SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
24845	55213	Α	24983	1	2180	METLNLYADLRSVTGEALLLL
						DEPGVGVDPISRRELWQMVHE
		l				LAGEGMLILWSTSYLDEAEQCI
						DVLLMNEGELLYOGEPKALTO
		l				TMAGRSFLMTSPHEGNRKLLO
		l				RALKLPQVSDGMIQGKSNIVGI
						KDTIDSVGHLRTMINTVKSVRP
	i	1			ł	SFSVFCGYDDHLLNTMLLGGD
		1			1	GAITASANFAPELSVGIYRAWR
						EGDLATAATLNKKLLQLPAIYA
	1	1				LETPFVSLIKYSMOCVGLPVET
		1				YCLPPILEASEEAKDKNRPLVD
	1	1			l	LEHAALQVGKGIIPPPLREYGAS
						EVRSVTRAFNHMAAGVKQLAD
		l				DRTLLMAGVSHDLRTPLTRIRL
	1	l				ATEMMSEODGYLAESINKDIEE
		l		1		CNAIIEQFIDYLRTGQEMPMEM
						ADLNAVLGEVIAAESGYEREIE
				İ		TALYPGSIEVKMHPLSIKRAVA
	1	l		l		NMVVNAARYGNGWIKVSSGTI
						PNRAWFQVEDDGPGIAPEORK
						HLFQPFVRGDSARTISGTGLGL
				1		AIVORIGDNHNGMLELGTSERG
l						GLSIRAWLPVPGTRAOGTTKE
						GAREDAVEFFAKLGFVNQGEIT
						TPTTTPIRHFLMIKPVATLDDIL
				i		HRGDWCAQLQQAWYEHIPLSE
		1				KMGVRIQQYTGQKFITTMPETO
						NONPHHTLFAGSLFSLATLTGW
						GLIWLMLRERHLGGTIILADAH
		1				RYSKPISGKPHAVADLGALSGD
				1		LDRLARGRKARVQMQVEIFGD
24846	55214	Α	24984	875	1150	
24847	55215	A	24985	1507	1974	
24848	55216	Α	24986	1	1006	
24849	55217	A	24987	1491	1703	RECRYATNGKNNGCCRSAGSD
				ĺ		FSSRLRYVR*PFIYTQ*SCGIGH
		1			l	CPGTDIRAKIRRTARFIKNYGTY
		1				CPS
24850	55218	Α	24988	I	1758	
24851	55219	Α	24989	1773	2165	PSRGVEVNSGWNWQATNRRVI
		1				RNFDDLDQLIIPGTARNAQTCIF
		1		1	1	NFVTVTMTLNNCRRIVQLANQ/
	1				1	DYRQPTGTAVAETHGTAEIALL
				1	1	ATNFNVA VFIAPLGNQRHNRVI
1		1		1	I	TVWHKFRRVGVLHVGNMASVI
		1		l	1	N
24852	55220	Α	24990	1	141	SPGKIRPVIAAAMKQIKEFMSP
						DSDFFRYMKTPTSATR*YNDCG
		1	1	I		TGQ

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24853	55221	A	24991	1430	1933	PHVCMGSLTMPDSACMAPFPPS
				l		AVRRWNSSFPPTFSAHTSSPCA
Į.						CYPRCYRTVKGVL**HHR*W/V
						LISTPGRGAYAASKYALEAWSD
İ						ALRMELRHSGIKVSLIEPGPIRT
		1		l		RFTDNVNQTQSDKPVENPGIAA
		1				RFTLGPEAVVDKVRHAFISEKP
	}			1		KMRYPVTHGDLWR
24854	55222	A	24992	1318	4265	LAIVALFLDLQNHIFSKGFWPS
		ŀ				DKFYAAKVEEQNQRHQRYHGT
		l				SYNLEPDIKSSPGGLRDIHTLO
		l				WVARRHFGATSLDEMVGFGFL
						TSAERAELNECLHILWRIRFAL
					l .	HLVVSRYDNRLLCVHPTLLTTL
		[				DIHGEAQIWRREVSSRYGQYPK
Į.		ı		l		AQAAQPDQLMSDYFFRVSLAM
		1				QNKTLLFSLDDTLVNNALQTLN
		l				KTRPAMVDVIPTDGIVPLYINPQ
		1			1	GIAKLLRNETLTSLPKNLEPVFY
		ŀ				NAAQTLLMPKLDAL
24855	55223	Α	24993	I	454	MGFDDTRDRALFEDSAMSQQP
		l				TVPDRLRWLLQTFKYQKNIRI*
				l		STPRKKPMRHSIWNIWGSRRC
		i				WSNPKRTFMSISVRGNMAAIM
		l				SFHTSAVMRSHCSILTTIKSRW
		1				ATLNTLILR
24856	55224	Α	24994	65	330	
24857	55225	В	24995	1	1998	
24858	55226	Α	24996	1175	1877	QQVPQKGPGRAKRHLHAAGW
						HWHQRDRCPEEKNVRQ*RRYR
						AVRFIII
24859	55227	В	24997	I	3117	
24860	55228	A	24998	1888	2412	ARFKHVGDGTVTHRLFRRAAQ
		1				IVRVV*RAVSHRQHFTGVDIHQ
		1		ļ		HGATRFSLVKGHRIVQFAINQR
1		1	1		1	LQAFINTQRQVVRSLAVSRRNI
1						FNYATIAVFTHNALTRLPGKPFI
1	1	1	1		1	ETLLNALNPLTEHAARDLEDSP
1		1	1	1		VRITAYIEDVDALAQAGADIIAI
						DGTDRPRPVPVETLLARIHH
2486 I	55229	A_	24999	I	2457	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first		*=Step codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	· ·			sequence		
		L				
24862	55230	Α	25000	1	3019	MAALRQSFWSQLFDRVHIGLD
		1				FFDASINRIAAWVIGTRNMKKA
		1				LLRALLEPTAELRNWKRRAITL
		ĺ	1			RVWHCWKSRNRCRGRRSGKCI
						ANVTIROODHOIETVFINORLH
				i		ERMFPPFVLFAERLSGDEDLGL
						KAPILEALNDLGYEKPSPIQAEC
			İ			IPHLLNGRDVLGMAQTGSGKT
				ľ		AAFSLPLLONLDPELKAPOILVL
					i	APTRELAVOVAEAMTDFSKHM
1						
	ļ		1			RGVNVVALYGGQRYDVQLRA
						LRQGPQIVVGTPGRLLD
24863	55231	A	25001	60	545	PSPFTAGASMAVERSTG\HEGE
1			ļ			LVLETLVIDGDENT/CAGTRRSL
						RANA*CLFHPFRAGAEKLAEEV
						WFCRYPHCGCEQNTTTEEQRR
			l	l		TEWMVTESLADFLDPHDPGKT
				l		VEGYPAPKRARNRNRAEDHRQ
l		l		1		RLRHRTRKKQTHGQRRRHRPE
1	-		l	ŀ		PAQRQPQTGTTD
24864	55232	A	25002	1410	1575	<u>````</u>
24865	55233	A	25003	200	691	
24866	55234	A	25004	1336	2028	
24867	55235	A	25005	1	345	
24868	55236	A	25006	671	1204	RTSDKLPFCRRSRMENLARFLS
24000	33230	ľ.	23000	l***	1201	TTLKQLRQQRGWSLSRLAEAT
l	1					GVSKAMLGQIERNESSPTVATL
				1		WKIATGLNVPFSTFISPPOSAT/P
						SLFPYDPQLCFEHLAIQMASGAI SESTPHEKGVIEHVVVIDGQLD
1				l	`	
						LCVDGEWHTLNCGEGVRFAAD
1				1		VTHIYRNGGEQTVHFHSLIHYP
		_				RS
24869	55237	Α_	25007	2251	2466	
24870	55238	A	25008	181	626	WQNFDTCGGDMLDKLDAALR
1					1	FQQEALNLRAQRQEVLAANIA
1				ŀ		NADTPGYQARDIDFASELKKV
i						MQRGRDATSVVALTMTSTQHI
ł						PAQALTPSTAELQYRI\PANPSL
[						DGNTVDMDRERTQFADNSLQY
				l		QMSLSALSGQIKGMMNVLQSG
						N I
24871	55239	Α	25009	57	278	
24872	55240	A	25010	171	532	KPVOFAIADGNNOPLALLNIHL
	1	Γ.			I	PVMMLAIAHGPLLPAFPPELLV
			l	ŀ		LFDDS/PLSSRVLLINAFSGGSDT
		l		ŀ		AMRRAGKGAPAFLLPELPIITV
		1	l	l		VSPFLPOSSPRRKPIMSKRIPSAV
			l	l	I	
		ļ		l		NQRNPRQ
24873	55241	Α	25011	I	648	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		•
24874	55242	A	25012	158	514	VLOLIKAVWTORTOKPSWLHP
24074	33242	ľ	23012	130	511	VDSAPGLOMELPASPVPCTCTP
						OPLGGRWDWALWSRGWRLLR
	1	1				RLGPHRSPRRS*GSGLWPWPAQ
		1		l		KGAPIVORWAKGLLKCHOSGS
		l				PGRGGAESERGL
24875	55243	A	25013	1	693	
24876	55244	A	25014	119	304	DRRRCAHKITVIPKRMTIAGIRL
						PPOTVNI*LGNFLRALIASTAGI
		l				MTAQMVAHSPAPPIP
24877	55245	Α	25015	361	540	
24878	55246	A	25016	191	446	AKRRLGVYDADCCSIDKTQSLS
	į.					ACTTRNCGAYSKCLCGKYAKP
						VGGIPQPLQESHVR*CCNVMEL
l	1					SPCSDFT**HPPGAVSQPQT
24879	55247	Α	25017	1	2259	
24880	55248	Α	25018	1	1170	
24881	55249	Α	25019	3	1240	
24882	55250	Α	25020	1	1259	MAGPRYPVSVQGAALVQIKRL
	l	l				QTFAFSVRWSDGSDTFVRRSW
						DEFRQLKKTLKETFPVEAGLLR
l	ŀ					RSDRVLPKLLGQASLDAPLLGR
						VGRTSRGLARLQLLETYSRRLL
		ı				ATAERVARSPTITGFFAPQPLDL
		1				EPALPPGSRVILPTPEEQPLSRA
	1					AGRLSIHSLEAQSLRCLQPFCTQ
			1			DTRDRPFQAQAQESLDVLLRHP
					i .	SGWWLVENEDRQTAWFPAPYL
		1				EEAAPGQGREGGPSLGSSGPQF
1						CASRAYESSRADELSVPAGARV
						RVLETSDRGWWLCRYAGAGPE
			1		0.0	ELDTSARNAGALTRRREIRDAA
l				1		TLLRLGLAYGPGGMSLREVTA
		1				WAQLHDVATLSDVALLKRLRN
				1		AADWFGILAAQTLAVRAAVTG
l				1		CTSGK/QIASCRWNSNQCARGR
l				1		QR*MATTYGI*SSYLSVH*F*AN
l	1	i i		1		RQQRR

3303

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24883	55251	Α	25021	803	2061	AKPAARGGILAAPVRDTLFLYF
						RLKKNQRQEGFINTYPWPKKP
						GIFYMCVPIKGANAQDVAAFC
						VTARGRQNCLWESIARGPALIN
						NRGAARGRCNDRVVEVDHGFA
		1				VLTFNFQGVSPGEFTQTVDHFD
						FAAFRHTSQTTGQLIDHFLFPGT
						NLVDIGFRFAEDDTVFSQRFGF
						FDNFCYVQQCFRRDTADVQAN
		l				TAKGVVTFYDYGFQTYWVKV
						LDPGSEVVAEAGDGASAIDLAH
i i		İ				RLDIDVILLDLNMKGMSGLDTL
						NALRRDGVTAQIIILTVSDASSD
		İ				VFALIDAGAAGYLLKDSDPEVL
						LEAIRAGAKGSKVFSERVNQYL
						REREMFG AEEDPFSVLTEREL\D
					ľ	VLHELAQGLSNKQIASVLNISE
						QTVKVHIRNLLRKLNVRSRVA
						ATILFQSAAFRSRFRRATSDNV
24884	55252	Α	25022	1	1569	
24885	55253	Α	25023	2151	2709	YLREASETARRQFTLP\VILYNF
						RDLTGQDLTPETVTRLALQNEN
						IVGIKDTIDSVGHLRTMINTVKS
						VRPSFSVFCGYDDHLLNTMLLG
		ŀ				GDGAITASANFAPELSVGIYRA
		ļ				WREGDLATAATLNKKLLQLPA
		ŀ				IYALETPFVSLIKYSMQCVGLPV
						ETYCLPPILEASEEAKDKVHVL
		l				LTAQGILPV
24886	55254	В	25024	1	1201	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24887	55255	Ā	25025	1	2209	MIGEIRDGETAEIAIKAAOTGHI.
1						VLSTLHTNSTCETLVRLQQMG
ĺ						VARWMLSSALTLVIAQRLVRK
ĺ						LCPHCRROOGEPIHIPDNVWPSP
ĺ						LPHWQAPGCVHCYHGFYGRTA
ĺ						LFEVLPITPVIRQLISANTDVESL
ĺ						ETHARQAGMRTLFENGCLAVE
ĺ						QGLTTFEELIRVLGMPHGDGAA
ĺ					İ	MDREENELGVSCIAVPVFDIHG
ĺ						RVPYAVSISLSTSRLKQLYAGLP
ĺ						VWCDGSRFFAQKARAİKCKQW
ĺ						GYVGAKSRQRWLFYAYDRLRK
ĺ		l			i	TVVAHVFGERTMATLGRLMSL
ĺ		1				LSPFDVVIWMTDGWPLYESRL
ĺ		1				KGKLHVISKRYTORIERYNLNL
ĺ		l				ROHLARLGRKSLSFSKSVELHD
ĺ						KAAGGVPVLVRELLKAGLLHE
İ		l			İ	DVNTVAGFGLSRYTLEPWLNN
ĺ		1				GELDWREGAEKSLDSNVIASFE
ĺ						OPFSHHGGTKVLSGNLGRAVM
ĺ						KTSAVPVENQVIEAPAVVFESQ
ĺ						HDVMPAFEAGLLDRDCVVVVR
ĺ	1					HQGPKANGMPELHKLMPPLGV
ĺ						LLDRCFKIALVTDGRLSGASGK
ĺ	1			•		VPSAIHVTPEAYDGGLLAKVRD
ĺ		1				GDIIRVNGQTGELTLLVDEAEL
ĺ					!	AAREPHISELSAFTFGTGRGYSA
ĺ						AFGVKCPFRKRALSDPCYAMR
ĺ						EVADFLINKGVDGLFYLGTGGE
ĺ						FSQMNTAQRMALAEEAVTIVD
ĺ						GRVPVLIGVGSPSTDEAVKLAQ
ĺ						HAQAYGADGIVAINPYYWKVA
24888	55256	Α	25026	1	3395	MSELPFTIASKRIKYLGIQLTRD
ĺ						VKDLFKENYKPLLKEIKEDTNK
ĺ		1				WKYIPCSWLGRINIVKMAILAK
ĺ		1			İ	VIYRFNAIPIKLPMTFFKELEKT
ĺ		1				TLKFIWNQKGAASRSNPEPKNK
ĺ						LEDHITNSTIYRLSTKSCSVSGL
ĺ						KQTLLAESEALTSYSHRVFSAW
ĺ		1		1		DFGLCGDVHVRLRQRIILYELK
ĺ				1		GQVPALLLDDGTLLTEGVAIM
ĺ		1		l		QYLADSVPDRQLLAPVNSISRY
ĺ		1		1		KTIEWLNYIATELHKELKFSFH
ĺ						WSTTSHKGLGM
L						WSTTSHKGLGM

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codun, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24889	55257	Α	25027	145	681	FNGATQRIFDARGKPSTYIGSIQ
						HVNADVDQRATTLQFFIGKDTP
						AGNAAATQGAGGGNVNLSQN
						AVGHLFTQLLRIERKTMVKVV
	1	l				GQHLAQFARGIDISRACYHMA
						ARFQCHQGMFVMKTVR*ADA
						NHIRFHCQQHGLRIVPHGCIPVF
						FCQRLPLGKAAVTDSYQFQIRC
						GCSSTKH
24890	55258	A	25028	696	953	LSGLCSVRRAYPGGRSCPGVP*
			ŀ			FVGLVARRPGGG*GSCFVLLHP
						QRSGTGGCL*QPPFPGAGAGRK
						IRECIRVGRSAGHAAGGET
24891	55259	Α	25029	3	506	RGKPSTYIGSIQHVNADVDQRA
						TTLQFFIGKDTPAGNAAATQGA
						GGGNVNLSQNAVGHLFTQLLRI
						ERKTMVKVVGQHLAQFARGID
						ISRACYHMAARFQCHQGMFVM
						KTVR*ADANHIRFHCQQHGLRI
		İ				VPHGCIPVFFCQRLPLGKAAVT
						DSYQFQIRCGCSSTKH
24892	55260	Α	25030	291	560	
24893	55261	Α	25031	63	404	
24894	55262	Α	25032	660	1073	LSHECSFWLTNQLVSPRAQTVS
						GELQPAYAHGVLCRQYPSAFE
						KASETPQSSNPCPSSYTIHPTVE
						NFQTCRNQHLSKGCLINAGRA
						GPSPGTGGWGELEVAAAARLQ
					1	GAWKRHLQSSRPPGQALFASPP
						*WTGSVQ
24895	55263	A	25033	272	511	GSDTALPSAIAAPLLAAMAWLP
						PRERGTLAH/QVLEHYQLAQLP
		1				VSAL/QMPLHCPPQAIAHHQQL/
						EQQALASLQNWGVFHV
24896	55264	Α	25034	1	3300	
24897	55265	A	25035	1117	1376	PPPIGLTYSSSASPLSLFCTVRKP
			ĺ	1	1	FSRSCW*QTNSNPISSCPELVTP
				1	1	SE*L*PRRSIRLDSLSAVRGFAS
						RIWLSSAITFPSGSLA
24898	55266	A	25036	207	427	DEHLQQRKKPLFLNYGRTEQA
				1	I	SVK*RISWVQNPERSSLC*GILA
						A*NPMSVSGL*LT*HCLSARRY

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Nucleotide Incation of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	1100	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24899	55267	A	25037	2012	2547	LKFARPKLWGIFRNRQYHHML ER\RSOAIDAPALDRGAALGAL
		1				MRLEHPNASAEAALTMLAOLS
		ļ				PAOSGEALHGLLALARHOLAC
	l	ł				OPAFIAGESSHLNOLSEADFINA
l		1				LPDLRAAMAWLPPRERGTLAH
ŀ						QVLEHYQLAQLPVSALQMPLH
1						CPPQAIAHHQQLEQQALASLQN
		ľ				WGVFHV
24900	55268	Α	25038	1	150	DKASRGRSRQQS/CAVLQPLLVI
						PRQT/WVWSGPPANSSRPGEEG
						PDC*KEN
24901	55269	Α	25039	1	150	DEASRGRNRQQS/CAVLQPLLV
						IPRQT/WVWSGPPANSSRPAEEE
		_	<u> </u>			PDC*KEN
24902	55270	A	25040	96	389	PCLSP*LYPSGVHKSTFIYGFYN
						T*PCTSQSLFWQHSC*GSITSSS
1	l .					YFYLLPEEGTGSNLCCSAASAG
						DTQANRVWSGPPANSSRPAAE
		1				GHDCWKEN
24903	55271	A	25041	1181	1364	VSLGNIKFRQTGAPLGQSFQRK
						EQSAIFAVLQPPLVIPRQI/WVW
						SGTPADSSRPAAEGPDC*KEN*
	1		l			RVNRQPTEWEKIFPIYPYDKGLI
						SRIYKELKQIYKKKIKPPHQKV
						GKGYVFSKEDIYAANRHMKKC
						SSSLAIREMQIKTTMRYHLTPA NRGIEIINCPFLDDAASCIDPTYS
ļ						SNIFPPVNLSWGLPMKPKEVKI
						KRQKKEHLLKDRDFSFQEPIMA
l						LRTVILEILMEKEMDNSQRECIK
				ŀ		DILTKHLVELSILARTFKNTOLP
						ERAIFQIKQYNSVSCGVSEWQL
						EEAQVFWAKKEOSLALSILKO
		İ				MIKKLDASCAANNPSLKLTYTE
						CLRVCGNWLAETCLENPAVIM
	1				1	OTYLEKAVEVAGNYDGESSDE
						LRNGKMKAFLSLARFSDTOYO
	1					RIENYMKSSEFENKOALLKRAK
						EEVGLLREHKIOTNRCPSGTKL
					1	PEEGTVSNLCCSAASTGDTOAN
1		1			I	RVWSGTPADSSRPAAEGPDC
	L		L	l		K V WOO I FADOOKFAAEOFDC

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleutide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodnn far last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nueleotide insertion)
				sequence		
		_				
24904	55272	Α	25042	42	963	VQEGCVRPFCCRSAGVCWRST
						PDSVCLGITSGGCRTAKTAACS
						FLWKLCPRGTPARCQVECSYTR
						CLS\SLLGGVSQAGGTRVRDPL
				1		EEEVCPLAELERCAGRSVAVFR
						ASRQEHLRLLKLTSQPPLPPGA
1						LSQGDGSFIYKPLTGVAAFLSD
			ĺ			ALPKRRNLERQSGYSTFEELCF
						QKRTWGRDAVRISDLLLGDHS
						HFGKCPISRLERAENMPVVSEL
						SAAGCSTEVNHVFVGIIWQKGK
						CSKYTAPSKSSVPVSSTRGHVHI
						TVQNPTLVPFVGKLNIDSPIGDR
						NIPVLTAGNCKTLGDLRSFPHN
24905	55273	Α	25043	98	352	
24906	55274	A	25044	3	414	PEEALCALAELERCAGRAAALF
						RAEROKRLRLLKLHPOPPLPPG
						ALSORDGS\LSISP*LGL\RLSFR
						DALPREQFYRLFTDRSDRVPEN
						SVTDVCHIESKMEPLRLGP/SNV
						SIMRPSLVCSFTTLVFISSNAOSS
						LVA
24907	55275	A	25045	2	1544	STTRGSPPOEAROYRHNOAYA
						YSIQGDGAEDDDERIVRFHTRL
						PVFMLPPTPRKTSWIVAPVLEV
						LARAIRHETEIQGIHTGTEDVPV
						SLFADDMIIYLDNLKDSSRKLL
						EVIRDFSKVSGYKINVHESVAL
						LYTNNDYAENHIKNSTPFTIGY
						VLAFVVMVIAVSCVRLLYAHN
						CTQHTSLKHKCQAWVVTTVDA
						AAFMTQATREERRIAYSAPGGY
						FFHILEVLARTIRQEKEIQGIQTG
						KEEVKVSLFADDMIIYLENLKD
		ĺ				SSRKLLEVIKEFSKVSGYKINVD
						SRGSPTDLVIYKEEIVFLIVPKA
		l				KKSKIKVLASDPLCYAATTWR
			İ			MTIIAGLPVEYNDRFIRGIAVFA
l	l			l		
	l		l			PWRKTPGIYHQSHDPLCYAATT
1	l	1	l			WRMTIIAGLPVEYNDRFIRGIA
1						VFAPWRKTPGIYHQSHGACLG
						RRSRTITVVDAQPQVMDMDPT
1	l		l			CSLFTTGQCLGEPDLLASARRL
1						QFFSHQYSIAVLMANARGNSA\
			L			LW\DNYGGLIVRADRGSLLLVG

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24908	55276	Α	25046	1	1228	MLQSNRTAASHSPSIQPAIQPAI
						<b>QPASQLSIHNLWTQFRHSTKIPV</b>
	l					EWVNGEWLNGRMPEDHHEWO
		l				CNYQNVQQFIDEGNYTSGDNH
	ŀ	ĺ				TLRDPHYVEDKGHKYLVFEAN
						TGTENGYOGEESLFNKAYYGG
		1				GTNFFRKESQKLQQSAKKRDA
						ELANGALGIIELNNDYTLKKVM
						KPLITSNTRETVDFNGKHIHVR
		l				GAKLLFPAIQOPYPPLYFGGSSD
						VAQELAAEQVDLYLTWGEPPE
		l				LVKDFIEQVRAKAAAHGRKIRF
		l		i	}	GIRLHVIVRETNDEAWQAAERL
						ISHLDDETIAKAQAAFARTDSV
				l	İ	GQQRMAALHNGKRDNLEISPN
						LWAGVGLVRGGAGTALVGDG
						PTVAARINEYAALGIDSFVLSG
						YPHLEEAYRVGELLVPLLDVAI
						P\EIPQPQPLNPQGEALRKK
24909	55277	Α	25047	1	1075	MTIKGEQAKKQLIAAALAQFGE
				l		YGMNATTREIAAOAGONIAAIT
				i		YYFGSKEDLYLACAQWIADFIG
						EQFRPHAEEAERLFAQPQPDRA
						AIRELILRACRNMIKLLTODDT
						VNLSKFISREQLSPTAAYHLVH
						EQEAEHRFAMGELPDEVLEICQ
						RLAKLTEMLRGLAELFLNDLSE
						KTGSHDIVRLHRLILQMNRALG
						MFEAQSKLWRLASLAQSSGAP
		l	İ			VTKWATREEREGQLHLWFHCV
	i	i				GIRVSDQLERLLWRSIPHIIVTS
						ATLRSLNSFSRLQEMSGLKEKA
ł						GDRFVA/SGFP/HLTTANRAKLL
						FPGCALSLPSTTKSSILPKWRPF
						SVSRWRAKNISVCWYCLPADG
						RCSAFSTM
24910	55278	A	25048	530	642	LKTLW/PAVQEPVPHRYHGATV
						FRIMQTIFIKQICRLLL*GTAGHF
			l			VCGITACHAAEAAHRLTVQPVP
						RILDQRRPAQLHSRQVTAAIRQ
			1	I		PLHRRQAVRRDAVCQPLLVVC
	l					VFRLMLPQQFPRLRVLHRLAFA
	1		1			GQAAFIVIAIVDGNTVAFAQVA
			1			DVCQPAVAIILPLLLCEFSGQVI
	1		1			MITLRPPVKAALLYQPVQRIVT
						EDAVAAVQEPVPHRYHGATVF
	1	1	I	I	I	RIMOTIFIKOICRLLL
1 4 4					l	KINQTIFIKQICKELL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24912	55280	A	25050	2	588	RWSSLTSSRYGFCRCPESADKE CLHYKSAAGKATAVGHYAG WLRTYSPHLAAHRVNFFFGINA HMDQRGFGKLMISCNBACGSA CYSNIBSYMRNDKHAVRRADSG RAEGGGPRVKSVIKAPVITEKK KPVYSTLKHWVLMLAWVTCSP LTVL\SPDGEMFDVMEKYAFSA WKWKRLRLAISQATFHALLPE KIG
24913	55281	Α	25051	912	1169	
24914	55282	В	25052	1	1665	
24915	55283	A	25053	43	302	
24916	55284	В	25054	116	1534	
24917	55285	A	25055		1017	NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGED GYQGESLFNKAYYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLIN NTRETVDFNGKHIHVRGAKLLF PAIQQPYPPLYFGGSSDVAQEL VIQVETVEGVAKAAAHGRKIRFGIRLH VIVRETNDEAWQAAERLISHLD DETIAKAQAAFARTDSVGQQR MAALHNGKRDNLEISPNL WAG RQLVRGGAGTALVGDGPTVAA RNEYAALGIDSFVLSGYPILEE AYBVGELLVPLLDVAIPEIPQP QQPLNYQGEALRKK

SEO ID	SECULO NO.	Mar	SEQ ID NO:	Nueleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nuelcotide insertion)
				sequence		
24918	55286	A	25056	1	2677	MVLNRLLTGLFFGSTPPRCHYD
21,710	55200			1		LIGADPDRTIRSVRLYWRHSLN
		l				ELISMLPKFNKELTRKLFKLQE
						MLPFLNLHMSPERMLORMDSE
						KVVTFTTALMTGLSGAMASVL
						LLVMTVVFMLFEVRHVPYKMR
		1				FALNNPQIHIAGLHRALKGVSH
						YLALKTLLSLWTGVIVWLGLEL
						MGVQFALMWAVLAFLLNYVP
		1				NIGAVISAVPPMIQVLLFNGVY
		1				ECILVGALFLVVHMVIGNILEPR
						MMGHRLGMSTMVDGVRVLKD
				1		GTDLNQTGSFYLAARPYAEKN
		l				GAFIQGVLATFSEADALTRSQR
						EOSIALLAKTMGLPAPVIASLLE
		1				ISOPVSNHPIRTRLTAEVAALQQ
						OTADLFYENRLVPKKVDIRQRI
						WQPTRLEGKQFMSLNMFWFLP
			i	1		THGDGHYLGTEEGSRPVDHGY
		1		1		LOQIAQAADRLGYTGVLIPTGR
						SCEDAWLVAASMIPVTOR\LKF
						LVALRPSVTSPTVAAROAATLD
		1		ı	1	RLSNGRALFNLVTGSDPQELAG
		1			į .	DGVFLDHSERYEASAEFTOVW
						RRLLORETVDFNGKHIHVRGA
		1				KLLFPAIQQPYPALYFGGSSDV
						AQELAAEQVDLYLTWGEPPEL
		1		l		VKEKIEQVRAKAAAHGRKIRFO
		Ì	1	Į.		IRLHVIVRETNDEAWQAAERFV
					i	LSGYPHLEEA/YRVGELLFPLLD
		1				VAIPE/IPOPOPLNPOGEAVAND
		1	İ			LSPRRTVAASGDQLLAGAVGFS
24919	55287	A	25057	114	372	LSI KKI TAASODQEEAGA TOI S
24920	55288	Ä	25058	2270	2760	TSPIPSQIRQYSIA/VGSTGNLGL
21,720		ľ				SIGIMSARIGFKVTVHMSADAR
		1		l		AWKKAKLRSHGVTVVEYEOD
	ŀ	1		1		YGVAVEEGRKAAQSDPNCFFID
		1	1			DENSRTLFLGYSV/AGQRLKAQ
	1	1	i	1	1	FAQQGRIVDADNPLFVYLPCGV
		1	1			GGGPGGVAFGLKLAFGDHVHC
						FFAEPTHSPCMLL
24921	55289	В	25059	1	2460	
24922	55290	Α	25060	I	993	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
24923	55291	A	25061	332	1349	ILYDSDIYRFSCRSGGHIPAVIY
24923	33291	^	23001	332	1349	HLSAKRTMENAKMNSLIAOY
	ı	1			1	PLVKDLVALKETT/WGFIPATL
		l				HGVKGLPYVGLTEODVODAH\
5-0						ARLSRFAPYLAKAFPGKWLPTG
		l				
						GIIES\ELGAL\PAMQKRL\EKEY
		ŀ				QQPISGQLLLKKDSHLPISGSIK
1	1	l				ARGGIYEVLAHAEKLALEAGLL
	1					TLDDDYSKLLSPEFKQFFSQYSI
!	1	l				AVGSTGNLGLSIGIMSARIGFKV
		!				TVHMSADARAWKKAKLRSHG
		ı				VTVVEYEQDYGVAVEEGRKAA
						QSDPNCFFIDDENSRTLFLGYSV
					i	AGQRLK\AQFAQQGRIVDADNP
						LFVYLPCGVGGGPGGVAFGLK
	1	1				LAFGDRVHGLQA
24924	55292	Α	25062	284	1494	RLSLPDMFPPVQQFPVSLHRAF
		l			İ	YRYDKSAYYALRIAGIASRLNP
		1				RRFSPSILTPERRCVVTLRNDIR
		1				RDVLRHNQPRSTASTRQARRR
		1				MKSSCWHMPTTSKPQALSHTS
	1	1				NSPTTSISRPNWSYSNVCNRSRT
					i	MANLSGYNFAYLDEQTKRMIR
	1					RAILKAVAIPGYQVPFGGREMP
				1		MPYG\WGTGGIQLTAS\VIGESD
		1				VLKVIDQGADDTTNAVSIRNFF
	ŀ	1				KRVTGVNTTERTDDATVIQTRH
		l				RIPETPLTEDQIIIFQVPIPEPLRFI
						EPRETETRTMHALEEYGVMOV
		1				KLYEDIARFGHIATTYAYPVKV
l					1	NGRYVMDPSPIPKFDNPKMDM
l					1	MPALQLFGAGREKRIYAVPPFT
l		l			1	RVESLDFDDHPFTVQQWDEPC
l	1	1				AICGSTHSYLDEVVLDDAGNR
l					1	MFVCSDTDY
24925	55293	A	25063	1	333	
24923	23273	1/4	23003	11	222	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24926	55294	Α	25064	1368	2451	PAHAAPGGGC/VRSLACRFLWN
		l				MRVTGKSYSTLRRVLSAIWNW
		l		l		RMMRCALTRALVAFRVR/SSVP
		l		l		LAAVLAIYARENGAGTMFEPE
		l				AAYDEDTSIMNDEEASADNET
		ı				VMSVIDGDKPDHDDDTHPDDE
		i				PPQPPRGGRPGLRGLTLRWFSV
		l		l		AAQRSDILDAVTLSLKVAALAT
		l		l		LIALVLGTLAAAALWRRDFFG
		l		l		KNAISLLLLLPIALPGIVTGLALL
		l				TAFKTINLEPGFFTIVVGHATFC
		l				VVVVFNNVIARFRRTSWSLVEA
		l				SMDLGANGWQTFRYVVLPNLS
	1	1				SALLAGGMLAFALSFDEIIVTTF
	1	1		ľ		TAGHERTLPLWLLNQLGRPRD
		1		ļ		VPVTNVVALLVMLVTTLPILGA
						WWLTAKATYLEKLKV
24927	55295	Α	25065	I	2072	MSEQLTDQVLVERVQKGDQKA
				i .		FNLLVVRYQHKVASLVSRYVP
						SGDVPDVVQEAFIKAYRELTPR
				!		RPYLLRAFYEWLLDNQLTPHL
	1	l				VVDVTLPGVQVPMEYARDGQI
				1		VLNIAPRAVGNLELANDEVRFN
				1		ARFGGIPRQVSVPLAAVLAIYA
	i	l		i		RENGAGTMFEPEAAYDEDTSI
		l				MNDEEASADNETVMSVIDGDK
						PDHDDDTHPDDEPPQPPRGGRP
	1	l				ALRVVNVIVAIIFTTKPTAMGIA
						VRFTTAKGETPAIPDVTTTTAVI
		l				GETARASVVAKCIGIIITTAVPIV
		1		l		VKPFANISPATTSVPRFFGLPAS
	1			l		SSHTLIGATIGIGLTNALLTGSSV
		l				MDALNLREVTKIFSSLIVSPIVG
		l				LVIAGGLIFLLRRYWSGTKKRD
		l				RIHRIPEDRKKKKKGKRKPPFWT
	i	ŀ				RIALIVSAAGVAFSHGANDGQK
		l				GIGLVMLVLVGIAPAGFVVNM
		l				NASGYEITRTRDAVTNFAARES
		1				EAS VIRHSNRFIETINGGRRCSR
		l	•			GITLTLHKLR\SAQPLL\AVLNR
						LEQKKPVGLRYDPQAQSLVCLP
			1	ĺ		TOTRTGWNLNGFEVGFRPCVR
				1		LMIYGRSLEAQATASLAAATG
		l	l	I		YDSHIFDLFPASASAQIDTDTAV
		1		I		ILLCHOLNRELPVLQAAREAKP
	1	1		l		FYLGALGSYRTHTLRLQKLHEL
		l				GWS\RQETTQIRAPVGIFPKARD
		L	L			AHTLALSVLAEVASVRLHQEE

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	deletion, \=possible nucleotide insertion)
24928	55296	A	25066	2	332	AGYSTRTALAIVNKPPSSAIPPT SGLASRKRNPASNDFNGCSRGC GGGGNAGRLNNGSKRSASTPP TIRPTNIAPP\AASPKAPPARWN VSSSGSAPAPRRRANPETQLR
24929	55297	A	25067		3192	MNKKFKYKKSLLAAILSATLLA GCDGGGGSGSSSDTPPVDGTGS LPEVKPDPTPNPEPTPPPPP PTPEPIPDPEPTPPPPPP PTPEPIPDPEPPNQMGALSYN TEKILTIRDSVFTYTENADGTIS LQDSNGRKATINL WQIDEANNT VALEGVSADGATK WQYDLING ELVITGDNATVNNNGKTTVDG KDSTGTEINGNNGKVIQDGDLD VSGGGHGIDITGDSATVDNKGT MTVTDPESM
24930	55298	A	25068	1078	1317	
24931	55299	Λ	25069	135	361	SCSMLAGLCG*GSSSSVSITTCF ALSASTIA*PREPQQALPV*PLA LPNSSQDGTPMKATSIFSSPLCT RCTRPP
24932	55300	Α	25070	469	841	RWWKQYAAAGFQCMCATAVS NLTRPVAA*TAAIPESKSPVLPN SPASTVRRS*PVSTMPPIRPGDG DHDPRFKAPSGTPHQPPRAGHS LIRRHG*TENCTAA*GQLRTPG DNGTVMSADTITFP
24933	55301	В	25071	1	2922	
24934	55302	A	25072	1	3849	
24935	55303	Α	25073	1	2280	
24936	55304	A	25074	672	1045	GAVLSINCRTLSPAAASGENVA TPPAVTSNNNTPIINKPKPLALAE ATGVIIAPKPPSSAAPMASPVTF CAVHKPLIRPNIASGVCVCSIVY CSNELTALNQPNSARQTTPKIHI GIRPNRPMARN
24937	55305	A	25075	650	1465	RKPICAADICQI-SASAGYSTRT ALAIVSGL ASKRKNPASNDFNG CSRGCGGGNAGRLNNGSKVI NVPAAASP*FQATPPVASNKPPI MGEITDPRRTVNMVIAPACIKF SRPTSAGVAANSAVTPSDAKKP SHKPSK*IASNDGGGSSALRHSP MKPMPQVPRASKITELBS*RSA STPPTIRPTNIAPPVSVTESPTCQ VECVIIWICTGATPSKPRDTQI EMKRARNTARNAGCVSAGSGS SAEVGSSNSKTSGSIASARAIET RCC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24938	55306	A	25076	156	3092	LNRRWIANIAKLEAEQARKLK KTEKDSLKDEVLISLLPRAFS KSOTMMWIDTVNGLIMVDCAS AKKAEDTLAVLRKSLGSLPVVP LSMENPIELTLTEWVRSGSAQI GFOLLDEAELKSLLEDGGVIK KKQDLTSEEITNHIEAGKVVTK LALDWQQRIGVPWCDDOSLKR LKFCDELRDQNEDIDREDFAQR FDADFILMTGELAALIQNLIEGL GGEAQHISGTGSLPEVKPDFTPN
						PEPTPEPTPDPEPTP
24939	55307	В	25077	61	2118	
24940	55308	A	25078	132	280	RRRAALPERSGPGLDHRRVRH/ GCHVLPTPVTLVKRRKVSRVD AQWKSSV
24941	55309	Α	25079	1	1449	
24942	55310	В	25080	110	550	
24943	55311	Α	25081	657	805	RRRAALPERSGPGLDHRRVRH/ GCHVLPTPVTLVKRRKVSRVD AQWKSSV
24944	55312	Α	25082	756	938	
24945	55313	Α	25083	781	1257	
24946	55314	В	25084	1	2727	
24947	55315	Α	25085	1	2286	
24948	55316	A	25086	1161	2024	VRSAVWPCLQRDPDCHHINRCG TGGTSRPGPARNPRIEPETCVG RIRNLGVLLVDADAMERAAST ENEKDLYQRQLDVFLDPNDPK VIEQAIKDGIPLSVIEAAQQSPV YKMAMEWKLALPLHPEYRTLP MVWYVPPLSPIQSAADAGELGS MGILPDVESLRIPVQYLANILTA GDTKPVLEALKRMLAMRHYK RAETVDGKVDTRALEEVGLTE AQAQEMYRYLAIANYEDRFVV PSSHRELAREARPFEKNGGLPF GDGCHGSDTKFNLFNSRRIDAI DKTEPHP
24949	55317	Α	25087	664	1065	VAPEPHHGRKQLCREGLGVFH PTHHITHHLGVSLSLLITIFDAQS VHGPDDGCQGLDSVAVDNRLV LFHVFSGEAIFMDDLHLLHNGA FS*FSSPEQE*F/PRLWRR*CHPL *GFSQSPCSARGRLSPLRSEYIP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	bod	in USSN	location of first	codon for last amino acid	*=Stop endon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
24950	55318	A	25088	434	1663	PAGAFPDIANDFGEKSLLMPGG
24930	33316	^	23000	434	1003	AVINGDF\NNVLPVDLVDPQQV
				l	ļ	OEFVDHAWYRYPNDOVGRHPF
				l		DGITDPWYNPGDVKGSDTNIQ
		l		1		OLNEOERYSWIKAPRWRGNAM
		1				EVGPLARTLIAYHKGDAATVES
		i			1	
1						VDRMMSALNLPLSGIQSTLGRI
		1			İ	LCRAHEAQWAADAIENNYSRN
ĺ		l		1	Į.	PSQGYSTVPRSPHPKVDPILTKP
		l				SGPAGPEMTRKQTQREDRPRSR
		1				PSMTTSPTSNLKPSVPAFKGVG
	l	l				YLDSLDRIGAADYQPTEQDILR
	1	l				TRVKTTGIVETHFTFKNLHFRT
	l	1				EQASVHACYCRLFDVEGQRSE
		ı				RKKWIHCFEDVTAIIFCVALSG
	1	1				YDQVLHEDETTVLSTRIVDGHR
		l				YSDHSTIACPAFGTYTLLELKEL
	1	1				ALSCSTLLHIPHQRSPAGSFLAD
	1	1				NLNCTQAAVIPEFGGF
24951	55319	Α	25089	1	1247	MTFGGDQIFESLVYRSAFRHVY
		1				SRGSPWYLHTNSDLSFVESKKE
						LIAEHILETFPWNLKGLTEIPWG
						DASGESGAVGLGVLAAVHYHP
		l				QRQSLMEKLALNKDAVVLVIS
1	1	l				TEGDTDQVIERLESDAVLRYGI
		l				EDVVTNLDVLERMQPSESLLRA
1		l				VLHTKHLMNPEVLAAARRIVC
	1	1				OVVEEIMARLAKEVROAFSGV
						RDRRRRSFIPLARNFDFKSTLRA
		i				NLQHWHPQHGKLYIESPRFNSR
	1	l				IKROSEOWOLVLLVDQSGSMV
		l				DSVIHSAVMAACLWOL\PGIRT
		1	1			HLVAFDTSVVDLTADVADPVE
		1	1			LLMKVOLGGGTNIASAGEYGR
		1	1			QLIEQPAKSVIILVSDFYEGGSSS
		l				LLTHQVKKCVQSGIKVLGLGA
		1				LDSTATPCYDRDTAQALGNVG
1			1			AOI\AALMPGELGSLAWENLLA
		_	i	1		AQNAALWIPOELGSLAWENLLA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hnd	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24952	55320	А	25090	1	1691	MGAYLIRRLLLVIPTLWAIITINF
				ŀ		FIVQIAPGGPVDQAIAAIEFGNA
		1		l		GVLPGAGGEGVRASHAQTGVG
		l				NISDSNYRGGRGLDPEVIAEITH
		l				RYGFDKPIHERYFKMLWDYIRF
						DFGDSLFRSASVLTLIKDSLPVS
		l				ITLGLCWYFVCRACVVTHALSL
ľ		l				WQSASIEVPRTSATAKARKTEP
						GRQTKRKVRSSQTVAARQRIAT
						LPHSMTVCNPGLFHSQMADAL
		1				AHRYYGFNIAEPWDNGSEAML
		1		ĺ		QRDIGLKSESRGLMAGKRCSCL
1		1				KGECGWSLDMQARVSTCFYVR
		ŀ		i		LLCGTELEDHRICHDTCDNKCG
		1				PQRRYVIKFRELCLVNSTVTLV
						DQEYELTVTDPELYDGSSQALA
1		1				GISDLSSIYATCDPGYSCTDRVT
		1				LVDVRKRQSKTGPYKEIGRYGI
		1				DRNRSPLNPGFRGKPDLMPSQC
İ		1			1	IACGACACACPANALTIQTDDQ
		1				QNSRTWQLYMGRCIY/CDGRCE
		1				EVCPTRAIQ\LTNNFVLTVTNKA
		1				DLYTRATFHLQRCSRCERPFAP
		i	1			QKTIALAAELLAQQQNAPQNR
		l			1	EMLWAQASVCPECKQRATLIN
		1			1	DDTDVLLVAKEQL
24953	55321	Α	25091	Ī	866	

3317

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn nf first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon,/=possible nucleotide deletion, \=possible nucleotide insertion)
24954	55322	A	25092	338	2388	CVQEPLITVSWRLFAIPAGMKF SLFLRCLFCFHLAARYLVLLCQ LH/SQGIKVLDFTGVQSGPSCTQ MLAWFGADVIKIERPGVGDVT
						RHOLRDIPDIDALYFTMLNSNK
	1	1				RSIELNTKTAEGKEVMEKLIRE
						ADILVENFHPGAIDHMGFTWEH
						IQEINPRLIFGSIKGFDECSPYVN
						VKAYENVAQAAGGAASTTGF
	l					WDGPPLVSAAALGDSNTGMHL
		l				LIGLLAALLHRELNMTVAEIVE
	l					REEWAGFRARETAALEAVTAP
		l				STVIATGGGIILTEFNRHFMQNN
	1	1				GIVVYLCAPVSVLEDFRQRTME
		l				VLRLAFLSSGILEFFTSLSIALVA
						VYFGFSYLGELDFGHYDTGVTL
						AAGFLALILAPEFFQPLRDLGTF YHAKAQAVGAADSLKTFMETP
						LAHPQRGEAELASTDPVTIEAE
						ELFITSPEGKTLAGPLNFTLPAG
						ORAVLVGRSGSGSRYCPYINHR
						NVRLGPIVTDVPWENSGDKSLP
l		1				EATAOVISSGSGATKVEDGLGD
						LNKPVSNONLVTGIDTPVYNAP
		l				SAGSAPFGVLADNMRYPILHKL
1		l				KDRLNQTWYQIRIGDRLAYISA
		l				LDAQPDNGLSVLTYHHILRDEE
						NTRFRHTSTTTSVRAFNNQMA
		1				WLRDRGYATLSMVQLEGYVK
İ						NKINLPARAVVITFDDGLKSVS
		$\vdash$				RYAYPVLKQYGMKATAFIVTT
24955	55323	Α	25093	1810	2399	STFRNSDDEPYIVRPVAVAWRD
		1				YVPQPARNGLSNFTGNLEEPAV
		1				MVNYFLQGDPYQGMVHFTRFF
		1				HQHPSGLS*WVAGNIFQILCAN
		1				QPVRKRTRDNVQLLHSRGQRG
		1				VFRCSRRVLTGLVDRFGRTQTF
		1				HREAAGEFSGEITGVTDGAWR HFRLVLTTQAQRAEEARQQAIS
		l				GGTEPSAFPDTLPVDTEYVMNF
24956	55324	A	25094	1	577	MPVSTAVATVIKTKOVEFOLO
24930	33324	<u> </u> ^	23094	ľ	311	VGVPLYFRLRANPIKTILDNOK
	1	l				RLDSKGNIKRCRVPLIKEAEQIA
1	1					WLORKLGNAARVEDVHPISER
1						POYFSGDGKSGKIOTVCFEVIG
l	1	1				CREEPDAEECHGDREQRRVFIR
			1			EDGFFVTKDLYPNRRA\GIISTT
	1					AVISPSQPPIIAPRVAQSSEPRSA
1		1				AHALARAIRQSTTV

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
24957	55325	A	25095	51	407	TCPIRAQRVETLYDRAYREVFG WNPRGPTGRPNARHTC*SKEG GRTEADETDAADSGQRGMEQR SEMDRKPTGTTGQRSEKPRRTL ECLALHETRIFLPQRKETHSSDA HDMPGPPML
24958	55326	A	25096	3047	4131	ÄHSGOMYMPLSSCIRSCILGSV WMTCGFPGKSAGOKRGKTADE RKRPQLYTKSLSLS/AVKAILAK GYDPVKWRKKDKVLDAVLKE LESGKYSDGDKHAFDQMLHSI GKQGGDPYLVMADFAAYVEA GKOYDVLYBQDEAWTRAALIA TARCGSSMESKRLDNAALAAGI SPNYINAHGKPQSISAETKRRLI DAMHQRATAKVAVTPVPNUM VYTSGKKMPMVVEGSGEYSW LITTELGTGYKGHVTGGKAFN LPTKLPEGYYHTTLTJODDQRAH CRIVVAPKRCYEPQALLNKPKLL WGACVQLYTLRSEKNWGIGDF GDLKAMLVDVAKRGGSFIGLM WHALPSELSEKNWGIGDF GDLKAMLVDVAKRGGSFIGLM
24959	55327	Α	25097	524	697	AANWWWKSRRNWR*KMTAM LDRIISHIIRTVRMSGSVAVTRAI AVPGLLLLLIIATA
24960	55328	Α	25098	I	1938	
24961	55329	Α	25099	33	226	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24962	55330	IA	25100	li	2314	MDRAGDGPIRPLSGPTDVYGD
21702	33330	ľ.	25,00	ľ	2314	VYLRDPGPNHGKTTNGPLRFVI
		1				LLPFGQQVFPRVTPNFWNPVSS
	i					AALPARYMQTIENAAVWAQIG
						DKMVTVGNIRAGQIIAVEPTAA
		1				SYYAFNCGFGKAFIDKGHLEPV
						QGRQKVEDGLGDLYKPLSNQN
						LVTWKDTPVYNAPSAGSAPFG
		1				VLADNLRYPILHKLKDRLNQT
		İ				WYQIRIGDRLAYISALDAQPDN
		1				GLSVLTYHHILRDEENTRFRHT
1	ŀ	1	İ			STTTSVRAFNNQMAWARVDRO
1	ŀ					YATLSMVQLEGYVKNKINNRA
1						TEREELRVSKITVLILGVIAIILG
1						VLFENQNIAFMVGLAFAIAASC
						NFPIILLSMYWSKLTTRGAMMC
						GWLGLITAVVLMILGPTIWVQI
				l		LGHEKAIFPYEYPALFSITVAFL
l						GIWFFSATDNSAEGAHLRPIRR
				l		KKVYRFNYLRSDGPYQGWVSE
1				l		RLLILRAISPGCSKLVHFPTLFDS
		1				LYRTLVKAGEKSGLLAPVLEKI
l		l				ADYNENRQKIRSKLIQSLIYPC
						MLTTVAIGVVIILLTAVVPKITE
		1				QFVHMKQQLPLSTRILLGLSDT
				ł		LORTGPTLLATVFIVAVGFWL
			i			WLKRGNNRHRFHAMLLRVALI
ŀ						GPLICAINSARYLRTLSILQSSG
ļ						VPLLDGMNLSTESLNNLEIROR
						LANAAENVRQGNSIHLSLE/QT/
l		ŀ				AIFPPMMLYMVASGEKSGOLG
		ŀ				TLMGAQSHWECATVNAASRIR
24963	55331	A	25101	20	825	GFPRSRSCYASCTACRTHTYSA
21,703		ľ.	22.0.	120	025	EK/QLTRALAKLARATSNEKLS
1			l			QAFHAHLEETHGQIERIDQVVE
						SESNLKIKRMKCVAMEGLIEEA
			İ			NEVIESTEKNEVRDAALIAAAQ
1		1				KVEHYEIASYGTLATLAEQLGY
		ı		ł		RKAAKLLKETLEEEKATDIKLT
		i		ł		DLAINNSFYKEDIFMNRIEHYH
				İ		
						DWLRDAHAMEKQAESMLESM
						ASRIDNYPELRARIEQHLSETKN
						QIVQLETILDRNDISRSVIKDSM
						SKMAALGQSTADTTKNSTHRQ
21061	66330	<del> </del>	25102		0/0	SNTRQGN
24964	55332	Α	25102	2	269	GIIGLHLQQQEAVAVAIVRGAT
1		l	1	l		RMLFATLVAVAAGERHYQRW
				l		ADC*CAAAG*NVVTVESRTAA
				l		ASSHYVGVSRQSHITAVISAPV
				L		DVPW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24965	55333	A	25103	607	727	RQAVYRG**TAGQRANLLLLR RHSACALAAGESQSSCPAG
24966	55334	Α	25104	465	574	
24967	55335	Α	25105	3	636	AHTSGFGDKESEKVSPÖRKLIHM MSRIFFWEMALRCHGALGSPTY AFQISAIDRVNFALVVGHHRH DYRNEKLGRSGRHYQAPVGNR SSADGMHRDPCSQ, DICCILLG AGSIYGLYRVIEPQLPDVATLK DVRLQIPMQIYSADGELJAQYG EKRRIPVTDGPVMWFPFMITTC VKGNFALNNQFREDMLHYNTE GIYGKNVNFENNKQT
24968	55336	Α	25106	434	1205	
24969	55337	Α	25107	368	532	
24970	55338	Α	25108	722	934	
24971	55339	A	25109	82	420	ARADPHRAHTAGVNGVNARLR IFNADTCLRRHAQPCTGGEKDF RVRFRVFKLGSIRAEGEKLAQL QRR*NRRRIQGDRSQPNRD/RA VPEDLPSKERMPGRTALTVNSR SEWT
24972	55340	A	25110	618	788	WYPCCRNWRYLAGGDSGFCR GERA*R*IASQSGVT*AVATVV FPSVLAGLRITGHS
24973	55341	A	25111	186	1198	OKTAVSTSITALTRWOSSRA/G KRGAVLRSRVTRGKYHYPSSW RETSSSVQNAPLMRQIKEVELAI RIEQLLTKDEILELYLMKIYLGY RAYGVGAAQVYFGKTYDQL TLNEMAVIAGLPKAPSTFNPLY SMDRAVARRNVVLSRMLDEG YITQQQFDQTNETAINANYHE EIAFSAPYLSEMVRQEMYNRY GESAYEDGYRIYTTITRKVQQA AQQAVRNNVLDYDMRHAIAA RHYVLWKPTANIRARYKAQQI ELPAVVPAGPDNPMGHHAIRL AAYGGVYLLHGTNADFGIGMR VSSGCIRLRDDDIKTLFSQVTPG TIXVNINTPIKYSAEPN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24974	55342	Α	25112	1087	3289	RLRSCGAQKNTFCNAAAGCRW
						RTTLSKMGGLLIAADLODPVO
						DMEMWOFHPTGIAC/AGVLVT
		l			l	E/GCRGEGGYLLNKHGERFMER
						YAPNAKDLAGRDVVARSIMIEI
		l				REGRGCDGPWGPHAKLKLDHL
						GKEVLESRLPGILELSRTFAHVI
		l				PVKEPIPVIPTCHYMMGGIPTKV
						TGOALTVNEKGEDVVVPGLFA
	•	l				VGEIACVSVHGANRLGGNSLL
						DLVVFGSARQVLHLQESIAEQG
		l				ALRDASESDVEASLDRLNRWN
		l				NNRNGEDPVAIRKALQECMQH
	ŀ					NFSVFREGDAMAKGLEOLKVI
						RERLKNARLDATSSEFNTORVE
		l				CLELHNLMETAYATAVYATFR
		ŀ				TERRGAHSR\FDFPDRDDENWL
	ŀ	ŀ		i		CHSLYLPESESMTRRSDYTLEA
						DEGRDMMLLDALIQLKEKDPS
						LSFRRSCREGVCGSDGLNMNG
		ŀ	İ			KNGLACITPISALNQPGKKIVIR
		l				PLPGLPVIRDLVVDMGQFYAQ
		l				YEKIKPYLLNNGQNPPAREHLQ
						MPEQREKLDGLYECILCACCST
						SCPSFWWNPDKFIGPGSLLAGY
						RSGLIAGIPKCSARYLSGEKRSV
				l		AWQQIAAEIGISIDAQFNESLKG
						ISRDESLRRILQHGGKEGDFNSQ
						ERAQLAYRKNLLYVHSLRELT
						VNAVLPGIRSLLADLRAQQISV
						GLASVSLNAPTILAALELREFFT
		ŀ				FCADASQLKNSKPGPGIFLAGC
24975	55343	A	25113	47	630	VGWETSFAQIRSRFLRIRFCRAY
						SSTLFVSAANPTT*G/QMVF*CG
						NGAQHKNILLLYRSIHGGFHFQ
		l				RGHHINTFNKRWRR**NRT*YO
		l	1	1		RDVRATTGSGGGDRKTHLAGA
		l				VIRDITHRIERFTRRAGGNHNV
		l	-			QMFQVVDGRKCATAISTVLDM
		l				FGDHFGRQKIASCQRWLAKTIR
		l				TVQQPICKNIVRKPGCHSLA
24976	55344	A	25114	731	829	- CQ L Carlo Collocat

SEQ ID	SEQ ID NO:	Mei	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
l	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24977	55345	Α	25115	2	3744	RLPFKYPVKVKPLPAPFSKILLN
		l				SPAIPQLPITMNGSDFSLPEGPM
1						NRWENIQLTPETRLAPRAYFFS
		1				YDSVAQARTFARETSSLFLPLS
		1				GQW\NFHFFDHPLQVPEAFTSE
1					İ	LMADWGHITVPAMWQMEGHG
		1				KLOYTDEGFPFPIDVPFVPSDNP
		1				TGAYORIFTLSDGWOGKOTLIK
						FDGVETYFEVYVNGOYVGFSK
		1				GSRLTAEFDISAMVKTGDNLLC
						VRVMQWADSTYEKDODMW,W
						SAGIFRDVYLVGKHLT
24978	55346	A	25116	1	2643	SAGIRET TETORIET
24979	55347	i A	25117	2499	2935	RSGGVACNCAVSASCMLVTVL
24919	33347	<u>۱</u> ^	23117	2477	2733	PWLSLPV/SVFGLWDGFFASLG
						VTALLAATPA\W*GVKT*CRPG
		1				
						RSP/SLTVRLGSVISPMIGGLLLA
1		1			ŀ	TGGVALLPLLSLPALPPPPQPRE
						HPLKSLLAGFRFLLASPLVGGIA
		L.				LLGGLLTMASAVRV
24980	55348	A	25118	676	1035	
24981	55349	Α	25119	1	1842	
24982	55350	A	25120	1	1341	DOLLIN D. OD
24983	55351	A	25121	563	1360	PSVLRCRNWVI*SPYCISLPSRV
1						SSLPFLVWIPVAR/CTAIGASRE
1	1	1				AMLGVLVEPMLLLGLWVAAQ
1	l					VAGSTNISNITDTVYHWPLSQSI
1	1					PLVLALCACAFATFIEMGKLPF
						DLAEAEQELQEGPLSEYSGSGF
	1					GVMKWGISLKQLVVLQMFVG
	1					VFIPWGQMETFTAGGLLLALVI
						AIVKLVVGVLVIALFENSMARL
l						RLDITPRDMIRIELDSWEQNGE
1	1					AIKRTGQPLLLSLLVRNLLDNA
						VRYSPQGSVVDVTLNADNFIVR
24984	55352	Α	25122	382	1424	VLLENLSEPPNQHDHEILTVQR
		1				KEEETALSCRLVLRKLTETEPVI
		1	l			IFEGIEAPATLPADEVPVGKDEN
l						DNVEVSRWGTPREFDFEVRDH
						VTLGEMHSGLDFAAAVKLTGS
						RFVVMKGQIARMHRALSQFML
		1	1			DLHTEOHGYSENYVPYLVNOD
						TLYGTGQLPKFAGDLFHTRPRH
1		1				ECFRHIGSLGLATPLVTECMQW
		ı				LFGIPHTLQLDAIIITCWIILNAIC
l		1				VACGLQKGVRIASDVRSYLSFL
l						MLGWVF\IVSGASFIMNYFTDS
1		1				VGMLLMYLPRMLFYTDPIAKG
l		1				GFPQGWTVFYWAWWVIYAIQ
l	1	l l		l		MSIFLARISRGRTVRELCFGMV
1	1	1		I		QEFGCKSSTKIDNADFNQA

ŠEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide scquence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide detetion, \-possible nucleotide insertion)
24985	55353	A	25123	416	610	
24986	55354	A	25124	662	811	AQQLPGMSDWQNSQEQHQMK N*VRLFMRTSRKLMDRLNVLIK LWSPNRT
24987	55355	В	25125	1	3264	
24988	55356	A	25126	489	3256	PRVFSATRSLVAMRRWYVRV RRIOYRRTOTAVFISTHGNYR EGQPVGTLIDDRYKANENVEL VHYAQPLLNEADSLAKVMPSDI PLKQRRWLGLOMLEGDIYSRA YAGEASQHLDAALARLRNEND PALHHADARYQCIAAICDVVS NTLTAEPSRFTTAVDKIVLNRFL GLPIFLYWYLLMFLANIGGAL QUEFDVGSVALFVHGIQWIGYT LHFPDWLTIFLAQGLGGGINTV LELYPQIGMWYLFLF
24989	55357	A	25127	779	910	
24990	55358	Α	25128	2203	2665	ACWARISAAVIQRSGMPGVRV CGRIKSCSKAVRCQRHVFATCV WNGRQVTSGAGTWSTIAWYSG VMSSAISSWSRPAIPFSAEA*TIG KSSC/YVGRVEVNEQIEYLIHNP IBTRARAVVIFVDNNNRLQAVS KRFFGYEARLRHRAVKCVNHQ QH
24991	55359	Α	25129	241	918	
24992	55360	А	25130	2142	2646	KGVCGTTNPAKIQAILQAFHEI FGEGSCHIASVAVESGVPEQPE GSEETRAGARNRVANARRLLP EADFWVAIEAGIDGDSTFSWVV IENASORGEARSATLPLPAVILE KVREGEALGPVMSRYTGIDES KKEGAIGVFTAGKLTRASVYH QAVILALSPFHNAVY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
24993	55361	A	25131	473	1765	KAWLMTGIVRHWKGRAVPPA
21775	33301	1	25151	1	1.700	EQLLEHLGNGKSFDSVAQAWD
		l				AAMADAKAEDTVLWGVEAFRI
l		l				NAAVAKDDTQIHTHMCYCEFT
l		i				DIMDSIAALDADVITIETSRSDM
		l				ELLESFEEFDYPNEIGPGVYDIH
		l				SPNVPSVEWIEALLKKAAKRIP
						AERLWVNPDCGLKTRGWPETR
		l				AALANMVQAAQNLRRGARAG
	1	l				CAADFAASARLAVGEALTNIA
	1	1				ATQIGDIKRIKLSANWMAAAG
		1				HPGEDAGLYEAVKAVGEELCP
		1				ALGLTIPVGKDSMSMKTRWQE
		l				GNEEREMTSPLSLVISAFARVE
						DVRHTITPQLSTEDNALLLIDLG
						KGNNALGATALAQVYRQLGD
1		1				KPADVRDVAQLKGFYDAIQAL
	ł	l				VAQRKLLAYHDRSDGGLLVTL
	1	l				AEMAVLSSLGQGGYFGHMII/D
	ŀ					SGQYPGKSKTGQSTPDVAAQA
				1		RQSWIP
24994	55362	Α	25132	602	2563	VVTTLTLVLTAVGSVLLLLFLV
1		l				MKARMHAFLALMVVSMGAGL
ŀ		1			ŀ	FSGMPLDKIAATMEKGMGGTL
l		1				GFLAVVVALGAMFGEILHETG
	İ	1				AVDQIAVKMLKSFGHSRAHYA
ĺ						IGLAGLVCALPLFFEVAIVLLIS
						VAFSMARHTGTNLVKLVIPLFA
						GVAAAAAFLVPGPAPMLLASQ
						MNADFGWMILIGLCAAIPGMII
						AGPLWGNFISRYVELHIPDDISE
		1				PHLGEGKMPSFGFSLSLILLPLV
1		1				LVGLKTIAARFVPEGSTAYEWF
		1				EFIGHPFTAILVACLVAIYGLAM
		1				RQGMPKDKVMEICGHAL\QPA
1		1				GIILLVIGAGGVFKQVLVDSGV GPALGEALTGMGLPIAITCFVL
1	İ	1			1	AAAVRIIQGSATVACLTAVGLV
		1				MPVIEQLNYSKRRGFTGRVEEN
		1				FGVCKGPSKYHSQHDAINRQG
					1	REASDAHGTLENLPLPLVPQPN
		1				AATALAALRASGLEVSENAIRD
l		1				GIASAILPGRFQIVSESPRVIFDV
		1	1		1	AHNPHAAEYLTGRMKALPKNG
		1		1	1	RVLAVIGMLHDKDIAGTLAWL
	1	1			1	KSVVDDWYCAPLEGPRGATAE
		1		1		OLLEHLGNGKSFDSVAQAWDA
					1	AMADAKAEDTVLVCGSFHTVA
				1	1	HVMEVIDARRSGGKLCQMHVN
				1	1	VQDKIDEEINQVHICLCLVLVIV
						SGCKYVGYSLKCSEHYYSLVR
	L	L_	L	L		BOCK I VOI BEKCSEHI TOEVK

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24995	55363	A	25133	518	1079	TQKETNKRCSPLVGWYPAFRM AHFLASERSCYQKLSNRKSHPM AVAGMYSGMTVANLLFEHSAG NVFKSGI*LALHLFIDRCF*YCG DGIGLFLGARYSRROERKSART ISLFAQPGPVVNFRRHDVWQRR CVCLVQLRKAIHDVYFRFFGNG DDLYYDVSWARDGAGKYAKW ODFRILFTAHCSSD
24996	55364	A	25134	322	798	AQRAHVVGTVGKFDEDDADIL HHRHNHLAKVFGLRLFLIAELE FIKFRHPLYQLGDAFTKKLFHIL ILVVGGSIFNHWQQRRHQRFI VEFHLGQNAGNATGCVI*GSPL ERVCPS*ASRATRYACRRILIW SIARPAAKVSACCSAIATSK*RS KGQRVLLGNCHVEVAIREFT
24997	55365	Α	25135	440	906	CGFSSLSRLPHSSYSAHHAVAPS VLMSASGRPRWSQWYRWIFRA GVYTGSIWFFICSTVRPHDASQ RRLSSLT/QVSQDFTFQPVNHQL WAGGRPTAGITVGKQ*W*PFIK FTVPGDDSGDGRGQGFLQIAAG KCRAQTFFSFCRAGKHDPCRRT VS
24998	55366	A	25136	1059	1541	TAPLLRPGCRLS*SAAHPAAPA QSTNQCPGDRYAATLPAHHRH TNHG*IADVHQHISATPASAAS YAPGFLKDGAPASERHRETGC GRORPHPSLYKLSGILRPYQPA SFPG*QQRAVLSAR*LLPVQCSL HSQRCRRRPHRLHRSAPAPGIR ERRSRR

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24999	55367	A	25137	236	2211	OGALMSEDIFDAIIVGAGLAGS
		1				VAALVLAREGAQVLVIERGNS
		ŀ				AGAKNVTGGRLYAHSLEHIIPG
						FADSAPVERLITHEKLAFMTEK
		1	İ			SAMTMDYCNGDETSPSQRSYS
		1				VLRSKFDAWLMEQAEEAGAQI
		1				ITGIRVDNLVQRDGKVVGVEA
		ŀ		İ		DGDVIEAKTVILADGVNSILAE
		1			·	KLGMAKRVKPTDVAVGVKELI
						ELPK\$VIEDRFQLQGNQGAACL
		l				FAGSPTDGLMGGGFLYTNENT
		1			ł	LSLGLVCGLHHLHDAKKSVPQ
		l				MLEDFKQHPAV\APLIAGGKLV
						EYSAHVVPEAGINMLPELVGDL
		1				HERSLIFVASGPAGNSKETASD
						KLEEALPTKNWEVPGANWNTP
İ						GNGIPSVPEKLKGMLSAPNYRR
		1				MVLPAPLQILLLQNAKGGELLC
						AAGGQIAFNLGSAVGAYCGGM
		l				MLTLGLAYNYVALPAALLSFA
		l				AMSSLLLYGRYKRQQAADTPV
		l				LAKPLGQLDNAPFRCENVNLIR
				l	ŀ	EEIGFNALDKFKRTTGALLQLQ
					l	QALHPALGADLCGSTGFAVLFI
						SPVRGNTHLRHLVHIFGTDLDL
				1		NRHSVRADHRGVQRLIAVRFW
		l		l		NGDIVFHAARTRLVQAVHLAQ
						HAITGVRIIDDHAESVDVHDRV
l		l				KTLLFEHHFAVNRIKMLLPTTD
						AARYSRFLQTPFDFRKNLLDHL
25000	55368	Α	25138	1	1932	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1	i		sequence		
		<u> </u>				
25001	55369	Α	25139	1	1200	MAIPAFGLGTFRLKDDVVISSVI
		1			i	TALELGYRAIDTAQIYDNEAAV
1		1				GQAIAESGVPRHELYITTKIWIE
1		l				NLSKDKLIPSLKESLQKLRTDY
		1			į .	VDLTLIHWPSPNDEVSVEEFMQ
	į.	l				ALLEAKKQGLTREIGISNFTIPL
	į	1		1		MEKAIAAVGAENIATNQIELSP
						YLQNRKVVAWAKQHGIHITSY
						MTLAYGKALKDEGIARIAAKH
		l				NATPAQVILAWAMGGGPVE\W
						RR*QIWRGFSSAS*RHELYITTK
						IWIENLSKDKLIPSLKESLQKLR
						TDYVDLTLIHWPSPNDEVSVEE
1		1				FMOALLEAKKOGLTREIGISNF
1		1		1		TIPLMEKAIAAVGAENIATNQIE
		1				LSPYLONRKVVAWAKOHGIHI
		1				TSYMTLAYGKALKDEGIARIAA
		ľ				KHNATPAQVILAWAMGGGPVE
		ŀ				MAKVADMAGIFVSKLKTFNAG
						VKGSTLGASGPQYVMVPKKHA
	l					DOLRESLASGEIAAVOSTLVAD
1		i .				NTPLNSRVYTVRSGDTLSSIASR
1						LGVSTKDLQQWNKLRGSKLKP
						GOSLTIGAGSSAORLANNSDSIT
1	1	1				YRVRKGDSLSSIAKRHGVNIKD
1	İ					VMRWNSDTANLQPGDKLTLFV
		1				KNNNMPDS
25002	55370	A	25140	2237	2404	
25003	55371	A	25141	307	642	
25004	55372	A	25142	1449	2084	NAPRCAYY\VDVIAVTMPTTCC
Ι.						TLKISPLCRELILTLANRTTTQR
	1					AEPMTRRLIQVLFDELPQQPQQ
						QLHLPVSSHPKIRTMVEMMAK
						GPVEWGALGOWAGFFAMSER
		l				NLARLIVKETGLSFRQWRQQLQ
		1				LIMALQGLVKGDTVQKVAHTL
1		1				GYDSTTA\FITMLRKPGKTAGTS
1		1				LYHRRYGVSLLSSAWGQVGPP
1		1				RYCROANSVLSDRFCVLI
25005	55373	A	25143	981	1103	K TORQTHO TESSMI O TEX
25006	55374	A	25144	222	379	-
25007	55375	A	25145	I	1452	
25007	55376	A	25146	500	854	
25009	55377	A	25140	1	1374	
25010	55378	A	25148	2	167	
25011	55379	A	25149	781	1047	
25012	55380	A	25150	1	783	
23012	22300	1^	123130	1.	1,00	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	coden for peptide	of peptide sequence	deletion, :possible nucleotide insertion)
1				sequence		
25013	55381	A	25151	1442	857	LVKNPVKRMEIQQKNLTLFEYL
		1				DWWDVLFLLLESELLFANTWL
1		1				AATSESVDDCSGVKPPSGKNGT
1		1				*AMPSWAKASIIASSARCAMLY
		1				SFCTQTISAILRASATCVGVTLL
						RPICFTRPCCCISASTVRLASIDP
						SAGP
25014	55382	Α	25152	3	4105	
25015	55383	Α	25153	2	269	YKNPYIAAKIQPKTHDTLTPINP
		1				GRIKLWLMTKRPMWVVPERSN
		1				*IAARSLG*VGRM**P*QAGAE
		1				ATMYAGSTPIASATGTIAASAA
		1				A
25016	55384	Α	25154	1	1370	MCPIEETASSFGGKPLSMVLVIQ
						MFMLLTGALIIILTKTNPASISK
		1				NEVFRSGMIAIVAVYGIAWMA
İ		1				ETMFAPACYGYYILPTYPSDLA
1	1	ı				AIQFDRSGTTHIGRFVINHSFILP
1		1				GLIGVSVSCVFGWIFAAIKRDA
						AAGRAKENVIFHHFPFQSVKAD
						IATNPFKRPGGAFIRITQTFRTV
		ŀ		l		QTFRLSAYRLDFAGDRLRISTPR
						AKMRTAFKKDHLRQRRRCIRQ
						RAPPARHNLVGAVALPATVAG
				l		VNFTFSNVPLDSSVLSSLLTDFS
						TAVGSIVMLAVIMGLMLAFDM
						GGPVNKVAYAFMLICVAQGVY
				l		TVVAIAAVGICIPPLGMGLATLI
		1				GRKNFSAEERETGKAALVMGC
		1		l		V\GVTEGAIPFAAADPLRVIPSI
		1	l			MVGSVGGAVTAALVGAQCYA
				l		GWGGLIVLPVVEGKLGYIAAV
						AVGAVVTAVCVNVLKSLARKN
		_				GSSTDEKEDDLDLDFEIN
25017	55385	A	25155	1	789	MKIIAGITPADSGTLEIEGNNYV
					1	RLTPVHAHQLGIYLVPQEPLLFF
				l	1	SLSIKENILFGLAKKQLSMQKM
						KNLLAALGCQFDLHSLAGSLD
						VADRQMVEILRGLMRDSRILIL
	1	1	l	1		DEPTASLTPAETERLFSRLQELL
	1	1		I	ĺ	ATGVGIVFISHKLPEIRQIADRIS
		1	1			VMRDGTIALSGKTSELSTDDIIQ
		1				AITPAVREKSLSASQKLWLELP
	1	1		1	1	GNRPQHAAGTPVLTLENLTGE
	1	1	l			GFRNVSLTLNAGEILGLAG/TEL
		L				AETLYGLRTLRGGRIML
25018	55386	Α	25156	I	1332	

SEQ ID	leco in vo.	D4	SEQ ID NO:	Inc. de alla	[Nt. 4/3. tt614	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence		
25019	55387	IA	25157	1594	2220	MWVNPERGRAENTIIGGNATGI
23019	33361	^	23137	1394	2220	GTLNVQDQDSVITVRRLS*SAL
		1				KPGILVFKLTPAETERLFSRLQE
		1				LLATGVGIVFISHKLPEIRQIAD
		l				RISVMRDGTIAGTGFGDDFGFT
		l			İ	HPLRQQRLPQHLVSFMRAAVQ
1		l			1	QIFTLEIQRGVRPGCNVLAFGQ
						RGWTPGIVFQQVVELSLKFRIFL
		1				RTDKSFFQLAQSRHQDLWHVH
l						AAKLTKIGVK
25020	55388	A	25158	14	237	KTTSFPAKLFNACRISLLASAE/
23020	22360	<u>۱</u> ^	23136	'"	237	CQSEYFSIFSNMDLADTVMFL*
	l					GAIRFSDLVNEQIQHTFLIPGETI
					1	CRLSEVV
25021	55389	A	25159	h	1506	CKLSEVV
25022	55390	A	25160	158	639	SGC*PGRPSLN/GRLDVLSAWS
23022	33370		25100	150	007	VSILRLGGMALEGSIAYIVINFC
		l				DVKPQRFRGLSVPAASITVVLIC
				1		QFVLHRRELRRKLALPAHHLVT
		l				FTWGNVSAVDETRQWMVIKPS
ŀ		l				GVEYDVMTADD\RWWLR*PAV
		l				RWWKAAKNPLPIHQRIWRSTV
		l				AMPKLAVLC
25023	55391	Α	25161	2	2886	SVPTIIFFFLPVLRFWRPGIQQA
		l				KKCHLFATGTQSRRNTLRQRT
ľ		l				AKGIPQQRMTAKREEISIGILHV
		l				TPOORRECRGDNRFTARFRRTP
		l	l			WRLLGHCVSAAVTGVLPAVAG
		l				SPLAYSDTDEFYPVAGGTMSQ
ł						HLPLVAAQPGIWMAEKLSELPS
ł		1				AWSVAHYVELTGEVDSPLLAR
1		l		ł		AVVAGLAQADTLRMRFTEDNG
i		1	l			EVWQWVDDALTFELPEIIDLRT
		ł				NIDPHGTAQALMQADLPQDLR
		1				VDSGEPLVFHQTTLGFI
25024	55392	Α	25162	I	1659	
25025	55393	В	25163	200	646	
25026	55394	A	25164	I	3197	MPHRQHGPQMTPSHQRTTINR
		ı			i	DQREQQPIGTAAPQTRPQSAPY
1		l				CEPHTRRRTLQPHNRGFRTAKY
		1		i		TSTQARKYHMARPERSNDSDH
				l		PVHTRSRWNATQTERHTQHHV
		1				SPPSSLRTLRTNCTSHAHHRYH
1						RHAQWHRVGLLDVKPTGVPSN
		1				TVFSPPKNALWADRVDTSRGR
1		1				TTVEQDNHPNGGNVVGTPSDN
			l			NFWLETTGGDPNKEYYHHHHY
1						NEDYCRYYPLLIAEPLLFPSLSI
		$\perp$				KENILFGLAKKQLSMQKMK
25027	55395	В	25165	1	2505	

3330

NO: of peptide sequence of	SEO ID	SEO ID NO:	Mat	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
sequence   09/540,217   code for peptide sequence   defeion, impossible nucleotide insertion)   sequence   sequence   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible n	NO:						
25028   55396   A   25166   159   1744   NSRISGLQQRYLMHIMVTQGG   MSLSIVHTRAALGVNAPPITVE   VIHSKGLPGLTMVGLPETTVKI   ARDRYWRSAINSGYEPAKKIT   NLAPADLPKEGGRYDLPIAIAL   LAASEQLTANKLDEVELVGEL   ALTGALRGVPGASSATEAISKS   RKIIVAKDNEDEVGLINGEGCL   ADHLQAVCAFLEGKHALERFK   PTDAVSRALQHDLSDVIGGEGC   GRRVLEITAAAGHNLLLIGPPG   TIGKTMLASRINGLIPDLSNEES   LESAAILSLVNAESVOKLWRQ   PERSPHHSASLTAMVGGAIPC   PFRSPHHSASLTAMVGGAIPC   PFRSPHHSASLTAMVGGAIPC   GRINNCTPECTLRYLNRLSGP   LDRFDLSLEIPLPPGILSKTVV   GRINNCTPECTLRYLNRLSGP   LDRFDLSLEIPLPPGILSKTVV   GESSATVKGRVMAARERQFKF   QNKLNAWLDSPEIRCPCKLEST   DAMWLEGTLHILGLSTRAWG   LLKVARTIADIDQSDITPTYGG   KADARNSGNVCPSSRALVQR   LKVARTIADIDQSDITPTYGG   KADARNSGNVCPSSRALVQR   LESEKLKNIFNRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPTAPFLLPLELRELLPLIP   AEKL*YTETDAPFLLPRDLSAK   STSRYHCVIEARAWFK   STSRYHCVIEARAWFK							
MSLSIVHTRAALGVNAPPITVE VHISKGLPGLTMVGLPETTVKI ARDRV/RSAINRSGVEYPAKKII NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEVELVGEL ALTGALROVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFW PTDAVSRALQHDLSDVIGQEG GKRVLETTAAAGHNLLLIGPFG TGKTMLASRINGLLPDLSSNES LESAAILSLVARESVORLWRQI PERSPHHSASLTAMVGGGAIPC GGHNRCTFEGTLRYLNRLSGP LDRAFEGGGHLSKTRAKI TYPARFQLVAAMMPSPTGHVY GGSSATVKQRVMAARERQFKI QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHLGLSIRAWG LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSOPAKTVMMI **RARLGR-**TTGLELRELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK				,			. ,
MSLSIVHTRAALGVNAPPITVE VHISKGLPGLTMVGLPETTVKI ARDRV/RSAINRSGVEYPAKKII NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEVELVGEL ALTGALROVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFW PTDAVSRALQHDLSDVIGQEG GKRVLETTAAAGHNLLLIGPFG TGKTMLASRINGLLPDLSSNES LESAAILSLVARESVORLWRQI PERSPHHSASLTAMVGGGAIPC GGHNRCTFEGTLRYLNRLSGP LDRAFEGGGHLSKTRAKI TYPARFQLVAAMMPSPTGHVY GGSSATVKQRVMAARERQFKI QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHLGLSIRAWG LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSOPAKTVMMI **RARLGR-**TTGLELRELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK							
VHISKGLPGLTMVGLPETTVKI ARDRVIRSA IINSGYEYPAKITI NLAPADLPKEGGRYDLPIALAL LAASEQLTANKLDEYELVGEL ALTGALRGVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHILQAVCAFLEGKHALERFK PTDAVSRALQHDLSDVIGQECC GKRVLEITAAAGHNLLLIGPPG TIGKTMLASRINGLIPOLSNEGE LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEFERI TLDALREPIESGQHLSRTRAKI TYPARFQLVAAMPSPTGHVC GNHNRCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVV GGESSATVKGRVMAARERGFK QNKLNAWLDSPEIRCFCKLESI DAMWLEGTLHILGLSIRAWGR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR KADARNSGNVCPSSRALVQR RMFPGIGVILTSGRGNEEEDNI 25029 55397 A 25167 127 503 NRCLLUTLLRCKGRNREEEDNI EAESEKLKNIFNRPSGRLSYGI RMFPGIGVILTSGRGNAETTGHEL RARLGRTTGLELRELIPLIP ARKLYYETDAPYLLIPROLSAK STSRYHCVIEARAWFK	25028	55396	Α	25166	159	1744	NSRISGLQQRYLMHIMVTQGGL
ARDRYIRSAIINISGYEYPÄKKIT NLAPADLPKEGGRYDLPIAIAL LAASSQLTANKLDEVELVGEL ALTGALRGVPGAISSATEAIKS RKIIVAKDNEDEVGLINIGGECL ADHLQAVCAFLEGKHALBERR PTDAVSRALQHDLSDVIGQEC GKRYLEITAAAGHNLLIGPPG TGKTMLASKINGLPDLSNEEA LESAAILSLVNSEVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFDLEPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHYC GGNHNRCTPECTIRYLNRLSGPI LDRFDLSLEPILPPPGILSKTVV GESSATVKGRVMAARERGPK QKLNAWLDSPEIRCPCKLESI DAMWLEGTLIHLGLSIRAVGR LLKVARTIADIDQSDITPTYGG KADARNSONVCPSSRALVQR RUKHANGLEPLESAKVV ESSO29  55397 A 25167 127 503 NRCLLUTLLRCKGRNREEEND EAESEKLKNIFNRPSGRLSYGI RMFDIGVNLTSSQPAKTVMM **RARLGLR**TTGLELRELPLIP AEKL**YETDAPYLLPROLSAK STSRYHCVIERAWFK				İ			MSLSIVHTRAALGVNAPPITVE
NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEYELVÜGEL ALTGALRGUPGAISSATEAIKS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFN PTDAVSRALQHDLSDVIGQEQ GKRVLEITAAAGHNLLLIGPFG TGKTMLASRINGLIPDLSNEES LESAAILSLVNAESVOKLWRQ PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPAREQLVAAMMPSPTGHVY GHNINCTPEQTLRYLNRLSGP LDRFDLSLEIPLPPFGILSKTVV GESSATVKGRVMAAREROFKF QNKLNAWLDSPEIRCFCKLESI DAMWLEGTLHILGLSIRAWGR LLKVARTADIDQSDITPTYGG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLUTLRCKGRNREEEND EAESEKLKNIFNRPSGRLSVGI RMFPGIGVILTSGRAFATVGR RMFPGGVILTSGRAFATVGR RRFPGGVILTSGRAFATVGR RRFPGGVILTSGRAFATVGR **RARLGR**TTGLELRELLPLIP AEKL**YETDAPYLLPRDLSAK STSRYHCVIEARAWFK				ŀ			VHISKGLPGLTMVGLPETTVKE
LAASEQLTANKLDEYELVGEL ALTGALRGVPGAISSATEAIKS RKIIVAKDNEDEVGLINGEGGL ADHLQAVCAFLEGKHALERPR PTDAVSRALQHDLSDVIGGGEG GRRVLEITAAAGHNLLLIGPPG TGKTMLASRINGLIPDLSNEA LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFDLEPEFERI TLDALREPIESGQHLSSTRAKI TYPARFQLVAAMNPSPTGHYQ GGSATVKQRVAMARERQFK QKILNAWLDSPEIROFCKLESI DAMWLGGTLHLGLSIRAWG LLKVARTIADIDQSDITPTYCG KADARNSONVCFSSRALVQR RVETTAAPULFTCLSAK Z5029  55397 A 25167 127 503 NRCLLUTLLRCKGRNEEEDH EAESEKLKNIFNRPSGRLSYGI RMFPGIGVNLTSSQFAKTVMM **RARLGLR**TTGLELRELIPLIP AEKL**YFTDAPYLLFROLSAK STSRYHCVIEARAWFK	1						ARDRV/RSAIINSGYEYPAKKITI
ALTGALROVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFR PTDAVSRALQHDLSDVIGQEG GKRVLEITAAAGHNLLLIGPEG TGKTMLASRINGLLPDLSNEE LESAAILSLVNAESVQKLWRQ) PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNEPSTGHVC GGHNRCTFEQTLRYLNRLSGP LDRFDISLEIPLPPFGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRGPCKLESI DAMWLEGTLHILGJSRAWGR LLKVARTIADIDQSDIITPTYGG KADARNSGNVCPSSRALVQR LLKVARTIADIDQSDIITPTYGG KADARNSGNVCPSSRALVQR EASESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSQPAKTVMM **RARLGR.RTGLELEELLPLP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK				ŀ			NLAPADLPKEGGRYDLPIAIAL
RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFK PTDAVSRALQHDLSDVIGQEGC GRRVLEITAAAGHNLLLIGPPG TGKTKILASRINGLIPDLSNEE LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLIPDLEIPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHVY GNHNRCTPEGTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR RULLVLLRCKGRNREEEND EAESEKLKNIFNPSGRLSYGI RNFPGGVNLTSSQPALTVMMI *RARLGLR*TTGLELRELLPLIP AEKL*YFETDAPYLLGPROLSAK STSRYHCVIEARAWFK				l		İ	LAASEQLTANKLDEYELVGEL
ADHLQAVCAFLEGKHALERPK PTDAVSRALQHDLSDVIGQEG GRRVLEITAAGHNLLLIGPPC TOKTMLASRINGLPOLSNEE LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPFERR TLDALREPIESGGHHSSTRAKL TYPARFQLVAAMNPSPTGHYC GRHNRCTPEQTLRYLNRLSGPI LDRPIJSLEIPLPPFGILSKTVY GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNV CPSSRALVQR 25029 55397 A 25167 127 503 NRCLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPGIGVNLTSSQFAKTVMMI **RARLGLR**TTGLELEELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK							ALTGALRGVPGAISSATEAIKSG
PTDAVSRALQHDLSDVIGQEQ GKRVLEITAAAGHNLLLIGPFG TGKTMLASRINGLLPDLSNEE LESAAILSLVNAESVQKLWRQI PERSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMPSPTGHVY GRHNRCTPEQTLRYLNRLSGPI LDRFDLSLEFILPPFGLLSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDITPTYG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLUTLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSGPAKTVMM *RARLGLR-TTGLELRELLPLP AEKL*YPETDAPYLLPRDLSAK STSRYHCVIEARAWFK					1		RKIIVAKDNEDEVGLINGEGCLI
GRRVLEITAÄAGHNILLIGIPG TGKTMLASRINGLIPDLSNEA LESAAILSLVNAESVOKLWRÖJ PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEEFRI TLDALREPIESGOJHLSRTRAKI TYPARFQLVAAMNPSPTGHYC GGHNRCTPEGTLRYLNRLSOPI LDRFDLSLEIPLPPFGILSKTVV GESSATVKGRVAARREPKEY QNKLNAWLDSPEIRCFCKLESI DAMWLEGTLHILGJSRAWOR LLKVARTIADIDQSDITFTYCG KADARNSONVCFSSRALVQR ROMELLTLLRCKGRNEEEDN EAESEKLKNIFNRPSGRLSYGI RMFDIGVNLTSSGPAKTVMMI **RARLGLR**TTGLELRELLPLIP AEKL**YETDAPYLLFROLSAK STSRYHCVIEZARWFK				ł			ADHLQAVCAFLEGKHALERPK
TÜKTMLASRINGLPÖLSNEE LESAAILSLVARESVÖKLW?QI PPRSPHHSASLTAMVGGGAIPC POEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHYC GNHNRCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSQFAKTVMMI *RARLGLR-TTGLELRELLPLIP AEKL-YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	1						PTDAVSRALQHDLSDVIGQ\EQ
LESAAILSLVNAESVOKLWRQI PFRSPHHSASLTAMVGGGAIN PFRSPHHSASLTAMVGGGAIN PRESPHHSASLTAMVGGGAIN POEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHVY GNHNRCTPEQTLRYLNRLSOPI LDRFDLSLEIPLPPPGILSKTVV. GESSATVKQRVMAARERQFK* QNKLNAWLDSPEIROFCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR RESEKLKNIFNPSGRLSVGI RMFDIGVNLTSSGPAKTVMMI *RARLGLR**LTGLELRELLPLIP AEKL**YETDAP*LLIPROLSAK STSRYHCVIEARAWFK				l			GKRVLEITAAAGHNLLLIGPPG
PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELEPFERI TLDALRPIESGGHLSATRAKI TYPARFQLVAAMNPSPTGHYQ GNHNCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPERIGPGCLESE DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYGG KADARNSGNVCPSSRALVQR EASSEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQGAKTVMMI *RARLGR*TTGLELRELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK		ł		ŀ			TGKTMLASRINGLLPDLSNEEA
PGEISLAHNGVLFLDELPFERI TLDALREPIESGQIHLERFERI TLDALREPIESGQIHLERTRAKI TYPARFQLVA AMMPSPTGHVC GNHNRCTPEQTLRYLNRLSOP LDRFDISLEPIELPPFGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIROFCKLESI DAMWLEGTLHLGLSIRAWOR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPGIGVNLTSSQFAKTVMM *RARLGLR-TTGLELRELLPLP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	ł						LESAAILSLVNAESVQKLWRQR
TI.DALREPIESGQİHLSRTRAKI TYPARFQLVAAMNPSPTGHYÇ GRHNRCTPEÇTLRYLNRLSGİP LDRFDLSLEIPLPPFGILSKTVV. GESSATVKQRVAARREPÇKE QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLİHLGLSIRAWQR LLKVARTIADİDQSDİİTPTYGG KADARNSGNVCPSSRALVQR ROMENDE VESTAVILY SOS NECLLITLERCKGRNEEEND EAESEKLKNIFNPSGRLSYGİ RMFDİGVNLTSOŞQA KIVMMİ "RARLGLR"TTGLELRELLPLIP AEKL"YETDAPYLLPROLSAK STSRYHCVIEARAWFK	l						PFRSPHHSASLTAMVGGGAIPG
TYPARFQLVAAMNPSPTGHYQ GNHNRCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPFGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNV CPSSRALVQR EASSEKLKNKFNRSGRLSYGI RMFDIGVNLTSSQFAKTVMM **RARLGR**TTGLELRELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l						PGEISLAHNGVLFLDELPEFERR
GNHNRCTPEOTLRYLNRLSOP LDRFDLSLEIPLPPPGILSKTVV GESSATVKQRVMAARERQFK QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR RS55997 A 25167 127 503 NRCLLITLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMM *RARLGR*TTGLELRELLPLIP AEKL*YFETDAPLLIPROLSAK STSRYHCVIEARAWFK		}					
LDRFDLSLEIPLPPPGILSKTVV. GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR EASSELTLRCKGRNREEEND. EASSEKTLKNKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGR*TTGLELÆELLPLIP AEKL*YYETDAPYLLPRDLSAK STSKYHCVIEARAWFK							TYPARFQLVAAMNPSPTGHYQ
GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYGG KADARNGGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSQFAKTVMMI *RARLGLR*TTGLELEELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK			- 30		l		
QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIOSDHITPTYGG KADARNSGNVCPSSRALVQR NRCLLLTLRCKGRNREEND. EAESEKLKNIKFRNEPSGLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGR-*TTGLELRELLPLIP AEKL-*YETDAPYLLPRDLSAK STSRYHCVIEARAWFK							
DAMWLEGTLIHLGLSIRAWOR LLKVARTADIDOSDIITPTYCG KADARNSONVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLTTLRCKGRNREEEND EAESEKLKKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGR*TTGLELRELLPLIP AEKL-YVETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l						GESSATVKQRVMAARERQFKR
LILKVARTIADIDQSDITPTYÖC KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLUTLERCKGRNREEEND EAESEKLKNIFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMM *RARLGER*TTGLELRELLPLIP AEKL*YETDAPYLEPROLSAK STSRYHCVIEARAWFK					l		QNKLNAWLDSPEIRQFCKLESE
25029 55397 A 25167 127 503 NRCLLITLIRCKGRNREEND. EAESEKLIKNERNEPSGLESYGI RMFDIGVNLTSSQFAKTVMML *RARLGR*TTGLELRELLPLIP AEKL-VYETDAPYLIPRDLSAK STSRYHCVIEARAWFK							DAMWLEGTLIHLGLSIRAWQR
25029 55397 A 25167 127 503 NRCLLTTLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQGAKTVMM *RARLGR*TTGLELEELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l						LLKVARTIADIDQSDIITPTYCG
EAESEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGLR*TTGLELRELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK							KADARNSGNVCPSSRALVQR
RMFDIGVNLTSSQFAKTVMML *RARLGER*TTGLELÆELLPLIP AEKL-YVETDAPYLIPRDLSAK STSRYHCVIEARAWFK	25029	55397	Α	25167	127	503	NRCLLLTLLRCKGRNREEENDA
*RARLGR*TTGLELRELLPLP AEKL*YETDAPYLLPRDLSAK STSRYHCVIEARAWFK							EAESEKLKNKFNRPSGRLSYGD
AEKL*/YETDAPYLLPRDLSAK STSRYHCVIEARAWFK					l		RMFDIGVNLTSSQFAKTVMML
STSRYHCVIEARAWFK							*RARLGLR*TTGLELRELLPLIP
					l		AEKL*/YETDAPYLLPRDLSAKP
25030   55398   A   25168   3   406							STSRYHCVIEARAWFK
	25030	55398	Α	25168	3	406	

SEO ID	ISEO ID NO:	Me	SEO ID NO:	Nucleotide	Nucleotide location of lost	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
		1		sequence		
25031	55399	I <sub>A</sub>	25169	11	1252	MFDIGVNLTSSOFAKDRDDVV
25051	33399	<u> </u> ^	23103	ľ	1232	ACAFDAGVNGLLITGTNLRESO
		l				QAQKLARQYSSCWSTAGVHSH
		1				DSSQWQAATEEAIIELAAQPEV
		1				VAIGECGLDFNRNFSTPEEOER
		l				AFVAQLRIGADLNMPVFMHCR
İ						DAHERFMTLLEPOMVENYETLI
					l	FEAHSTDYOTPOSLROLVIDHF
		1		1		AILKVGPALTFALREALFSLAAI
		1				EEELVPAKACSGLROVLEDVM
				İ		LDRPEYWQSHYHGDGNARRLA
		ı				RGYSYSDRVRYYWPDSQIDDA
		1				FAHLVRNLADSPIPLPLISOYLP
		l				LQYVKVRSGELQPTPRELIINHI
		1				ODILAHTTOPVKANKONKEEH
		1				AMPNIVLSRIDERLIHGOVGVO
		İ		l		WVGFAGANLVLVANDEVAED
		ı				PVQQNLMEMVLAEGIAVRFWT
		l				LOKVIDNIHRAADROKILLVCK
		i				T*WKWYWOKGSPYVSGRCKK
		1			l	LSTTFIAPPIDRKSCWFVKHPPIS
25032	55400	A	25170	2	319	YSSVFSLSASASFSSSRFRPLPT*
						KREKKTPISNROYIGIANSVCEK
		1			1	TSGGVSNIPTTNAPTSTYGRFLR
		1				KSSGEVIPIQHSSTIATGTSKETP
						NAINSAITKLK
25033	5540I	Α	25171	1	1011	MIPHPKLEGDRSTQALPPTPVIR
		1				VTERRNLNWVGTTIGFVHTGK
	Į.	1			ł	PLSFVYDMADIIKFDTVVPKAF
	1	l		l	ļ	EIARRNPGEPDREVRLACRDIFR
		1				SSKTLAKLIPLIEDVLAAGEIQPF
		l				APPEDAQPVAIPLPVSLGDAGH
	İ	ı				RRRRSGRVSEVSWRSGVMSFR
		l				RASGDKPQPKPKVMPEHAECPF
	1	l		l		AARRGQMMSICPCFALKIDIAD
		l				NKFFNGETSPLFSQSQAKLARQ
	1	1				FHQKIAGYRPTPLCALDDLANL
		l		1		FGVKKILVKDESKRFGLNAFK
	1	ı				MLGAPEKCHRRKNDF*RRSDRI
		1				VLIRL*REFSSHQKGLRDRPAH
						KAVLGDNQLFSGGTGAPVWPG
		1				FAKRAVMF/TPLKNLLSAISIFN
						AKHGHILIIWPRLAAGGHSACS
		1			1	GITFGFGCGLSPLARRKLMTPE
						RQLTSDTRPDRLLRWPASPSET
1		1		1		GSGMATGCASSGGAGGCISPA
		1				ASTSSISGINLANVLLLRKISLH
1		ĺ				AKRTSRSGSPGLRRAISKAFGTT VSNLMMSAIS
25034	55402	-	25172	ı	510	A 2INFIMIM2VI2
25034	55402	A B	25172	1	1482	
23033	153405	ρ_	2110	11	1702	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
25036	55404	А	25174	704	1069	RLWQADCKENAGGDYYWTFF PQPTFVSTQKYYCHVDNSCYM NFDFSAPEYHAHWRYGLLMVG ESQHGLGANAIQASQCFKAAN QPLGADATFLQQIKGEIICFGLFI TGVFSIDSAFCDIT
25037	55405	А	25175		639	MARWUCDFPYGVLPTLNAM PESTRKQIMPWTRLSGSLHTWN FTPNRRIGRYPSGLPPDSANRPR REPDACRSLHSPAKYRGNPNBD RLDHQQNGLPARGKDTPRSNK PSISQWTNTKPQPRHQPRGKG HKSPAPEMPKPPQATSSTREQT KYGAAELWRSPWKTRYIELKA RGPMACVTISLNVCCAHLVRL VMVTLKQTDPIRNLGEMPSKSQ TKKAREVHLHSLHLQELQQE EPPARKRKTQWAVSEKK
25038	55406	Α	25176	82	356	AQCEEYRVPQTLKRNPKQCFDI SIRGGSQPCGIFSTPVRNTLQNM GQMGWLVAPG*WLWREIRKH NRWCACPRKPGRAGISMALRW GSGHA

NO: 0	f peptide equence	hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25039 5	is407	A	25177		2635	MNKSGKYLWTYLSIMGAFAL GYALANREGINAL WIVVASV IYLIAYRFYGLYIAKNVLAVDP TRMTFAVRHNDGLDYYPTDKK VLFGHHFAAIAGAGPLVGPVLA AQMGYLPGMIWLLAGVVLAG AQMGYLPGMIWLLAGVVLAG AVDFMVLYSTRRDGRSLGE LVKEEMGPTAGVIALVACFMI MYIILAVLAMIVVKALTHSPWG RIGEVSVIGLYFLIFAIISGGWV ASSPTWAPFYEDFTGVQLTWLLAS IRELITTINFPEEYPFTTGVGLTWL RLINKSIMMDFSLTEGGELLAS IRELITTINFPEEYPRTCDQNGTY PREFMRALADNGISMLGYPEF GGIPADYVTGMLALMEVSKCG AFAFLITNGGCHISMRFGSAE QLRKTAESTLETGDPAYALALT EPGAGSDNNSATTTYTRKGW VYINGQKTFITGAKEYPYMLVL ARDPOPKDPKKAFTLUWVDSS KGIKINPLHKIGWHMLSTCEV YLDNV*TSVWRTCACPALRRA DMEWTSLRSEIDWEKGDTIKQC ISAATSC VYGVTGGAILEGGDA DRAWTSLRSEIDWEKGDTIKQC ISAATSC VYGVTGGAILEGGDA QLREELPGTKLGLLNWYPEDA LESRSTKERDGRPGGGICGETA NILRGPENRTSCHLGGLLNWPYPDA LESRSTKERDGRPGGGICGETA NILRGPENRTSCHLGGLLNWPVPDA LESRSTKERDGRPGGGICGETA NILRGPENRTSCHLGGLDRWPYPDA LESRSTKERDGRPGGGICGETA

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25040	55408	A	25178	216	1829	TVCRCHFVTTKHIGRERNQRAR
23040	33404	ľ`	23170	1.0	1025	OCLVGKTTDTQQHNCDIRVGE
1		1				OADHTRANHOHCTORYDHLTG
						NDOVHTKPTLEQRRQVTTEDT
]						TEVSKQHRHPGEHRDLFQRTLN
1						ISADDORRLLLELONDNLNHNR
		ļ			i	IWLRLAAQPEDHIYGCGEQFSY
				l	l	FDLRGKPFPLWTSEQGVGRNK
				l		QTYVTWQADCKENAGGDYYW
		l			i	TFFPQPTFVSTQKYYCHVDNSC
		l		l		YMNFDFSAPEYHELALWEDKA
					1	TLRFECADTYISLLEKLTALLGR
						OPELPDWIYDGVTLGIQGGTEV
						COKKLDTMRNAGVKVNGIWA
						ODWSGIRMTSFGKRVMWNWK
						WNSENYPOLDSRIKOWNOEGV
						OFLAYINPYVASDKDLCEEAAO
ļ						HGYLAKDASGGDYLVEFGEFY
						GGVVDLTNPEAYAWFKEVIKK
					İ	NMIELGCGGWMADFGEYLPTD
						TYLHNGVSAEIMHNAWPALW
		l				AKCNYEALEETGKLGEILFFMR
		l				AGST/GDIGG\YTTLFEMKRSKE
						LVLRWCDFSAFTPMMRTHEGN
						RPGEHWAF/DGDAKHRHLAVY
25041	55409	Α	25179	277	488	
25042	55410	В	25180	260	1500	
25043	55411	Α	25181	1	764	MQEWGRYTILSGCCNSALKGD
		l				VCLLYGFRVAGRRQASE*TPGA
		l				YNRVPSSKK*GFQLVLLPFSAN
		l				GKSPAY*RFSKSFAEDGEKDAG
		ı				FPHPYAEAGYDNGGRRSGAGT
		ı				LLSR*I*TGAGRGAWRV*RLTG
		l				E*MAGKRT*VTASGYSQR*IMV
l		l		1		FLWSLYRSYRL/GRVRQHNGPR
		l				YLPVLARNWKMSAWVAAAW
		l				QGLTDMKRKTMKIRSGS\IVILA
		l				SGYAATAA*PLSGDRIFLP*PGK
		L				TG*RHGGTPSCAGFTGDY
25044	55412	В	25182	1	3117	
25045	55413	В	25183	270	388	
25046	55414	Α	25184	2154	2279	
25047	55415	Α	25185	614	623	RPNSGAR*GRGDKRSTQSVPET
	1	1		I		VRLLFCAGTFDQQPGNARWDD
		1		1		QYRCIRSGIVGVRAVLLGGDIL
				<u> </u>		DTQPLPVELAETLGKSAE

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		05/540,217	sequence	or popular sequence	, , , , , , , , , , , , , , , , , , , ,
25048	55416	A	25186	1208	2813	CYGVAWPFDPTLKFEFWRYFT
						HALMHFSLMHILFNLLWWWY
			i		l	LGGAVEKRLGSGKLIVITLISAL
		1				LSGYVQQKFSGPWFGGLSGVV
						YALMGYVWLRGERDPQSGIYL
						RRGVIIFAPIWIVRRWFEMTPTQ
						WSNYFFENLFKYEWVQTRSPA
						GAIQFEAVDAPEIIPDPFDPSKK
						RKPTMLVTDLTLRFDPEFEKISR
						RFLNDPQAFNEAFARAWFKLT
						HRDMGPKSRYIGPEVPKEDLIW
						QDPLPQPIYNPTEQDII\DLKFAI
		l				ADSGLSVSELVSVAWASASTFR
					l	GGDKRGGANGARLAL\MPQTR
						TGDVTRRQPIRAL\PVLE\KIQKE
		l				SGKASLADIIVLP\GLFVVEKSA
		1				SAAGLSIHVPFAPGRVDARQDQ
					l	\TAIGMFELLEPIADGFRNYRAR
						LDVSTTESLLIDKAQQLTLTAPE
				l		MTALVGGMRVLGANFDGSKN
						GVFTDRVGVLSNDFFVNLLDM
		l				RYEWKATDESKELFEGRDRET
		l				GEVKFTASRADLVFGSNSVLRA
		l				VAEVYASSDAHEKFVKDFVAA
		l				WVKVMNLDRFDLL
25049	55417	Α	25187	1520	1960	PVPLNFGWQRSTEVLICHVNSP
		1		1		STAAMTISPWRR**RRRTKQLS
		l				APLLLGVSAIGW/LTIILVAFMA
		1				WLLAKT/AFGRSFYATGDNLQG
		1				AR/QLGVRTEAIRIVAFSLNAER
		1				DFDDLRDSGPLIAMILFIMPTLS
						SISSRRLNPGVPSEI
25050	55418	A	25188	1155	1778	SASGGVMLKFIQNNREITALLA
		l	1			VVLLFVLPGFLDRQYLSVQTLT
						MVYSSAQILILLAMGATLVMLT
		1				RNIDVSVGSITGMCAVLLGMLL
						NAGYSLPVACVATLLLGLLAGF
		l				FNGVLVAWLK/IPAIVATLGT\L
					1	YRGLMSLWTGGHWFEGYPRIE
	1	l				KPSPPVAGVHHWCVTQIGGLRF
						AVAKRVGPDLPGDNKGAKGVL
	1	1	1			NTLDNYGVDGKCV

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide		in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25051	55419	A	25189	1	2227	I MVTIAGIILGGLALVGLITYFGK
23031	33417	^	23107	1	1221	WTYLWKEWLTSVDHKRLGIM
					ĺ	
			ŀ		1	YIIVAIVMLLRGFADAIMMRSQ
						QALASAGEAGFLPPHHYDQIFT
						AHGVIMIFFVAMPFVIGLMNLV
			İ			VPLQIGARDVAFPFLNNLSFWF
			İ			TVVGVILVNVSLGVGEFAQTG
			i			WLAYPPLSGIEYSPGVGVDYWI
						WSLQLSGIAVAHIAAQNVAVLI
						ISSDLEEIELMADRVYVMHQGE
						ITHSALTERDINVETIMRVAFGE
						SQRGVMLKFIQNNREITALLAV
						VLLFVLPGFLDRQYLSVQTLTM
						VYSSAQILILLAMGATLVMLTR
						NIDVSVGSITGMCAVLLGMLLN
						AGYSLPVACVATLLLGLLAGFF
						NGVLVAWLKIPAIV\ATLGTLG\
						LYRSIMLLWTGGQWIEGLPAEL
						KQLSAPLLLGVSAIGWLTIILVA
						FMAWLLAKTAFGRSFYATGDN
						LQGARQLGVRTEAIRIVAFSLN
						GCMAALAGIVFASQIGFIPNQT
				1		GTGLEMKAIAACVLGGISLLGG
						SGAIIGAVLGAWFLTQIDSVLV
						LLRIPAWWNDFIAGLVLLAVLV
						FDGRLRCALERNLRRQKYARF
			i			MTPPPSVKPASSATSDFICIGIVA
						LPLTMVIVSGGIDISFGSTIGLCA
						IALGVLFQSGVPMPLAILLTLLL
1 1						GALCGLINAGLIIYTKVNPLVIT
						LGTLYLFAGSALMLSEEQKNTK
						KTRQREDKKKEKKKQRKREEK
25052	55420	Α	25190	1055	1206	SFALFSSSSPRSRP*FASTKS*TL
		l				TTGQVLPSTNVRFLTGNWGPPV
						VATG
	55421	В	25191	1	1386	
25054	55422	A	25192	1	449	MQDPLLALLEDYNKGDLEKQV
						PPAQSGPQPGKAGRDRPIVIML
						DPGHGGEDSGAVGKYKTREKD
						VVLQIARRLRSLIEKEGNMKVY
						MTRNEDIFIPLQVRV/AKAQKQ
				I		RADLFVSIHADAFTSRQPSGSSV
						FALSTKGGMCSYRGSGCLQ
25055	55423	Α	25193	1536	1941	STSNQNSTALCRRRGLVHCIDG
						ANDDDSVMVWPSGSGRPWSAE
						PGAPQR\YAQLVVEDVELDLLH
				l		FIVFGDDVMLNVVLQGQAFML
				l		ALGLVTNVGVLAHAHHHALVS
				l		GVPNDGGGTWVGGRCVQQSQ
ı I		i	1	l		LCTCWSHCQ

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25056	55424	Α	25194	240	855	SRAGYAPAAAQKVASPYVRRE
		1				R*NOSD\PAVLTGIGERGK*LLS
		1				RDFFIAPLAGMIVEKRGAVHLA
		1				RWSVPVERKGQWQPAGLWAQ
		l				FFLADIVCPAATALPDTTAEDQ
		i				HIDHPAVVHVHVIPVVNTCAED
		l				NHRAPMRFMGGIGKFTGDGFN
		l				LARHPGNLLTPGWGVRFDFSVI
		l				FRTVFIFQPAIEAVIRQYQIINAD
						HRTGVAID
25057	55425	A	25195	840	1157	QYAPTAQPARPADPFALPTVQA
		l				RLTPFCYLVAKGDWCVYRRSY
i						SLWHSVASPRVRQSPRLGY*GY
		l				TANSPGILLAPLSLRGEMFLPQD
		l				APKSVPPYKRGKSVAIN
25058	55426	Α	25196	1076	1339	LVCVASMPVEISTDASASSGVI
		1				VISSAMSGSWSAETKRRLAMV*
		ı				PEPLHLWAISIPTTSGRFTSSLIS
						PFPAR*YSPARYIPRVWRV
25059	55427	Α	25197	2	118	
25060	55428	Α	25198	1809	3145	ARHKQHAYGYRYRQSPRCYGV
		l				SGKKRGLRYYGSWLAISGSSRI
		l				TR/LLCMYLRRFFIGVIGADIAN
						MGISAGAMWLLSVSQVSLAAV
						SQVVAVRVWPASSYTRVTVES
						NRQLKYKQFALSNPERVVVDIE
					l	DVNLNSVLKGMAAQIRADDPFI
		1			ľ	KSARVGQFDPQTVRMVFELKP
	l			ĺ		NVKPQLFALAPVAGFKERLVM
				1		DLYPANAQDMQDPLLALLEDY
				1		NKGDLEKQVPPAQSGPQPGKA
		1				GRDRPIVIMLDPGHGGEDSGAV
		1				GKYKTREKDVVLQIARRLRSLI
		1				EKEGNMKVYMTRNEDIFIPLQV
1		1			İ	RVAKAQKQRADLFVSIHADAF
		l				TSRQPSGSSVFALSIQRGARPVG DRYVDHTMFDMVQSLTIADSL
		l				KFGKAVLNKLGKINKLHKNOV
		l				EQAGFAVLKAPDIPSILVETAFI
		l				SNVEEERPNGQPGHPLDPATTM
		l				GTLIDCAHADSVQ
25061	55429	A	25199	1	277	O I DIDONII NDOVQ
25062	55430	A	25200	902	1006	
25063	55431	Α	25201	2	1265	
25064	55432	Α	25202	409	525	
25065	55433	Α	25203	91	431	NHKPGNIDVARRIQRGFAGDQI
		ŀ				GHLRPVERQCSPDKRRFIAADG
	1					REIRGKQRAGHIFQLLSRCLLQI
	1	l	1			LNHCQRRAAHFRFQLSNQRHQ
	1	1		1		QLLPV/HYHAAEREYPAGACLV
	1			l	i	RWLL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25066	55434	Α	25204	3	71	
25067	55435	Α	25205	1	1212	
25068	55436	A	25206	1	2786	MAAVIEQIRRAVLALVTGVVIH GOIPPVVDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGFGRLPFNRIGLIRRITRRIRGR LFGLYFILLLINRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRW FTDKTGSSNGLAPQGQCSAQ GELINEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQULDAIAAFILAALDGTLD DFIVARETEGQSGLKRVYHSPG APDIREFIRDAIP
25069 25070	55437	A	25207	48	402	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPPS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI DETCGHLWAYVWPSCAAVIGL
23070	33436		23200			YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
2507I	55439	Α	25209	1	912	

SEQ ID	SEQ ID NO:	T54-4	Icro in vo.	ISC. d. ala.	Thirt-day to come of the	I V V V V V V V V V V V V V V V V V V V
NO:	of peptide	hod	in USSN	Nucleotide location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide
1.0.	sequence	""	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	l '			sequence		
		L				
25072	55440	Α	25210	1	1857	MRVCARACVRTRTRMCVYAH
		1				TCVCVRTYAYVRVRVRVHVRA
l						RVRVCAYARTRVRNSLSILPFIQ
1						LTLATPIHHIHQEEFNIRGIVPVL
		1				RRVKPDLAIGIDITPSCDTPDLH
		l				DYSEVRINGGVGITCLNYHGRO
		1	İ			TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
						GWEIGFSPLALLLAFLCSTSPGF
						GDPDGLGVIAYQDTVRPNAAT
						AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
						KAVTELNQHAPLAMVGDGIND
				ì		APAMKAAAIGIAMGSGTDVAL
	1	i				ETADAALTHNHLRGLVQMIEL
						ARATHANIRONITIALGLKGIFL
		1				VTTLDDRVVAGSAGRYGGDGA
	1	[				GDSECVKIVAQEIRQTDRNIER
						DRSPRPSGERVRVRGKGGIEAN
						QPLSTAFTNQITIRQSIRLFSNQF
		ŀ				VFHKGISRVVAGSSAIISNVSPG
						CILRTPNCRRGFPISCTGEGKAA
						YGWQRDGGHAEYLLAEEKDLI
						LLPDALSYEDGAFISCGVGTAY
		ŀ			1	
						EGILRGEVSGSDNVLVVGLGPV
		1				GMMAMMLAKGRGAKRIIGVD
						MLPERLAMAKQLGVMDHGY*I
		l				LPDVY/V*IGVARVSWMNGRID
		1			i	SELRTRVRAYAHTRTRARTCTR
		1				TRTRTYAYVRTHTHVCAYTHM
		ļ				RVRVRTHARAHTR
25073	55441	Α	25211	3	1180	SKLGTRRSVVWA*SPSTSPTLW
1						CSTFSAAGHSSMKRMNEFVDL
l						LPAQQRMKGENWYRGTADAV
	ŀ		ŀ			TQNLDIIRRYKAEYVVILAGDHI
						YKQDYSRMLIDHVEKGARCTV
			l			ACMPVPIEEASAFGVMAVDEN
			ŀ			DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
		1				RDENSSHDFGKDLIPKITEAGLA
				1		YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
						PAGPPLPLPAARSEAPKAAGTV
1		1	l	l		ASVPSIAPARLRPVPDPVELVLV
İ	1	1	l	l		AAEFITPGDPTPRLHGSGFIDIR
1		ı		l		QIHHQTRSHLEGVKTGIRFLNH
l				1		FSGNPQGGIAHVNGVARFQVK
		1		l		QCHQAWGQQYAARLRFQARGI
						SLQIAIHRVDIIHRFDVRQL
25074	55442	Α	25212	16	543	
25075	55443	Α	25213	1	3387	

SEO ID	ISEO ID NO	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25076	55444	ĪA.	25214	1688	2234	LSVGKTFPVLVPAAFRKVSATO
		1		1.000	1	AAVPGTPSILALPSYSTTPFGVC
1		İ				TSASMNVPVLTLRIRTRVTGEV
						AAIKPFSMANAPTPDSILPQLGV
						VSTRCS*TITCANR*STSARGSL
1		İ				ERLIMATLL/WVAGTFD*SVWF
ł						GHDTDVVTLYRFHEALCYSVT
1				1		LRTPHRRVLRFKSQHPGELACF
				1		SPVA
25077	55445	A	25215	905	4761	PPHNWMPSNATPGIAFVWCAY
23077	33443	ľ	23213	100	17701	GAI/LPGDAPVPVVDDYRKVVR
				1	1	KDTKGLIARWKYFWMSVIALG
İ				1	l	VAFALYLAGKDTPATQLVVPFI
						KDVMPOLGLFYILLAYFVIVGT
				1		GNAVNLTDGLDGLAIMPTVFV
		1			ŀ	AGGFALVAWATGNMNFASYL
				1	1	HIPYLRHAGELVIVCTAIVGAG
1				į.		LGFLWFNTYPAQVFMGDVGSL
				•		ALGGALGIIAVLLRQEFLLVIM
					i	GGVFVVETLSVILQVGSFKLRG
25078	55446	A	25216	269	1219	QRIFRMAPIHHHYELKGWP
23076	33440	Α.	23210	209	1219	QTRTRRVQLQDLIEYVAIHQW/ FSDKHPVPFYSCIFDDSITNCYS
					1	WSISKDGYFIFGGAYPMKDGQT
					ļ	RFLTMKDKMSAFQFQFGKTVK SEKCTVLFPSRGODFVCGKDNA
						FLIGEAAGFISASSLEGIIYALYS
						TDIPRSVLLKQPDKLNPAYWRA
					1	TRLVCITLFGOIVNTICMAAPDL
		1				,
		1				RKWIMLSPVAHKGHHLEWVLF DMQILPVPRPSGCICSGSSTFFC
		1				NWGCPYDRPQWQLYPSMCLC
		1				VHIGPAPVRSEKVESKRAISKV
						DQDSAFRGCCRSGNRNGGRKI VAVSLKKVSGAAKPCGHFRST
						RYRVAYSTIIN
25079	55447	A	25217	1	1158	KIKVAISIIIN
25080	55448	A	25218	1156	1899	LKLGIRYPQCQRLVTHSLDGISL
		1				PLHTAH*SQSNSAENTHRAISLK
						AVPPFFTAERRGVNAEEHRNGR
						LINGECRORFNVLRVANGVRN
						VQFAKARDRNDIASFRQIGFDT
						FQTEVAQHFTDFRVAGFAFAID
		1	l			DSDLLVRLHFTALDAANADNA
		1	l			NIAVVIELRNLHLERTVKVNVR
		1	1			RRNVVNNRLVQRGHVFRHIFV
		1	l			VQTRDTVQRRSVNDREVQLLV
l	1	1	l			GRVEVNEQIEYYADAFVIMLER
						LCKVLCCR
25081	55449	A	25219	1	2583	LCKYLCCK
23001	22449	J^A	23217	1	2203	

OFO ID	lero in vo		lero in No	St. J. et l.	IN	Amino acid sequence ( X=Unknown,
SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		*=Stop codon, /=possible nucleotide
NO:	sequence	nou	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	sequence		0,7,5,40,217	sequen <b>ce</b>	or pepilar sequence	decition, a possion matternate insertion,
25082	55450	A	25220	278	787	TLLSATRQVYALLSTKPAFFSS
						HSSFSTSSRLISSRAASSMDVAF
						PIAFSASKTVSIKFFSR*KLLRNS
		1				HRPPFMVMRSIIRSPSNVFMAS*
						FRFVSIPTLRIDAVRRSTIWCSTT
	1					ARFSSRADAKFIKNVFQQAIPDS
						AAKWFFPVPGFPLNAKFVHPVI
						SSSAMDFA
25083	55451	Α	25221	866	1144	
25084	55452	A	25222	19	1203	NWNLTPYASLTGFTADNPEYH
						LSNGMKSKSVDTRSIYRELGAT
	1					LSYNMRLGNGMEVEPWLKAA
						VRKEFVDDNRVKVNSDGNFVN
						YLSGRRGIYQAGKDLDRFKNL
						VLVHAARYAADLSYLPLMQEL
						EKRYEGKLRIQTVVSRETAAGS
					İ	LTGRIPALIESGELESTIGLPMN
						KETSHVMLCGNPQMTRRLIPAS
						VEVYHDSLC\RKIWHGWEQHIT
	ļ					ARYLVGADGANSMVRRHLYP
						DHQIRKYVAIQQWFAEKHPVPF
						YSCIFDNSITNCYS WSISKDGYF
						IFCGAYPMKDGQTRFTTLKEK
						MSAFQFQFGKTVKSEKCTVLFP
						SRWQDFVCGKDNAFLIGEAAG
		1				FISASSLEGISYALDSTDILRSAL
						RKPIRTEQGANGAIRELEKFRPA
25085	55453	В	25223	58	359	
25086	55454	A	25224	4	329	
25087	55455	A	25225	1	1008	
25088	55456	A	25226	1	1335	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	deletion, \=possible nucleotide insertion)
25089	55457	A	25227	3	1886	HRINITAENDCRRLHGSIRDI.S SLIQAVGRIAAFYIGDVFAARF NDALTVVERLVKYTLYGSQIKL YNIETAVPSVLEVPDLIDVHAQYS LAGGCRLSSAHWLAQYCSBIHR QNTQOFVTLISTTMDAITPLIST KVQDKLLISACHILVSLATINAT PVFLISIPAVGKYFNRITDASAL RLVDKAQVLVCRALSNILLIPW PNLIPINEQQWPVRSINHASLISA LSRDYRNLKYPSAGAPQRKMPL PNEQQWPVRSINHASLISA LSRDYRNLKYPSAGAPQRKMPL FUNTENERGQWFVRSINHASLISA LSRDYRNLKYPSAGAPQRKMPL FUNTENERGYQWFOTFEQIQT FLIMPTREQLASSILHEGSTGC RVVEKFLKILQVVVQEPGQVFK FFLPSIIALCMEQVYPIIAERSP DVKAELFELLFTLHHNWEYF KSTVLASVQRGIAVEGOPPHLFK KSTVLASVQRGIAVEGOPHLFK FRITAMLFQFVNVLLQVLVH KSHDLLQGEGHRISYMMASV DFUDGFFAAFLPEFLITSCUDGV DANGKSVLGRNFKKMPLCPCL DGGNDSLAPWGLWKLLGPCLL DSGNDSLAPWGLWKLLGPCLL DSGNDSLAPWGLWKLLGPCLL DSGNDSLAPWGLWKLLGPCLL DSGNDSLAPWGLWKLLGPCLL PGGTRDFLLVAT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25090	55458	A	25228	689	3053	VDCRMS/FSYIEKFTDFLRLFVS VHLRRIESYSOFPVVEFLTLLFK
	1		İ	1		,
1				ŀ		YTFHQPTHEGYFSCLDIWTLFL
						DYLTSKIKSRLGDKEAVLNRYE
						DALVLLLTEVLNRIQFRYNQAQ
						\LEEL\DDETLDDDQQTEWQRY LRHSLEVVAKVMELLPTHAFST
	l					LFPVLQDNL\EVYLGLQQFIVTS GSGHRLNITAENDCRRLHCSLR
					Į.	DLSSLLOAVGRLAEYFIGDVFA
						AR\FNDALTVVERLVKVTLYGS
						QIKLYNIETAVPSVLKPDLIDVH
				i		AQSLAALQAYSHWLAQYCSEV
						HRQNTQQFVTLISTTMDAITPLI
					!	STKVQDKLLLSACHLLVSLATT
		1			1	VRPVFLISIPAVQKVFNRITDAS
					1	ALRLVDKAQVLVCRALSNILLL
						PWPNLPENEQQWPVRSINHASL
					ŀ	ISALSRDYRNLKPSAVAPQRKM
						PLDDTKLIIHQTLSVLEDIVENIS
	l				l	GESTKSRQICYQSLQESVQVSL
					İ	ALFPAFIHQSDVTDEMLSFFLTL
						FRGLRVQMGVPFTEQIIQTFLN
	ĺ					MFTREQLAESILHEGSTGCRVV
						EKFLKILQVVVQEPGQVFKPFL
						PSIIALCMEQVYPIIAERPSPDVK
i		1				AELFELLFRTLHHNWRYFFKST
ł		ı				VLASVQRGIAEEQMENEPQFSA
i						IMQAFGQSFLQPDIHLFKQNLF
		l				YLETLNTKQKLYHKKIFRTAML
		ŀ				FQFVNVLLQVLVHKSHDLLQE
						EIGIAIYNMASVDFDGFFAAFLP
25091	55459	Α	25229	1	853	MISVANEIAEAGFDPQGRTSED
		l				LLDLAESRVFKIAESRANKDEG
		l				PKNIADVLDATVARIEQLFQQP
		1				HDGVTGVNTGYDDLNKKTAG
		l				LQPSDLIIVAARPSMGKTTFAM
1					1	TLVENAGR\MLQDKP\VLIFSLE
		1			1	MPSEQIMMRSLASLSRVDQTKI
		l				RTGQLDDEDWARISGTMGILLE
1		l	1	1	1	KRNIYIDDSSGLTPTEVRSRARR
		1			I	I\AREHGGIGLIMIDYLPLMRVP
		l	1			ALFONRTLEIAEISRSLKALAKE
1		1	1	ĺ	1	LNVPVVALSHLNRSLEQRAEER
					l	PGNSDLGESGSIEQDADLIL

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25092	55460	IA	25230	206	1073	VKITSWLMSNSALPGTLKLLAL
23092	33400	l^	23230	200	1075	ILKCSTCVRVLPRSELRNLER/O
		1				GQLDSVGGFA/YLAEL/SKNTPS
		1				AANISA/YADIVRERAVVREMIS
		1				
		1				V/ANEIAEAGFDPQGRTS/EDLL DLAESRVFKIAES/RANKDEGR
		1				
		1				NPMFDDRGKRGEPSDLIIVAAR
	1	1				PS/MGKTTFAMNLVENAAML/Q
		1				DKPVLIFSQTKI/RTGQLDDEDW
		1				ARISGT/MGILLEKRNIYIDDSSG
l	1	1				L/TPTEVRSRARRIAREH/GGIGL
						IMIDYLQLMRVP/ALSDNRTLEI
					l	AEISRSLKHFEKLALICGCRNNG
						TTRYCKSLLA
25093	55461	В	25231	1	483 635	
25094	55462	В	25232	287	2469	MRCDICL ACCRED ATCRETTION
25095	55463	Α	25233	1	2469	MPSDISLASCRLRATSRLFTDHR
		1				RQSDCMTAINRIPIVDDEDNVR
1		1				RFETHCANNVRTALHLFADIHP
1					l	DVVLMDIRMPEMDGIKALKEM
1		1				RSHETRTPVILMTAYAEVETAV
i		1				EALRCGAFDYVIKPFDLDELNLI
1	1	1			ŀ	VQRALQLQSMKKEIRHLHQAL
ŀ	1			1		STSWQWGHILTNSPAMMDICK
						DTAKIALSQASVLISGESGTGKE
		1				LIARAIHYNSRRAKGAFIKVNC
						AALRESLLESELFGHEKGLFER
		1			1	ANEGTLLLDEIGRM/PLVLQAIL
i		1				RILQEREFERIG/GHQTIK/VDIAS
	1					LLAPTRLQAMVKEGTFREDLFY
						RLNVIHLILPPLRDRREDISLLA
		i				NHFLQKFSSENQRDIIDIDPMA
	1	1				MSLLTAWSWPGNIRELSNVIER
		1				AVVMNSGPIIFSEDLPPQIRQPV
		1				CNAGEVKTAPVGERNLKEEIKR
		1			i .	VEKRIIMEVLEOOEGNRTRTAL
		1				MLGISRRALMYKLQEYDATGF
		1				FRDGMTIMVGGFMGIGTPSRLV
		1				EALLESGVRDLTLIANDTAFVD
						TGIGPLIVNGRVRKVIASHIGTN
1		1				PETGRRMISGEMDVVLVPQGTL
	1	1				IEQIRCGGAGLGGFLNPTGVGT
1		1	1		1	VVEEROTSIDTSTRKRPFELGRP
1	1					SRNNDKGIRPRSGAGSEEYPRT
1	1					
1		1	1		1	LHDSLKRLQTDYLDLYQVHWP
		1	İ	1		LRPFYCFGKLGYSWTDSAPAVS
1			ļ		1	QLDTLDALAEYQRAGKIRYIGV
	1	<b>!</b>		ļ		SNETAFGVMRYLHLADKHDLP
25096	55464	A	25234	1	891 1614	
25097	55465	A	25235 25236	1	946	
25098	55466	Α	23230	П.	240	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25099	55467	A	25237	1055	11474	NGVKSKPPPNHOTGSAPGFSAI
23099	33407	A	23231	1033	14/4	KNRTFAWPTLPNTSCWANTML
		Ì			1	
1	1	1				IGSRELGIRSSQSGPLLGVRVWC
1						/CRCRGTQG/HSQGKDG/IPENGI
						RAYKFTSS*ASFRNSACFRQPSR
ŀ		1		1		IKPLRKATWLLCGLSTRHLITK
L	<del></del>	ļ.,				RLSSPDWA
25100	55468	Α	25238	2036	2743	DLLIRQMPLLSRRVIPVIRVPVT
					1	GVLWKSFTPRITIFGH/ALIDQH
	}	ı			1	SMIVAAQGLTPDHQLLLQIYDR
	ł			1	1	ARVSASRIVHQAQIYGDAVVR
	ļ					YAFIEHRAEVFDFASIEGNEENN
	İ					VWLCDCAKVYGHAQVKAGIEE
	l					DAIPTIHYSSQVAEYAIVEGNCV
1	İ	1			1	LKHHVLVGGNAVVRGGPILLD
						EHVVIQGESRITGAVIIENHVEL
1		1		1		TDHAVVEAFDGDTVHVRGPKV
1		1				INGEERITRTPLAGLL
2510I	55469	Α	25239	2234	2571	IMSSVDSSLVLPLKAMVPSRITL
		1				IRSAIWRISG/RLMRDKNNTHAS
		1		1		SKQLLQATKQAFGFRRGKRGG
		ŀ			l	RFIEDQNPRVAHQPAEDFHHLA
1						IGDIQRSCQTMQIKLAAQRRQQ
1	ŀ	1		į.		VLH
25102	55470	Α	25240	659	1206	WKSTSNTAKAKPGSVMAVDLR
				1		IPIRFGVMLSAA/FGDDVVDLIA
		1		l	1	QVDLVTTAVGPVVLERIAPAIA
		ı		ı	ŀ	KGQVKRKEQGHESPLNIIACEN
		1		i	l	MVRGTTQLKGHVMNALPEDA
		ı			i	KAWVEEHVGFVDSAVDRIVPP
		1		1	1	SASATNDPLEVTVETFSEWIVD
		ı			1	KTOFKGALPNIPGMELTDNLM
		ı		1		AFVERKLFTLKH
25103	55471	A	25241	332	683	ALPGR*RHVHLPGSAYEWNDA
		Γ.				EPAQESDELSLKMLTAICWLTA
		1	l	I	1	TA/STSLKI*R*KVALRCLVGRIR
		1			1	RLRRIROOCOLLMRRSRVLSGR
		i i		i .		LSSV
25104	55472	A	25242	1	841	MVKVAGECRVRASAHLPGLNR
25101		Γ.		1	***	STKNTEDRGANNOEGTNTOKT
				İ		RGETNERLKKNEHRDLRLARY
						PAKENNKQGDKNKPRTYEKLT
					i	GTVTHQEPPHHADQSPGLCLFR
		ı		1		TSRAQVERGPTVLLLISQENQIE
1			1	1	l	RYDSDNHSQLNLCLRVPTVTTQ
		1		1	1	RRDYDIAERYRQKGIKLPARKE
l	l		l		1	RLMTIAERLRQEGHQIGWQEG
1		1	l	1		KLEGLHEQAIKIALRMLEQGFD
		ŀ		1		RDQGIA/RRASCQRQQRQSSLPT
						P/EHCCAISGATARKPAALPAAR
		L.,		L		IRRILVSIIRCTSGCPALSG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop eodon, /-possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \≔possible nucleotide insertion)
25105	55473	A	25243	240	651	RCPPQSCLLAEGRWCG*K/CRK
	i					VSV*SNRYR*SRLSLGELLRAYS
	1					RNRDLPGF/SSGSARVLVATDV
						AARGLDIKSLELVVNFELAWEP
		1				EVNVHRIGRTARAGNSGLAISF
						CAPEEAQRANITSRPPHPAHIAS
		1				DHQSTP
25106	55474	Α	25244	1455	1643	RDPHQICVAESVYLAAFVLLCA
		l				GLCVRRRSTTGARNAAAAC*N
						GLW*AEAQCPAYYVCPVVG
25107	55475	Α	25245	549	641	
25108	55476	Α	25246	1378	2084	PNFGYSPPASSCGQVSQNSS*LQ
		l				CSVSGRDKMLRTGPCARTVSSS
		1				YLMGVSFSRDA**DAR*VCACH
		1				NTIAALSASAERFTSCERASHSE
		1				ARSGCCNSVRVMSNNPCCPRSL
1		1				IGVYDILFFQESTAKRCKRSLSG
		1				SGSACGKSRVRFTPYRPARRTP
		1				LRSTTSPISAASFPSGWECNAAS
	1					TCSAALRSTAITSLPSLAKFRAS
						SPSNSQTPRTAGLTGSAASESSI
ŀ		1		l		PQPQAAANS
25109	55477	Α	25247	1134	1428	GPCGCCSSNVARCASQTSSRFA
		1				AV/WHGAIGAR*LNADNRPLWI
1		1				EITREHAELPGKTGRRMETKQR
1						RAITFTQRQNGFESHTPGAVFFS
	1			l		INNRCQFGDR
25110	55478	A	25248	96	535	RPQTTVQPALYVAEQSICSQPC*
			l			*FSTKCDRKPAAVLAPAGYAAL
ŀ				l		PVLFSSAKLDGSWLRWNSASG
				l		RRQNGSFSCAALASKRPASASS
				l	1	KLNSA**SLPSAVFAAPVRVAA
					1	SMIISGFCALASIRPSASTRRPSA
l	1	l			1	SVFITSTFLPLR

SEQ ID			SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
25111	55479	A	25249	1471	3026	SPLRSSVACRGWHRKNNRRGW
		Γ.				CPRRGDPARPVRDSLO\HATAII
ı		1				VATPGRLLDHLQKGTVSLDAL
i		1				NTLVMDEADRMLDMGFSDAIL
i		1				DVIRFAPASRQTLLFSATWPEA
i	1	1		ļ		AAISGRVQRDPLAIEIDSTDALP
i	ŀ	ŀ				PIEQOFYETSSKGKIPLLQRTLV
i	1	l				RFANGSARVLVATDVAARGLD
l	Į.	1	l			IKSLELVVNFELAWDPEVHVHF
l	ļ		i	1		IGRTARAGNSGLAISFCAPEEA(
ı		1		1		RANIISDMLQIKLNWQTPPANS
ı		1				SIATLEAEMATLCIDGGKKAKN
l	l			1		RPGDVLGALTGDIGLDGARAKN
ì		1		ļ.		
ì		1		1		IAVHPAHVYVAVRQAVAHKA
ì						WKQLQGGKIKGKTCRRCYPLA
ì				1		APYVRHCSLVGRAASHQALWH
l						VAGFGLYALFRRTGGCRLRCR
ì				1		YSGGLRLIRPTVAAGICRPDKT
ſ		ŀ		i		RKRRIRHRAPFPDAARAPYPAY
	l	1		1		RSQYNQFFFTNSDFSFIGPKPSM
í		1				LQSMLCAPCNQADVFHFGANV
	1	1				SASKSYLFTFRSLMMVTLSPCS
		1		1		QQIAVSIFNDQLVAFLCRFCVV
25112	55480		25250	196	330	PLRRHIHGQMYMPLSS
25112	55481	A	25251	62	617	NRRLPSGGDEMSAQVSLELHH
23113	33461	n	23231	02	017	RI/SQF/LVQESSCWTDW/KFRD
		1		1		GVAOLRPKEVRF\TMRTTVNGC
		i i				TRVPRKGVQPPTTWIFNDTKDQ
						LERRIARLETGMAWAEEPPSRT
		į.		l		RHLISNCQISETDIPNVFAVRVN
		1				YLLYRAQK\ERDETFYVGTRFD
	l	1		1		KVPPSE\DTTWRCLKRDIVLDO
	1	1		l		AVITSHNLSVLF
25114	55482	A	25252	1	318	AVITSHINESVEI
25115	55483	A	25253	1	510	
25116	55484	A	25254	9	79	
25117	55485	A	25255	ĺ	361	
25118					1245	FSQIYLARSALSSAHSSRSPWQF
	55486	A	25256	863		
	55486	Α	25256	863	1245	
	55486	A	25256	863	1245	SVWTLVRSVTNLETSANSALG
	55486	A	25256	863	11245	SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR
	55486	A	25256	863	1245	SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW
	55486	A	25256	863	1245	SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE
25119	55486	A	25256	909	1069	SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI
25119						SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW
25119						SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSKIJELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW YYP*GLCSVPLVDISVLVPVPCC
25119						SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW
	55487	A	25257	909	1069	SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLISLCLADEAFPSSKYIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW YYP*GLCSVPLVDISVLVPVPCC
25120	55487	A	25257 25258	909	1878	SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLISLCLADEAFPSSKYIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW YYP*GLCSVPLVDISVLVPVPCC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25124	55492	Α	25262	1599	1776	WFPASSMSQPKKAQDQTDSQP
		1				NSTRGTERSWYHSF*NGSKO*K
						KSNSSPTHFMRPASS
25125	55493	Α	25263	1	162	
25126	55494	Α	25264	1	3370	MNRAPIPKQSKDKTSRETKNTS
						RSKTRERTDELEGLSTDNHAET
		l				QHAETNTDMTHERYTQIRNHT
		1		l		YKTTHQMEDKRTKPKREKEIH
		1				NRPDDMAKAGIPRSILNTGHPG
l		1		i		KLMQTEVHHVRTLKIMLKVYS
İ	l	l				RALOEELOFSSKAIGRLFPCAD
		l				DLLETHSHFLAQTHERSGYVPL
	l					CVCATHTKFYEFMEDVNTAYT
		İ				KRHTMFRSLSMVSECLFSLING
		l				DDMFVTFAAMQAQQGRSSLV
l		l				WLFSQLYLYSFISLFIYMV
25127	55495	В	25265	44	238	· ·
25128	55496	Α	25266	1	444	MPAEFITG\ERS\SEGFF\RIHAGI
	İ				\	EQAISRGLAYAPYADLKNLDD
		l				KTIASFOOOLSDMGYKFOFITL
1		l			1	AGIHSMWFNMFDLANAYAQG
		l				EGMKHYVEKVQQPEFAAKKD
	i e	l				GYTFVSHQQEVGTGYFDKVTTI
		l				IQGGTSSVTALTGSTEESQF
25129	55497	Α	25267	710	1395	DLPGISSKWVIAVIFGHLIVGIFI
		i				PPAIIVRAGIT*RQVR/WIAAHE
		l				GKAPQQIIIMAHLDTYAPLSDA
		l			l	DADANLGGLTLQGMDDNAAG
		l				LGVTLQLAERLKNTPTEYGIRF
		l				VATSGEEEGKLGAENLLKRMS
		l				DTEKKNTLLVINLDNLIVGDKL
		l				YFNSGVQTLEARHQRSFNTVKP
		l				WPDSVISNRPFAGNTGSVDDND
		l				EIQRNLNDTNYNRMWEYNNRG
		1				VGSKVVAEAKK
25130	55498	Α	25268	2	2105	
2513I	55499	Α	25269	754	1133	RAANQHQTVDLTRLQTRIAQR
	1	1				LFNRHSQAIEQRQPQIFQFVLVK
	l				1	FAFPRFFLILPANVQWRLIATFC
						RFHTGVQGCQFTLVKRGPGDIR
						DYQQTNLDWYNSRNTTKLDES
						VNRV/HAAIQS*RQNGL
25132	55500	В	25270	1	1275	
25133	55501	С	25271	1	1167	

NO: of peptide sequence had in USSN mortal and in USSN more period sequence of peptide of peptide sequence of peptide of peptide sequence of peptide of peptide sequence of peptid	Common 1 4	Tono	1	1222-2-2-2-2			
25134   55502   A   25272   275   2424   SPAMHPQSFT/WQNNLDDNTIA SPQQHLSDMGYKFQFITLAGIH SMWFNMFDLANAYAQGGGMK HYVEKQQFFTAGIH SMWFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQFTTAGIH SWMFNMFDLANAYAQGGMK HYVEKQFTTAGIH SWMFNMFDLANAYAQGGMK ATALHYYTAKCAPPKTAGAK GENERAL SWMFNMFDLANAYAGGMTALSDLFG CRTSQRCPDKTRQRIRQPAR ALDVGCGYTALSDLFG CRTSQRCPDKTRQRIRQPAR ALDVGCGYTALSDLFG CRTSQRCPDKTRQRIRQPAR ALDVGCGYTALSDLFG CRTSQRCPDKTRQRIRQPAR ALGTSFKRLCAHYSRMKCWRI SGLRGAPFNICKCRRLRRIPG LRLRFPHSRVVFIFGGGNPR AKQRCTGEVEKCHQPQHGTK CCARGGFAACLVFEVVVVFWT SLPDSFCRKSFFTRIRGSMYPSL WDFPPGVDGRKGTSWMOYP PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSQPPIPLKFQAILQ/FHEIFGGSGHLASVAVESGYPP QFGSEETRAGARNRVANARR LLPFADFWAHEAGIGGDSTSS WVVIENASQRGARSATLPLPA VILEKVREGEALGFVMSRYTGI DEIGRREGAIGVTAGKTSKTWOYP QFGSEETRAGARNRVANARR LLPFADFWAHEAGIGGDSTSS WVVIENASQRGARSATLPLPA VILEKVREGEALGFVMSRYTGI DEIGRREGAIGVTAGKTAGA GMEKLPLGGFWTTQEAVRT GMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT AAASDLTTSGCOPTDEKATTG AAASDLTTSGCOPTDEKATTG AAASDLTTSGCOPTDEKAFT FORWARLQAQAHAKYPGKLLAYNCSSSSN WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIHARSP WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIFTAGKTTAG FAAKCGTTFTDLELARRI AQAHAKYPGKLLAYNCSSSSN WQKNLDDKTTASFQQQLSDMG YKFQFTTAGIFTAGKTTAG FAAKCGTTFTDLELARRI AQAHAKYPGTTAGKTTAG FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAAKCGTTTAGAT FAA	SEQ ID					Nucleotide location of last	
25134 55502 A 25272 275 2424 SPAMHFQSFT/WQNNLDDNTIA SFQMLSDMGYKFQFITLAGIH SNWFMMFDLANAYAQGEGM HYYEKVQOPEFAAAKDGYTFV SHQQEVGTGGYVASGNSLLIM RALNAAWGIIDCSNHFARLRC SVWSIPRSDLRCAAAFRTGRLA CCPAGDEKPYPSLRSSRWSGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGYTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLEG LHRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMKCWRII SGLRGARPKIVCRIRRLRRIRP IRLRFPHSRVYFFGGGNPRR AKQROTGEEVEKCHQPQHGTR CCARGFACLVFEVVVFWFY SLPDSFCRKSFFTRIRGSMVPSL WDFPPGVDGRKGKTSWNGVP PCVTCGIGLTCPSPCVGGLU PHEIFGEGSCHIASVAVESGVPP PCVTCGIGLTCPSPCCFGLU PHEIFGEGSCHIASVAVESGVPP QPFGSEETRAGARNANARR LLPEADFWVAIEAGIBGDSTFS WVVIENASQRGERASATILLPA VILEKVREGEALGFVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWTOZEAVRT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAJHAKYPGKLAVNCSSTW WQRNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWTNNFOLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJSDMG YKFQFTTLAGIBAWTNFOLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJSDMG YKFQFTTLAGIBAWTNMFOLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJSDMG	ino.		11100				
SFQQHLSDMGYKPQFITLAGIH SMWFMMFDLANAYAQGGGMM HYVEKVQQPEFAAAKDGYTFY SHQQEVGTGYYAASGNSLLLM RALNAAWGIIDSNIHFALRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA ALDVGCGYTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPCXTALSDLGG CRTCTA			l				, , , , , , , , , , , , , , , , , , , ,
SFQQHLSDMGYKPQFITLAGIH SMWFMMFDLANAYAQGGGMM HYVEKVQQPEFAAAKDGYTFY SHQQEVGTGYYAASGNSLLLM RALNAAWGIIDSNIHFALRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA ALDVGCGYTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPCXTALSDLGG CRTCTA							
SMWFMRFDLANAYAQGEGMM HYVEKVQPEFAAKDGYTFV SHQQEVGTGYYAASGNSLLM RALNAAWGIIDCSNHFARLRC SWWSIPRSDLRCAAAFRTGRIA. CCPAGDERPYPSLRSSRWGGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR LLRSCPFYFLRRAGAPVGI YCTGTPITPLESTRLFAPLPINC SMAGMYGIQPYPHPAIGARC LMRCTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMRCWRII SGLRGARPNKIVCRIRRLRRIPP LRLRFPRHSRVVFIFGGGNPRR AKQROTGEEVEKCHOPQHGTIK CCARGGFAACLVFEVVVVFVY SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLEFQAILQ/ FHEIFGEGSCHIASVAVESGYPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTFS WVVIENASQRGARSATLLPLA- VILEKVREGEALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGPVTGCEAVRT VRARLQADVTGVFTVLVARTT ADASDLITSDCDPYDSEMTIGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPUELARRR AQAHAKYPGKLLAYNCSSESN WQNILDDKTIASFQQQLSDMG YKFQFTTAGIBRMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSGVGTGY FFRAKTUTINGGTFDKAFT	25134	55502	A	25272	275	2424	SPAMHFQSFT/WQNNLDDNTIA
HYYEK VQQPEFAAALÖGYTFV SHQQEVGTGVYAASGNSLLLM RALNAAWGIIDCSNIHFARLRE SVWSIPRSDLRCAAAPTGRLA CCPAGDEKPYPSLRSSRWSGR ATALHYYTAKRCEPDKTRQRR RQPARALDVGCGYTALSDLPG CRTSQRCRPDKTRQRRRRIRPAR ALDVGCGYTALSDLPG GCTSQRCRPDKTRQRRRRIRPAR ALDVGCGYTALSDLRGAALHG SLANYRVNFLERIPDAMILES LLRSCPFVFPLLRRLRAGAPVGI YCTGFPTPLPSTRLFAPLPNEC SMAGMYGGLQPVPHPAIGARC LMRCLTHLRPTMGTGSMAEE ALGTSFKRLCAHYSMRCWRIII SGLRGARPNKIVCRIRRLRRIRP LELRPRHSRVYFFGGGNPRR AKQROTGEEVEKCHOPQHGTR CCARGGFAACLVFEYVVVFWT SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVP PCVTCGIGLTCPSPCCPGLSL DGYPEKVSVGPPPLKFQALQA FHEIFGEGSCHIASVAVESGVPE QPFOSEETRAGARNAVARRR LLPEADFWAIEAGIDGDSTFS WVVIENASRGERASTALPLAP VILEKVREGEALGPVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VRARLQADVTGVFTVLVARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAJHAKYPGKLLAVNCSSFN WQRNLDDKTIASFQQDLSDMG YKFQFTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQEVGTGY FGKVYTTIJQGGTFDKAFT			1				
SHOQEVGTGVYAASGNSLLLM RALNAAWPGIDCSNHFARLRC SVWSIPRSDLRCAAFTTORLA CCPAGDERPYPSLRSSRWGGRC ATALHYYTAKCREPIXTRORR RQPARALDVGCGVTALSDLPG CRTSQRCRPDKTTRQRRIRQPAR ALDVGCGVTALSDLRGALHGE SLANYRVVNFLFRLPDAMILSV LLRSCFPVFPLLSBLRGAALPGG YCTGTPITPLPSTRLFAPLPNRC SMAGMYGGLQVPHPAIGARC LMRCLTHLIRPTMGTSMAEE ALGTSFRRLCAHYSRMRCWRII SGLRGARPNICVCRRIRLRIRGP LRLRFPRHSRVVFIPGGGNPR AKQROTGEEVEKCHOPOHGTIK CCARGGFAACLVFEVVVVFWT SLPDSFCRRSFPTRIRGSMVPSL WDFPPGVDGRRGKTSWNOYPG PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLFFQAILO FHEIFGEGSCHLASVAVESGVPF QPFGSEETRAGARNRVANARR LLPFADFWAHEAGINGDSTSS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRREGAIGVFTAGKLTAG 25135 55503 A 25273 I 441 25136 55504 A 25273 I 441 25136 55504 A 25273 I 441 25137 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLTISDCDPYDSEMTIGE RTSGGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQRILDDKTIASFQQU.SDMG YKFQFTTLAGIBRWTNMFDLA NAYAQGEGMKHVVEKVQQPE FAAAKDGVTFVSHQUSGTDY FFEKTYTTINGGTFDKAFT			Ì				SMWFNMFDLANAYAQGEGMK
RALÑAAWGIIDCSNIFIARLRC SVWSIPRSDLRCAAAFRTGRLA CCPAGDEKPYPSLRSSRWSGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGYTALSDLGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLGG SLANYRVVNI-ERLPDAMILSV LLRSCPYPFLLRRLRAQAPVGI YCTGFTIFTLPSTRI-PADPINGE SMAGMYGGLQPYPHAJGARC LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMKCWRII SGLRGARPKRIVCRIRRLRRIRP IRLRPPHSRVVFIFGGONPRR AKQROTGEEVEKCHOPQHGTK CCARGFAACL VFEVYVVFWT SLPDSFCRKSFFTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PC-VTCGLGLTCPSPCVGGLLC DGYPEKVSVGPPIPLKFQAILQ/ FHEIFGEGSCHLSVAVESGVFP QPFGSEETRAGARNANARR LLPEADFWAIEAGIBGDSTFS WVVIENASQRGERASATLLPA- VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25135 55503 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFFWTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRR AQAJHAKYPGKLAVNCSSSFN WQRNLDDKTIASFQQQLSDMG YKFQFTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONDM	1		1				HYVEKVQQPEFAAAKDGYTFV
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CCARGGPAACLVFEYVVFWT SLPDSFCRKSFTTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PCVTCGGLTCPESPCCPGLSLC DGVPEKVSVGPPPLKFQAILQO FHEIFGEGSCHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGOSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTARS 25136 55504 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQADVTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FEKVYTTIQGGTPDKAFT			l				LRLRFPRHSRVVFIFGGGNPRR
CCARGGPAACLVFEYVVFWT SLPDSFCRKSFTTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PCVTCGGLTCPESPCCPGLSLC DGVPEKVSVGPPPLKFQAILQO FHEIFGEGSCHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGOSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTARS 25136 55504 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQADVTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FEKVYTTIQGGTPDKAFT	1		l				AKOROTGEEVEKCHOPOHGTK
WDFPPOVDGRKGKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVCPPPLKFQALQO FHEIFGEGSCHIASVAVESGVPE QPFGSETRAGARNVANARR LLPEADFWVAIEAGIBGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRVTGI DEIGRKEGAIGVFTAGKLTRAS  25136 55504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQADVTGVPTVLVARTI ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WGNILDDKTIASFQQQLSDMG YKFQFTLTAGIBAWWTNMFDLA NAYAGGEGMKHYVEKVQQPE FAAAKDGYTFVSHQGVGTGY FDKVTTIIQGGTPDKAFT			1				CCARGGFAACLVFEYVVVFWT
PCVTCGLGLTCPESPCCPGLSLC DGYPEKYSVGPPIPLKFQAILQA FHEIFGEGSCHIASVAVESOVPE QPFGSEETRAGARNRVANARR LLPEADPWAVIEAGIGDOSTES WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGVFTAGKLTRAS 25135 55503 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/VTGVPTVLVARTL ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAV APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAARCDGYTFVSHQQSVGTGV FFKVTTIIQGGTPDKAFT			l	1		ì	SLPDSFCRKSFPTRIRGSMVPSL
DGYPEKVSVCPPIPLKFQALLQA FHEIFGEGSCHIASVAVESGVPE QPFGSETRAGARNRVANARR LLPEADPWAIEAGIBGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VERALQADVTGVFTVLVARTT ADASDLITSDCDFYDESFMTGE RTSEGFFRTHAGIEQAISKGLAV APYADLVWCETSTPDLELARRI AQAIHAKYPGKLAVNCSSFS WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQSVGTGY FEKVYTTIJQGGTFDRAFT			l				WDFPPGVDGRKGKTSWNGVPG
DGYPEKVSVCPPIPLKFQALLQA FHEIFGEGSCHIASVAVESGVPE QPFGSETRAGARNRVANARR LLPEADPWAIEAGIBGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VERALQADVTGVFTVLVARTT ADASDLITSDCDFYDESFMTGE RTSEGFFRTHAGIEQAISKGLAV APYADLVWCETSTPDLELARRI AQAIHAKYPGKLAVNCSSFS WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQSVGTGY FEKVYTTIJQGGTFDRAFT			l				PCVTCGLGLTCPESPCCPGLSLG
FHEIFOEGSCHIASVAVESGVPE QPFGSETRAGARNRVANARR LLPEADPWVAIEAGIDGDSTFS WVVIENASQRGEARSATLPLPA VILEKYREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25135 55503 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQ/EAVRT VRARLQAD/VTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRS AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTLTAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FDKVTTIQGGTPDKAFT			l				
QPGGSETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVTGAGKLTRAS  4 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/VTGVPTVLVARTT ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRR AQAIHAKYPGKLLAYNCSSFSN WQRNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWTNMFDLA NA YAQGEGMKHYVEKVQQPE FAAARDGYTVSHQQEVGTGY FEKVYTTIJQGGTPDKAFT			l				
LIPEADFWAIEAGIDGDSTES WVVIENASQRGEARSAIT.PLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25136 55504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQAD/VTGVPTVLVARTI ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSPN WGNILDDKTIASFQQDLSDMG YKFQFITLAGIBRWFNMFDLDL NAYAGGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FPKVTTIQGGTPDKAFT			l	1			
25135 55503 A 25273 I 44I 25136 55504 A 25273 I 44I 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQ'EAVRT VRARLQAD/TGVPTVLVARTE ADASDLITISGCPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFGPTTAGIBRWFNMFDLA NA YAQGEGMKHYVEKVQQPE FAAARDGYTFVSHQQVGTGY FEKVYTTIJQGGTPDKAFT			l				
VILEKVREGEALGPVMSRYTGI			l	l			
DEIGRKEGAIGVFTAGKLTRAS	i		l				
25135   55503			l				
25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQAD/VTGVPTVLVARTI ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSN WQKNLDKTIASPQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIQGGTPDKAFT	25125	55502	<u> </u>	25272	1	441	DESCRICTION TO THE PROPERTY OF
GMEKLPLGGKFWPTQ/EAVRT VRARLQAD/VTGVPTVLVARTE ADASDLITSDCD/PYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FPKVTTIQGGTPDKAFT							A VSNCSEGI SK EWGPRPCRHP
VRARLQAD/TGYPT\L\ARIT ADASDLTSDCDPYDSEMTGE RTSEGFFRTHAGIEQAISRCLAY APYADLVWCETSTPDLELARRI AQAIHAKYPGKLAYNCSFS WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWFNMFMEDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FEKVTTIIQGGTPDKAFT	23130	33304	ľ	23214	ľ	2515	
ADASDLTSDCDPYDSEFNTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAIHAKYPOKLLAYNCSPSFN WQKNLDMKTIASFQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FPKVTTIQGGTPDKAFT			l				
RTSEGFERTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWWENMEDLA NAYAQEGMKHYVEKVQQPE FAAAKDGYTFVSHQSVGTGY FEKVTTIIQGGTPDKAFT	ı		l				
APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSTN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FPKVTTIQGGFPDKAFT			1		ì		
AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FPKVTTIQGGTPDKAFT			l		l		
WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT			l		i		
YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQFE FAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT			1	1	l	1	
NAYAGGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT	İ		1		l	1	
FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT			1			1	
FDKVTTIIQGGTPDKAFT			1	l	l		
			1	l	I		
[25137   55505   A   25275   432	25125	55505	I.—	250#5	430	5.00	FDKVTTIIQGGTPDKAFT
	25137	55505	A	25275	432	549	

NO: of p	O ID NO: No eptide l'ence		SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25138   555		A	25276	652	2689	KFSVGYAVONFNATVSTKOFO VFSEQNTSSYFAEPQLDVNYYQ NDVVHFVTTRDDMPEATRYHL EPTINLPLSNNWGSINTEAKLLA HYQQTINLDWYNSKNTTKLDE SVNRWMPOFKVDGRMVFERD MEMLAPOYTOTLEPRAQYLLYV PYRDQSDIYNYDSSLLQSDVSG LFRDRTYGGLDRIASANQVTTG VTSRIYDDAAVEEFNISVGQIV YFTESRTGDDNITWENDDKTGG QVDTRLDNVATSNSSIEYRRDE DRLVQLNYRYASPEYIQATLEPN VHHITMEHHMKTRTQQIEEL QKEWTOPRWEGITRRYSAEDV VKLRGSVPFECTLAQLGAK WRLLHGESKKGYINSLGALTG GQALQQAKAGIEAVYLSGWQV VKLRGSVPFECTLAQLGAK WRLLHGESKKGYINSLGALTG GQALQQAKAGIEAVYLSGWQV ADANLAASMYPDQSLYPANS VPAVVERINNTFRRADQIWSA GIFEOPRYVDYFLPIVADAG GFGGVLNAFELMKAMIEAGAA AVHFEDQLASVKRMRHMGRT ASDQPWLAYAPYADLVWCEPP PPDLELARRRAQAIHAKYPGKL LAYNCSPSHWGNLDHDKYGKL HYVEKYQGEGYAR WRYNMFDLANAVAQEGMK WRYNMFDLANAVAGEGMK WRYNMFDLANAVAGEGMK HYVEKYQGEFAAAKDQYTFV SHQQEVGTGYPDKYTTIIQGT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25139	55507	IA	25277	1134	1695	I FPDPARLPPVSVNHHITMEHLH
23139	33307	ΙΑ .	23211	134	1093	
	1	1				MKTRTQQIEELQKEWTQPRWE
	1	1			l	GITRPYSAEDGGKLRGSVNPEC
		1				TLAQLGAAKMWRLLHGESKK
		1				GYINSLGALTGGQALQQAKAG
	1	1				EAVYLSGWQVAADANLAASM
l		ŀ				YPDQSLYPANSVPAVVERINNT
1				į		FRRADQI/QWSAGIEPGDPRYV
1		1				DYFLPIVADAEAGFGGVLNAFE
1					1	LMKAMIEAGAAAVHFEDQLAS
1		1				VKKCGHMGGKVLVPTQEAIQK
1				ŀ		LVAARLAADVIGVPTLLVART
		i				DADAADLITSDCDPYDSEFITGE
1		1		1		RTSEGFFRTHAGIEQAISRGLAY
İ						APYADLVWCETSTPDLELARRI
1		1				AQAIHAKYPGKLLAYNCSPSFN
	1					WQKNLDDKTIASFQQQLSDMG
						YKFOFITLAGIHSMWFNMFDLA
						KAYAOGEGMKHYVEKVOOPE
						FAAAKDGYTFVSHQQENRSSK
		1				QQQPLLTVGRIRRSRRIRQSVPR
		1		l		TGIGCASRRFNTAKPWADAVIS
1	1					
1		1				NRPFAGNTGSVDDNDEIQRNLN
		1		i		DTNYNRMWEYNNRGVGSKVV
25140	55508	A	25278	230	380	AEAKK
25140	55509	A	25279	432	1247	PSQEPSVHGRWMA*KGHSRIV*
23141	33309	^	23217	1732	1247	WRAYD*TH\FNPVLKKSVSLGS
	1	1				NIRHMLAEEATTEELDGT\GPV
i	1	1	1			LV*PNRH*PAYWMRAYLNLKK
1						MSCRSFRRKA*RW*CETOTVV
1	1					
1	1					HRDRVDQGNNHFDVVARHYH
1						LYAFLRKERQLIFFKFKYARIQY
		_				AG
25142	55510	Α	25280	243	430	RRPSYSVLQRLPSAVLLPYY*R
						DWYHRTAGRRRDGNAGRQHQ
		_				NGCYPDPPDRDGRRSAFRNP
25143	55511	A	25281	10	638	SSVPTAGSRYNHLRAPRYSPLF
1		1	ŀ			ANYSMSDRCCKPFG/LDSSTG*
		1				WFQ*RSVPLPILLPDTSRHQL*C
1	1	1	ļ.			SDPTRNGPA\QACQRFFHIVERV
		1				ARVHHARFAATVTVDHVVIDQ
1	1	1	1	1		RFFQICRT/PWCRLHRHHWRSS
1	1	1				GTR*TF*SPARHFCLLHNDSSYR
i		1		1		STARPTCSGTDVPDRRCSDAHL
1	1	1	1			CDHWSGSRAHADTDAECWCL
		1				NPQPAPSLLQCRR
25144	55512	A	25282	803	1622	· · · · · · · · · · · · · · · · · · ·
25145	55513	A	25283	498	686	RRPSYSVLQRLPSAVLLPYY*R
1	1	1				DWYHRTAGRRRDGNAGRQHQ
1		1	1	1		NGCYPDPPDRDGRRSAFRNP
1	1		1	L	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nueleotide insertion)
25146	55514	Α	25284	1	2063	MKNFMENVLRYLSDDKWKPD
		1				AKASMTVGTNLDTVYFKRHGQ
	l	l				VTGNSAAFDFHPDFAGISVEHL
	İ	1				SSYGDLDPQEMPLLILNGFEYV
	İ	1				TQVGNDPYAIPLRADTSKPKLT
						QQDVTDLIAYLNKGGSVLIMEN
						VMSNLKEESASGFVRLLDAAG
	1			ł		LSMALNKSVVNNDPQGYPNRV
		1				RQQRATGIWVYERYPAVDGAL
		1				PYTIDSKTGEVKWKYHVENKP
		l				DDKPKLEVASWLEDVDGNRKR
						NFSNDARANGTAAFTDCETQT
		l				VVHRDRVDQGHNHFDLVARH
		1				YHLYAFRQFDGTSHVSSTEVEL
		1				RTVAFEERSMTAAFISWTECTL
					ļ	QIRTCPQNPTGKVWTCDELEIM
		1				ADLCERHGVRVISDEIHMDMV
						WGEQPHIPWSNVARGDWALLT
		l				SGSKSFNIPALTGAYGIIENSSSR
					İ	DAYLSALKGRDGLSSPSVLALT
	1					AHIAAYQQGAPWLDALRIYLK
			•		1	DNLTYIADKMNAAFPELNWQIF
	1	1			i .	QSTYLAWLDLRPLNIDDNALQ
		1				KAL\IDQEKVAIMPGYTYGEEG
		l				RGFVRLNAGCPRSKLEKGVAG
					1	LINAIRAKKSATMIDTTLPLTDI
		1				HRHLDGNIRPQTILELGRQYNIS
		1			1	LPAQSLETLIPHVQVIANEPDLV
					1	SFLTKLDWGVKVLASLDACRR
					1	VAFENIEDAARHGLHYVELRFS
	1					PGYMAMAHQLPVAGVVEAVID
						GVREGCRTFGVQAKLIGIM
25147	55515	Α	25285	3	371	
25148	55516	Α	25286	63	180	
25149	55517	Α	25287	2	205	
25150	55518	Α	25288	495	707	REFSSHQKGLRDRPAHKAVLG
		1			1	DNQLFSGGTGAPVWPG/HSENV
		1			1	VPVDPT\MKRLPDDVNHPALDY
	1	l				YWRLSFA

NO:	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
25151   55519   A   25289   I   1713   MTWAYSPSYGKPLSVPQGIIG MTRRGMDVTLAHPEGYDLIF VVEVAKNAKASGGSFRQV MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVALISHEM SCKEGRSDQKAYDEKSRPDE PIDDNVVLIKGGVLQVRSGDV RVKTLADRIGFISHSQVTDLL CAFFVIGIMIGMITFOFSTESF MCNAAGLIFAGIMLGFMRAA PTFGYIPQGALSMVKEFGLM MAGGIQVDGNTIYPHIWKSC GVLFAKQYLLRIGIILYGFRI SQIADWIGSIIDVLTLSSTFI ACFLQQK VFGLDKHTSWLIG GSSICGAAAVLATEPVVKAE KVTVAVATVVIGFGVAHFLY YPLMSQWFSPETFGIYIGSVII GVDVPNASLMIENPERILGL LHQLRGRVGRGAGLLTACCS KRRILKAAPEVTRTGLADDR GLPQTGYGLASMQGLDVVV LSPQGTDTFAMLDAFRANEA AAPLPLTANSDCNGYWRLDL LHQLRGRVGRGAGLLTACCS KRRILKAAPEVTRTGLADDR GLPQTGYGLASMQGLDVVV LSPQGTDTFAMLDAFRANEA AAPLPLTANSDCNGYWRLD HCWPADISGVSCKGGEVTEG EKYRIATYKEASWKPYILAA CPVNTTPNQVHCSSNC HCWPADISGVSCKGGEVTEG EKYRIATYKEASWKPYILAA CPVNTTPNQVHCSSNC CPVNTTPNQVHCSSNC CPVNTTPNQVHCSSNC CPVNTTPNQVHCSSNC GEVTEG EKYRIATYKEASWKPYILAA CPVNTTPNQVHCSSNC GUTEG EKYRIATYKEASWKPYILAA CPVNTTTPNAMATTPNAMATA CPVNTTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATT						of peptide sequence	deletion, \=possible nucleotide insertion)
MTRIGMDVTLAHPEGYÖLLE VVEVAKNNAKASGGSRQV MEEAFKDADIVYPKSWAPYY MEERTELLRANDHEGVKAP HCLAQNAQHKUWHISIEME EPITREGEAQNKHGRPAEING SCKEGRSDCKAYDEKSRPDE PIDDNVVLNKGDVLQVSGDV RVKTIADRIGFISHSQVTDLL CAFFVIGLMIGMITPOFSTSST MGNAAGLLFAGIMLGFMRA PITGYIPQGALSMVKFGILM MAGEIQVDGNTIYPHIWSSC GVLFAKQYLLRLGIILYGFRL SQIADVIGSGIIDVLTLSSTFL ACFLGQKVFGLDKHTSWLIG GSSICGAAVLATEPVVKAE KVTVAVATVVIGTVAILTY! YPLMSQWFSPETFGIYIGSVII GVDVPNASMIIENPERIGL. LHQLRGRVGRGAGLLTACC KRRILKAAPEVTRTGLADDR GLPLQTGYELASMQGLVDVU LSPQGTDTFAMLDAFRANEN AAPLPLANSDCNGYWRLL DHEGLKALLEKQCLAQNAQ-D WHCTEEMMELTRDGGALY HCWPADISGVSCKEGEVTEG EKYPIATYKEASWKPYIIAAN CPVNTPNQVHCSSNC  25153 55521 A 25291 235 780  TYRNNHQTIGVAFLFQTIKF HGGGKTGFGFRRGKA GIFLYNNQLQPDIVHGGFCTF HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNKMPRIGVG GWAYLQGYPVRFGVWPLEE AYACGKFNGAIRAGDAAQL YAQAFQLHGIPIDAGGAGVW					sequence		
MTRIGMDVTLAHPEGYÖLLE VVEVAKNNAKASGGSRQV MEEAFKDADIVYPKSWAPYY MEERTELLRANDHEGVKAP HCLAQNAQHKUWHISIEME EPITREGEAQNKHGRPAEING SCKEGRSDCKAYDEKSRPDE PIDDNVVLNKGDVLQVSGDV RVKTIADRIGFISHSQVTDLL CAFFVIGLMIGMITPOFSTSST MGNAAGLLFAGIMLGFMRA PITGYIPQGALSMVKFGILM MAGEIQVDGNTIYPHIWSSC GVLFAKQYLLRLGIILYGFRL SQIADVIGSGIIDVLTLSSTFL ACFLGQKVFGLDKHTSWLIG GSSICGAAVLATEPVVKAE KVTVAVATVVIGTVAILTY! YPLMSQWFSPETFGIYIGSVII GVDVPNASMIIENPERIGL. LHQLRGRVGRGAGLLTACC KRRILKAAPEVTRTGLADDR GLPLQTGYELASMQGLVDVU LSPQGTDTFAMLDAFRANEN AAPLPLANSDCNGYWRLL DHEGLKALLEKQCLAQNAQ-D WHCTEEMMELTRDGGALY HCWPADISGVSCKEGEVTEG EKYPIATYKEASWKPYIIAAN CPVNTPNQVHCSSNC  25153 55521 A 25291 235 780  TYRNNHQTIGVAFLFQTIKF HGGGKTGFGFRRGKA GIFLYNNQLQPDIVHGGFCTF HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNKMPRIGVG GWAYLQGYPVRFGVWPLEE AYACGKFNGAIRAGDAAQL YAQAFQLHGIPIDAGGAGVW	25151	55510	Ι	25280	1	1713	MTWAYSPSYGKPI SVPOGUGI
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HISEELATFIVRGFRFRRGKA GIFLYNNOLOPDIVHRGFCTE HIDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGGGVYR			1				DGGVKTFDGYRVQTQSRHAEQ
GIFLVNNQLQPDIVHRGFCTE HDVRGIKHFTLVEHVITGSGI NTIRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL. YAQAFQLHGPIDAGDGVNR			1				EVTDVEINLFCHPLCIIMQIFTV
HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGDGVAF			1				HISEELATFIVRGFRFRRGKAAI
NTRFTFFRAGNNKMPRLGVC GWAVLQGYPVRFGVWPLPE AYACGKFNGAIRAGDAAQL, YAQAFIQLHGPIDAGGVYR							GIFLVNNQLQPDIVHRGFCTEH
GWAYLGGYPYRFGYWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGDGYNF						1	HDVRGIKHFTLVEHVITGSGFG
AYACGKFNGAIRAGDAAQL, YAQAFIQLHGPIDAGDGVNR			1			1	NTRFTFFRAGNNKMPRLGVGA
YAQAFIQLHGPIDAGDGVNR			1			1	GWAVLQGVPVRFGVWPLPEYP
			1				AYACGKFNGAIRAGDAAQLAA
			1		1	I	YAQAFIQLHGPIDAGDGVNRA
DHRAGDFFEIVFQNLFAIADV			1			i	DHRAGDFFEIVFQNLFAIADVD
LAINHAVNAQLRLRNP	l .		L				LAINHAVNAQLRLRNP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first eodon for peptide sequence	codon for last amino aeid of peptide sequenee	*-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
		l				
25155	55523	Α	25293	365	722	TSCLSALAIK/QQHLDEKKELG
		1				HLSAGARRLILGIIVTF/CADSG
		1			İ	VNLRYSAV*PAGAVYLPDAAV
		1				GGSADRTADAGALLGANVDCA
				1	1	VADRFLPLYLVALHLYAELGRS
						GQPGVRAYSALR
25156	55524	Α	25294	798	1094	
25157	55525	Α	25295	1	2780	MGIVA\$A\$VQAAEIYNKDGNK
						LDVYGKVKAMHYMSDNASKD
						GDQSYIRFGFKGETQINDQLTG
	İ					YGRWEAEFAAWTDMFPEFGG
	1	1				DSSAQTDNFMTKRASGLATYR
ļ		1			İ	KTTSSAYRWPELNLQYHRCTS
		1				AARAMLLSGRPVMQINERTAV
l		1				RRQMTVYLRVERIHEIDPLVSL
		1		1		SHSMSVIPIDVERPIAAAPCTPG
		l				LWRTKTPLRVPSTYPLRLPGRA
			1			RVVCHRTFRLHLCKDWVFMFS
						GLLIILVPLIVGYLIPLRQQA
25158	55526	Α	25296	66	300	QSTYCDNPPVPVSRGL*P*RRSS
1		1				STSSAGYQK*RYCQHRHDPASR
1		ŀ				IRTVQRTDSQRTVKRKFMLLVP
1						EASVPASEIC
25159	55527	A	25297	240	424	RCSRDEHDFQLIANLRIVVITFA
		i i				TFA*CTA*LPLGNHSVVAAH*A
						G*GGAPVTAQVFVQHG
25160	55528	A	25298	1	1425	
25161	55529	Α	25299	I	471	
25162	55530	A	25300	1269	1390	
25163	55531	A	25301	601	1119	VAAGAV*RGH*NVQLGKLFFV
		1		1		ASDLRINAIAGGVVVFS*FIQGL
		1	l	i .		TNAIGSGFNNARCRKPTGQVA
		1		1		ADGGRDAGFFTIANNQCTYAA
				1		GIFFQCSGEFVGIQFQFAIAGIGR
		1		1		DTNLRQRFIAGRTDGITQHRFQ
1				1		LRLNRPQRGVAEQCTIARTLAIS
		_				SRMAVYLVRLLKVSISEL
25164	55532	Α	25302	1666	1769	RLKRHPPLRPSWPPY*TGAHVW
						HFSPLANWKPGI
25165	55533	Α	25303	1	1970	MKDDIFFRTSGGGVTLSGGEVL
				1		MQAEFATRFLQRLRLWGVSCA
	ŀ			1		IETAGDAPASKLLPLAKLCDEV
	1			1		LFDLKIMDATQARDVVKMNLP
	1	1	1	I		RVLENLRLLVSEGVNVIPRLPLI
		1				PGFTLSRENMQQALDVLIPLNIR
	1	1				QIHLLPFHQYGEPKYRLLGKTW
l	1	1		1		SMKEVPAPSSADVATMREMAE
l		1	1	1		RAGLQVTVGEKWGVSIETQGA
l		1		1		LGTENRLADEDIRRADVALLIT
1	1		1			DIELAGAERFEHCRYVQCSIYA
1	1		1	1	1	FLREPQRVMSAVREV

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25166	55534	A	25304	2804	3494	LSLAEWKCLNPSQRALYREVM
23100	33334	^	23304	2804	3434	LENYRNLEAVGQLQPQSTQRIP
						*GRICNGDRLTSQKGLDL\VLEA
			-			LPGLL\EOGGQLALLGAGDPVL
						QEGFLAAAAEYPGQVGVQIGY
						HEAFSHRIMGGADVILVPNRFE
i		l				PCGLTQLYGLKYGTLPLVRRTG
						GLADTVSDCSLENLADGVASG
i						FVFEDSNAWSLLRAIRRAFVLW
						SRPSLWRFVQRQAMAMDFSW
		L				Q\VAAKSYRELYYRLK
25167	55535	A	25305	1	1306 1658	
25168	55536	A	25306	2611	2826	
25169	55537	A	25307			
25170	55538	Α	25308	609	2359	PPPKIAPV WGCRKKSLPARSKSI
1						FCFALFFPFFLNGEIILPESPCPF
1	:					WTLFRNDGGKKRDPLAPVYLL
						GKLTISPGPICPDMIGVLFDSTV
						RREVAHIGNVQHRFCGPLFLKL
						VEFIDFILTIDIAAIIRQYLVVICE
					1	VDQRINQIAIATRIFRTGYTAAD
ŀ						LRQIILMQLLIFLVVFTRFVALT
l l	ł				1	TQFFHFFRCVTKNKDIVSTDMI
					1	QHLDIRTVQRTDSQRTVKRKLH
					1	VTGAGSFRPCQRNLFRQICRRN
	l				1	DQLRQANAVVRDEHDFQLIAN
l					1	LRIVVDHFRYVIDQMNNVLRH
ŀ					1	VIGRSRLTAKNIHARYPLRIRVG
ŀ						LDAVIAEMASGLDPFWRPDVV
l						HAHDWHAGLAPAYLAARGRP
1		ĺ				AKSEFTVHNLAYQGMFYAHH
1	1					MNDIOLPWSFFNIHGLEFNGOIS
l						FLKAGLYYADHITAVSPTYARE
1						ITEPOFAYGMEGLLQORHRERR
1						LFGVLNGVDEKIWSPETDLLLA
						SRYTRDTLEDKAENKROLONA\
1						MGLKVDDKVPLFAVVSRLTSQ
1						KGLDLVLEALPGLLEQGGQLA
l						
1				1		LLGAGDPVLQEGFLAAAAEYP
1		1	1		I	GQVGVQIGYHEAFSHRIMGGA
						DVILVPSRFEPCGLTQLYGLKY
1		l	1			GTLPLVRRTGGLADTVSDCSLE
		ĺ				NLADGVASGFVFEDSNAWSLL
I		l	1			RAIRRAFVL/WSRAGSWRYSAR
1		l				AIRCCRKVSLRRQRNTPVRWAF
1	1	ı	1	J _		RLAITKHFRIALWAARTSFWCP

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25171	55539	A	25309	1028	1632	TSASAGTARNFSSNFAVRTTGH STSEATSSSRSILS KSALPHEL SASALMFFVIGDDFPTSRRISG Y*SALSMVNSGSPIKRWPRITRS DYMPRMVAGMTLSPMQQGHG VHRTHEVHVVAPQRISFGIGSF AREVATIFESSASVFRR*YRNH APPALLTLCSVCLQRRTPGQSPG RVFRHDDPVAFRQVSYFQRQTP IA
25172	55540	Α	25310	1	336	
25173	55541	A	25311	1889	2257	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTVCTGRTKCTSL APQRISFGIGSFAREVATRRPYR DIKEGFSQREAALLPQSLRVPQ TGTWSAAGAQA
25174	55542	В	25312	1	735	
25175	55543	Α	25313	1439	1744	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPMQQGHVPWQLMVVL WNTRQRWKPSSPDRYVNRAMS LPSRKGEMLKPAPCRK
25176	55544	A	25314	1209	1972	SAMTPPRSRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTVCTGRTKCTSL AGVILSPSSRGYSFAREVATIFCSSA SVHFALHMGAIQQPFAFIGSQT LSLVNGNTATTPCPSALLGLP SASNAWAIAGPFRSISRSGASA RLATFSARRRGASKPLNGCLR ATLSSPDKFQQGSTGGMLWGV LKHSPKFSITADGREFTLHVPN TGAMTGCATPGEYVWYSTEDN TGRKYPHPWEL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, +=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
25177	55545	Α	25315	ļi .	1521	METQHRLMRTFQPRQQDWTY
						ALWGGVKLRWLFFFLWGLFLF
						AGEEELGIRQTRTNDFLVTGDN
						LLRIFRFDVGNEDKVRQQFAVV
						RIHREVFLVTFHGVNQRFSRHR
	İ				İ	EEFLFEFCVTPKLNEGTTQRTN
						NRGIAVLNTGHRHPDLVAAVE
į .						QQLQQFTHTAYQIVPYESYVTL
ľ	i					AEKINALAPVSGQAKTA\FFHP
					İ	GSETG\ENGVKMVRAHTGTPG
						V\IAFRGG\FHGRTYMTMALTG
						KVAPYKIGFGPFP\GSVYHVPYP
	1					SDLHGISTQDSL\DAIERLFKSDI
						EAKQVAAIIFEPVQGEGGFNVA
						PKELVAAIRRLCDEHGIVMIAD
l		1				EVQSGFARTGKLFAMDHYADK
		1				PDLMTMAKSLAGGMPLSGVVG
		1				NANIMDAPAPGGLGGTYAGNP
1					i	LAVAAAHAVLNIIDKESLCERA
İ		1				NQLGQRLKNTLIDAKESVPAIA
		1				AVRGLGSMIAVEFNDPQTGEPS
						AAIAQKIQQRALAQGLLLLTCG
				_		AYGNVIRFLYPLTIPDAQFDAA
25178	55546	Α	25316	114	187	RSTISSVRYGDDAFKP*RQAWN
						VL
25179	55547	Α	25317	105	317	YLFFLSRFNHWISMEKKLGLSA
		1			i	LTALVLSS\SWARVFSVCRKIW
		1			1	RQLPARQHCSSAGVLLALAFYC
						WPLPC
25180	55548	Α	25318	1	593	
25181	55549	Α	25319	1	729	
25182	55550	A	25320	l	1005	
25183	55551	Α	25321	1	1361	
25184	55552	В	25322	1	2793	
25185	55553	Α	25323	27	255	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25186	55554	A	25324	225	1408	RIIYMHMESOKIWFALSTPMEIR
						NECCLPSHSSPKMYLGACLF\PL
		1				SSSWGIDDRDDLLRTIHRMIDN
1		l				GHAARLAGFYHRWFRYSPCEW
		1				RDYLAELNEOGOAYAOFVAST
1						AECCGEGGIKAWDYVRMGFLS
		ĺ				RMGVLNNWLSEEESLWIOSRIH
						LRALRYYSNWRQYFAGYTFGR
						OYWOSPEDDHLPLLREFLAGET
						TDVDIIRRAYLALLPSFHTETDP
						QGFKQLRHAYDDALPIAQSPAK
						SVLOPEEYEWEALLVEMLGLL
		i				HRIAMVQLSPAALGNDMAAIE
						LRMRELARTIPPTDIQLYYOTLL
						IGRKELPYRTCQLHACTSADTP
						LRKIPRFSGKLHFYAFCPNIYSS
		1				YHSAAKYGGSCOPGSTAHRLG
						YYWRWHFIAGLCHADPHAHSS
25187	55555	Α	25325	230	380	
25188	55556	Α	25326	432	1247	PSQEPSVHGRWMA*KGHSRIV*
		1				WRAYD*TH\FNPVLKKSVSLGS
						NIRHMLAEEATTEELDGT\GPV
						LV*PNRH*PAYWMRAYLNLKK
					1	MSCRSFRRKA*RW*CETQTVV
						HRDRVDQGNNHFDVVARHYH
						LYAFLRKERQLIFFKFKYARIQY
						AG
25189	55557	Α	25327	10	638	SSVPTAGSRYNHLRAPRYSPLF
						ANYSMSDRCCKPFG/LDSSTG*
				ł		WFQ*RSVPLPILLPDTSRHQL*C
				1		SDPTRNGPA\QACQRFFHIVERV
						ARVHHARFAATVTVDHVVIDQ
		1				RFFQICRT/PWCRLHRHHWRSSS
						GTR*TF*SPARHFCLLHNDSSYR
						STARPTCSGTDVPDRRCSDAHL
						CDHWSGSRAHADTDAECWCL
		_				NPQPAPSLLQCRR
25190	55558	Α_	25328	803	1622	
25191	55559	A	25329	498	686	RRPSYSVLQRLPSAVLLPYY*R
						DWYHRTAGRRRDGNA GRQHQ
						NGCYPDPPDRDGRRSAFRNP

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO;	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	-	1		sequence		
		_		L		
25192	55560	Α	25330	I	2063	MKNFMENVLRYLSDDKWKPD
					1	AKASMTVGTNLDTVYFKRHGQ
		l				VTGNSAAFDFHPDFAGISVEHL
		l				SSYGDLDPQEMPLLILNGFEYV
		l				TQVGNDPYAIPLRADTSKPKLT
		1				QQDVTDLIAYLNKGGSVLIMEN
		l				VMSNLKEESASGFVRLLDAAG
		1				LSMALNKSVVNNDPQGYPNRV
		i .	i			RQQRATGIWVYERYPAVDGAL
		l				PYTIDSKTGEVKWKYHVENKP
		l				DDKPKLEVASWLEDVDGNRKR
		l				NFSNDARANGTAAFTDCETQT
						VVHRDRVDQGHNHFDLVARH
		ĺ				YHLYAFRQFDGTSHVSSTEVEL
1		1				RTVAFEERSMTAAFISWTECTL
		ı				QIRTCPQNPTGKVWTCDELEIM
		ı				ADLCERHGVRVISDEIHMDMV
		l				WGEQPHIPWSNVARGDWALLT
		l				SGSKSFNIPALTGAYGHENSSSR
		l				DAYLSALKGRDGLSSPSVLALT
		l				AHIAAYQQGAPWLDALRIYLK
		l				DNLTYIADKMNAAFPELNWQIF
		i .				QSTYLAWLDLRPLNIDDNALQ
1		l	į.			KAL\IDQEKVAIMPGYTYGEEG
		1				RGFVRLNAGCPRSKLEKGVAG
1		ĺ				LINAIRAKKSATMIDTTLPLTDI
		l				HRHLDGNIRPQTILELGRQYNIS
		ı				LPAQSLETLIPHVQVIANEPDLV
		l				SFLTKLDWGVKVLASLDACRR
						VAFENIEDAARHGLHYVELRFS
		1				PGYMAMAHQLPVAGVVEAVID
		1				GVREGCRTFGVQAKLIGIM
25193	55561	Α	2533I	2	696	FLLLLWEIRKSSQQTTPTEMNA
		l				AEMAQLVAGVDEVGRGPLVG
		ł				AVVTAAVILDPARPIAGLNDSK
		1	İ			KLSEK\RRLALYEEIKEKALSWS
		1				LGRAEPPEIDELNILHATMLAM
		1				QRAVVGLHIAPEYVLIDGNRCP
						KLPMPAMAVVKGDSRVPEISA
		1	1			ASILAKVTRDAEMAALDIVFPQ
		1	1			YGFAQHKGYPTAFHLEKLAEH
	1	1	1			GATEHHRRSFGPVKRA/LGTCV
						LILVSRLSKPESEDVL
25194	55562	Α	25332	2	63	
25195	55563	В	25333	138	182	
25196	55564	Α	25334	356	706	ISDICAPNMVSAIHAIPYTATMA
						IIPERKTSFFEIDAGLVLVRIIISA
		1				PVSSINI*ITSTIDSGLPPKDGRRS
1		1				ESAPRRATTAIAPRKIHIASQLL
	l			1		VVIIIRSLVGCRMRRWRVLSD
25197	55565	Α	25335	1746	1873	
$\overline{}$						

fero in	leco in vo		SEQ ID NO:	IN	Nestentide tenetion of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
10.	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,			sequence		
		ㄴ				
25198	55566	Α	25336	1998	3626	PKAARMANVPNNTTGTAMVGI
i		1				SVA/RHILQEQIHHQEHQHNGFE
1		1				QRFYHFVNRKLDEWRGVIRVE
		1				NLHS/AAGRMAVIPPVLP*WLS
						RYREHSRRLPA*SPKGEAASNP
1						EVIARTLRKLKNQPELSEDTIKK
		l				AVESLSLELVLTAHPTEITRRTL
1	l	l				IHKMVEVNACLKQLDNKDIAD
		ļ				YEHNQLMRRLRQLIAQSWHTD
						EIRKLRPSPVDEAKWGLCRNGK
l						TACGKAYQITWAELNKQLEEK
						PRLQTCPSKFGSGPFYF
25199	55567	Α	25337	243	604	PRFPFPLPPATSSVQTAMTDG*N
		l				ECERICVGYLRYSSHSAPDARR
						QRARTHVPVGKHALPALTKAT
1		1				HPSWWWQCAAMAEDSTDARQ
			İ			LKA*WGVNGFLDLRSATMDGR
						LYPVAMCLLPATK
25200	55568	Α	25338	1	3287	MPITERRSVEKEQLIEIANTIMPF
						GKYKGRRLIDLPEEYLLWFARK
						DEFPAEARYTHIDLHVPAPLLV
ì		l				MFTLDTRQSACDRNPHLPIHVC
		l				SSWTSPKCAPRLWTRALLPRTR
1						TPPYATGTTIGSRASWFVTFPD
İ		1				ASFYRRKAPRQEFHTSLQGRSL
1	1	1				YVRQRSTANPTEITRRTLIHKM
						VEVNACLKQLDNKDIADYEHN
1						QLMRRLRQLIAQSWHTDEIRKL
1						RPSPEAIMTEQEKTSAVVEETR
			<u> </u>			EAVDTTSQPVAT
25201	55569	Α	25339	1	1425	
25202	55570	Α	25340	534	1391	RQKRRLYQTYWYKQQPRYLPP
						EHRQRHRHQSAGVSRPYSGYG
	İ					EVRPLSQYQPEWQCWEPDVEW
		l				VRQPPQDAITDPDFFCFYQPGM
	ľ	1				TFEQFVREFAEWFSQKRPAAM
		1				MIGIRADESYNRFVAIASLNKQ
						RFADDKPWTGGHSWYIYPIYD
		1				WKVADIWTWYANHQSLCNPL
		ı				YNLMYQAGVPLRHMRICEPFG
		1				PEQRQGL\WLYHVIEPDRWAA
			ł			MCAR\VS\GYTTGGLYPGQARG
	1		1			AAV*TEALKPSGLPQVCALNQC
1	1	1	1			LLSVHRYAGHVRQERCDGADG
		L				RPAVHERRQLL
25203	55571	Α	25341	786	1009	HHSHEQQFQWPVGASGVDRW
	1	1	1			AVYLHQICPLTQFQY/WCRARQ
			1			EGIMSSPGQQVGFIA*VTSSFSP
						R*KGRRVSSA
25204	55572	Α	25342	2446	2970	
25205	55573	Α	25343	1	2184	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		İ		sequence		
25206	66674	IA.	25344	706	1293	IHRLLIRRIHOIIDLRIWORTVEI
25206	55574	l <sup>A</sup>	25344	/00	1293	HGAPVRFIOMAAWTHIAVLLT*
		1				
1		1				QLRQLRAGFQRNSWAIFYFFHH
1		1				RKQYIFHFDLRRFPVIMHALFC
i		Į.			1	AVQRCADLMAHRRQKRRFCLA
İ	i	1	l		1	GFFCFRPCLSVFYHQFLQFSCTR
		1				FDLRRQLFAVAIQCMNIAFAAA
		1				LVDFDLPDIDGITLARQLAQQY
						PSLVLIGFSAHVIDETLQ
25207	55575	Α	25345	I	329 I	
25208	55576	Α	25346	882	1019	
25209	55577	Α	25347	1	2265	
25210	55578	A	25348	284	535	CVAASVTGTRVLIPPLLNNRSR
		ı				RSPVRYVSKGNWWGSVCNCAS
		1				NNSNSVSR*SLPPMRSHAWRKV
		l _				RRIMRQLPLERPRPGFTI
25211	55579	Α	25349	13 I	208	LVRWLLSPGW*WKISPIISICLFP
						V
25212	55580	Α	25350	1	3108	MDSQDKYFEATQTVYEWCGV
	1	1	1			ATQLLAAYILLFDEYNEKKASA
		ı				QKDILIKVLDDGITKLNEAQKS
						LLVSSQSFNNASGKLLALDSQL
1	l l		ļ			TNDFSEKSSYFQSQVDKIRKEA
1		1				YAGAAAGVVAGPFGLIISYSIA
1	1		İ			AGVVEGKLIPELKNKLKSVONF
	1	1				FTTLSNTVKQANKDIDAAKLKL
	1					TTEIAAIGEIKTETETTRFYVDY
İ	1	1				DDLMLSLLKEAAKKMINTCNE
						YOKRHGKKTLFETYLTDHPVTF
						RERLQMSIYKIPLPL
25213	55581	A	25351	I	296	I I I I I I I I I I I I I I I I I I I
25214	55582	A	25352	3	164	VGD/NVGTTARWGIFALIIVETL
		1.		ľ.		AWFTVVASLFAQHKQRAENLI
						ORLHLLWSFNP
25215	55583	В	25353	91	990	
25216	55584	A	25354	1146	1881	RCGVQ\WTMYIRAVFVNLTNP
222.0	55501	1.		1		KSIVFLAALFPOFIMPOOPOLM
1	į.	1				OYIVLGVTTIVVDIIVMIGYATL
1		1				AQRIALWIKGPKQMKALNKIFG
		1	ŀ	,		SLFMLHNAFAWFYLGAFLLTVI
						AWFLLGNAQKMPOTTLOWGIL
						VFLGVVASGIGYFMWNYGATQ
1						VDAGTLGIMNNMHVSAGLLVN
	l	1	1			LAIWHOOPHWPTFITGALVILA
	1		1			
			1			SLWVHPNKRFRNWLTLLAIAH
	1		1			GGVQSAPQAFAQGFGHHQTLA
		<del>ا</del>		1010	2005	LKTLYYPMR
25217	55585 55586	A	25355 25356	1943	2287 274	
25218	155586	IA.	23336	144	274	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25219	55587	A	25357	876	1400	YRHVRDSPGNDRLFETWRSAG CAARLLRQSGETRLLSRVVRDY GGRWPVSLLDGLPDATWCTEK RGGFCTCATGRAGEKWAQFPEN SLLTNLANPKAIIYFGSVFSLFV GDNVGTTARWGIFALIIVETL WFTVYASLFALPØMRRGYQRL AKWIDGFAGALFAGFGIHLIISR
25220	55588	Α	25358	1	1428	
25221	55589	A	25359	421	797	IIFPFLLFHLCNQLSHLLQYAVV NAPVRRILPIQLLWQQLIQPGEK LKSIRRAIQHIGQTQIIGMFIQMP IMIAYETDRATGDGI/WAAH*T HEYPCHVRQSQFHENHDDVQE NPPHPWKIQTPGH
25222	55590	Α	25360	1	1320	
25223	55591	A	25361	1	1251	MLLSITVAFRNLEGIVKTHASI. AHLAQVEDISFEWIVVDGGSND GTREYLENLNGIFNLRVSEPD NGIYDAMNKGIAMAQGKFALF LNSGDIFHQNAANFVRKLKMQ KDNVMITGDALLDFGDGHKIK RSANRAGLFLIGYGAFRIVEFF RQPDAQFTGAWVQYISMGQILS IPMIVAGTMKQYLELMQKVLD EGTQKNDRTGTGTLSIFGHQMR FNLQOGFPLVTTKRCHLRSIIHE LLWFLQGDTNIAVLHENNVTI NQLKNDPDSRRIIVSAWNVGE LDKMALAPCHAFFGYVPDGK LSQLYQMSCOVFLGLFPNIAS YALLVHMMAQQCDLEVGDFV NTGGDTHLYSNHMDQTHLQLLS REPRILPKLIIKKPESIFDYRFE
25224	55592	A	25362	3	1327	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25225	55593	A	25363		2443	MGLIGFVLTALWIKLIHNFTDH PRMASPELKIFSENGAVVDMD HKKPGSAAASOPKLHYIKQLLS NRMMLGVFFGGYFINTTWFFI TWFPIYLVQEKGMSILKVGLVA SIPALCGFAGGVLGGVFSDYLI KRGLSITLARKLPIVLGMLLAS TIILCNYTNNTTLVVMLMALAF PGKGFGALGWPVISDTAPKEIV GCLGGVFNVFGNVASIVTPLVI GYLVSELHSFNAALVFVGCSAL MTMSARSATGHECVFWCNGKP RRLAMKLIYWCAAAPTGDVVQ KLTGKWALIANSHRAGQPTRN VNEEVGQRLLEEMEWYDNYL NMGKTDRSANPSPGNKKGGLA NVVEKALGSIAKSGKSAIVELS SGQRPTKRGLIYAATPASDFV CGTQVASGITVQVFTTGSFV YGLMAVPSH*NGNWKITASVT SIQPNTMELPNCCMMGVSTANT TSKSSLVICALR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25226	55594	A	25364		2701	TFFLPAGEILPPRLEPQITLPVGS RRISIAVTDLPEPESPHLRSGLG WASLCCFMVICKFPAAEGLIL AAVCDSRGSRYWCMGNRRYG YASDLLVRCGATVMFSEVTEV ROAHLLTPRAVNEEVGRLE EMEWYDNYLNMGKTDRSANP SPGNKKGGLGKRGSSKALWLE LQIQARKQVGLRVYTVACVL RTGTWYDRNGFDWRVPGQLN MGNPAPETGRYRLAHPATPHD PRTTPDHPSHIKPHAPTNQPDT LTPTHHHHITOTRDPSPPPTRTTR PRQSTHITTPPHPTTTTRHTDIHP PHTTPDHPPPTTVLTRQLHHTNRI IPHRTHTTTCRRNHHNQMNTIT PRYNTSIVGTIGGGMVERKVIE ESLQALQERKPRLFHGRMARN GADAVGSDCGGAMSVISVHG MRPRLVLIGGGHVNRAIAQSAA LLGFDIAVADIVRESLNPELPP STTLLHAESFGAAVFALDIRPP STTLLHAESFGAAVFALDIRPP NFVLIATNNQDREALDKLIEQPI AWLGLLASRRKVQLFLRQLE RGVALEHIARLHAPVGVNIGAE TPGEIARVLAEILQWKNNAPGG LMMKPSHPSGIMWNLEVE
						KPTVIRCTVAFAQAVFDGEMT VEGVTARLATSSAEAMKLTER

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	ł	
25227	55595	IA	25365	li .	1262	MGNWHLSPCPAPAPGHSCLFL
23221	33393	<u>۱</u> ^	25305	l'	1202	VGTSPRILAVPGHTGSKAINKA
						ALLLESYMSQALKNLLTLLNLE
	l	ĺ				KIEEGLFRGOSEDLGLROVFAG
						QVGG\QPLYAAKEPVPEERLVH
		ł				
1		1				SFHSYFLRPGDSKKPIIYDVETL
		1	1			RDVAPVLDVAGATPPTIRHQRV
		1				TALVAPKNGSRDVRSCAGKMP
						TDGSIRAVLLPFQVSTIGGVTYF
	1	l				RVGTKDQGPQCPHVQRSSAVR
	1	1				PGPEAAPGDNSYPPYEDRSTCG
		l				MQAPDASYSANPDLSFTWSPCI
		l				SEDALHTSPLYCTTPTSGGEAF
		l				KGLASDLVPHEDKMVLQNGKO
	1	l				FTSPRHTEWAVLRAGHALARG
		l				RNLLDLAAGGMAWVSMSQEC
		1				PGPGTICSRDLQGTECLRMIQIL
	1	1				PPKDPVTRGSTHCNAGTKRELE
						EFSSQVTLTALIQPLMQVSAQF
						RAADGAP
25228	55596	Α	25366	2	176	
25229	55597	Α	25367	ĮI.	1395	MRESLELPRDLLNCCDQNANS
		l				DMDMKSRLRGYQMEIMNLLG
		l				AGVKDFELESDDLVYLVEEISK
		l				QQSIHDVA WLLLVAFVYICEQR
i						NDLKSELIFTREAEHKSLENLEF
						DHVPEELDTSARNAGALTRRRI
1						IRDAATLLRLGLAYGPGGMSLF
1	1	1				EVTAWAQLHDVATLSDVALLK
		1		ļ		RLRNAADWFGILAAQTLAVRA
1		1				AVTGCTSGKRLRLVDGTAISAP
						GGGSAEWRLHMGYDPHTCQFT
		l				DFELTDSRDAERLDRFAQTADE
1		l				IRIADRGFGSRPECIRSLAFGEA
		l				DYIVRVHWRGLRWLTAEGMRI
		1				DMMGFLRGLDCGKNGETTVM
		l				GNSGNKKAGAPFPARLIAVSLP
1		1				PEKALISKTRLLSENRRKGRVV
1		1	1			QAETLEAAGHVLLLTSLPEDEY
1		1				SAEQVADCYRLRWQIELAFKR
		l				LKSLLHLDALRAKEPELAKAWI
		l	1			FANLLAAFLIDDII\SHRWISPPE
25230	55598	A	25368	482	765	
122230	122270	l'	20000	702	700	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25231	55599	A	25369	1	1575	MGSVTKSRGPTDSSAFFQINRD
23231	33399	<u>۱</u> ^	23309	1	1373	YSFLDYILGGCOLMFTPWARLL
		l				QSTCCEQCSKKAHDQFLADLA
		l	ĺ			SILPSNTTPLIVSDAGFKVPWYK
		l				SVEKLGWYWLSRVRGKVQYA
		l				DLGAENWKPISNLHDMSSSHSK
		l	İ			TLGYKSLTISNPISGOILLYKSRS
		l				
		l	ł			KGRKNQRSTRTHCHHPSPKIYS
		l				ASAKEPWILATNLPVEIRTPKQL
		1	ł			VNIYSKRMQIEETFRDLKSPAY
						GLGLRHSRTSSSERFDIMLLIAL
		l				MLQLTCWLAGVHAQKQAFRF
		l				MRLVDGTAISAPGGGSAEWRL
		l				HMGYDPHTCQFTDFELTDSRD
						AERLDRFAQTADEIRIADRGFG
		l				SRPECIRSLAFGEADYIVRVHW
		l				RGLRWLTAEGMRFDMMGFLR
		l				GLDCGKNGETTVMIGNSGNKK
		l				AGAPFPARLIAVSLPPEKALISK
1		l				TRLLSENRRKGRVVQAETLEA
		l				AGHVLLLTSLPEDEYSAEQVAD
		l				CYRLRWQIELAFKRLKSLLHLD
	ĺ	l				ALRAKEPELAKAWIFANLLAAF
		<u> </u>				LIDDII\SHRWISPPEVPDPKRRT
25232	55600	A	25370	1	1341	MAGGRKFPDGGDRTTLCGLSQ
		l				PGVLAPRSPEKRRAINQRYPSK
		l	[			TGQLPASITDMMRTARHHLSG
		l				NGISVPKGAELAHPSTVLELFAI
		l				SAKPIHPEELDTSARNAGALTR
	ŀ	l	l			RREIRDAATLLRLGLAYGPGG
		l				MSLREVTAWAQLHDVATLSDV
		l				ALLKRLRNAADWFGILAAQTL
			İ			AVRAAVTGCTSGKRLRLVDGT
			ľ			AISAPGGGSAEWRLHMGYDPH
						TCQFTDFELTDSRDAERLDRFA
						QTADEIRIADRGFGSRPECIRSL
						AFGEADYIVRVHWRGLRWLTA
						EGMRFDMMGFLRGLDCGKNG
						ETTVMIGNSGNKKAGAPFPARL
	1	l	1			IAVSLPPEKALISKTRLLSENRR
		l				KGRVVQAETLEAAGHVLLLTS
		l				LPEDEYSAEQVADCYRLRWQIE
						LAFKRLKSLLHLDALRAKEPEL
	1					AKAWIFANLLAAFLIDDII\SHR
		_				WISPPEVPDPKRRT
25233	55601	В	25371	1	1233	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location uf first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25234	55602	A	25372	1	2197	SHSRGSPGKAVDFTLVSHAAW
		1			l	FGLPHFSTPAFNGQAMMLIAPV
ļ		1				AVILVAENLGHLKAVAGMTGR
		1		İ		NMDPYMGRAFVGDGLATMLS
						GSVGGSGVTTYAENIGVMAVT
						KVYSTLVFVAAAVIAMLLGFSP
					1	KFGALIHTIPAAVIGGASIVVFG
		1				LIAVAGARIWVQNRVDLSQNG
		l		l		CNPAYAEHHQHPGYSDKLKTR
		l				VSFSCLRIISTNLRRECRAQFRF
		l			l	HVDASARHGFRLWQIQGVAQP
		l				VFIITIREVEAAMRATAFGTEVG
		l				RNSRCIRRFHQVIQFQALNALG
		1			i	VELAGIDSRDPRLKVLEEMKRT
			-	1		FHWGRQTISKHIKIWLGLMLGR
1		1				AMTPLMLDATSGKLTVWDGA
		1				HAGAAMGILAVTADQNSAELA
1		1			ľ	YYKSGSFRIEDVLWPSAVTDDN
1						IKRNAFAADGSVNSYSVPFSSV
1		1			l	PLLQRQGRIKYAVTLAKYRTNS
l		l		1	-	NEQQESKFAQATLQWGGPWGT
1						TWYGGGQYAEYYRAAMFGLG
		l				FNLGDFGAISFDATQAKSTLAD
						QSEHKGQSYRFLYAKTLNHLG
		l			ļ	TNFQLMGYRYSTSGFYTLSDT
					ŀ	MYKHMDGYEFNDGDDEDTPM
l		l			į.	WSRYYNLLYTKRGKLQSLISKT
1		l				RLLSENRRKGRVVQAETLEAA
		1	l			GHVLLLTSLPEDEYSAEQVADC
		l	1			YRLRWQIELAFKRLKSLLHLDA
1		l	1	l	1	LRAKEPELAKAWIFANLLAAFL
						IDDII\SHRWISPPERIPSARKWT
25235	55603	A	25373	1	2754	
25236	55604	A	25374	1	652	
25237	55605	A	25375	1	1800	

SEO ID	ICEO IN NO.	Date	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.01	sequence	1.00	09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	· .	1		sequence	' ' '	
		<u> </u>				
25238	55606	A	25376	1	2187	MAGPRYPVSVQGAALVQIKRL
						QTFAFSVRWSDGSDTFVRRSW
						DEFRQLKKTLKETFPVEAGLLR
						RSDRVLPKLLGQASLDAPLLGR
1		1	ŀ			VGRTSRGLARLQLLETYSRRLL
1						ATAERVARSPTITGFFAPQPLDL
						EPALPPGSRVILPTPEEQPLSRA
1					l	AGRLSIHSLEAQSLRCLQPFCTQ
						DTRDRPFQAQAQESLDVLLRHF
	1					SGWWLVENEDRQTAWFPAPYI
1	1					EEAAPGQGREGGPSLGSSGPQF
İ		l				CASRAYESSRADELSVPAGARV
1		1				RVLETSDRGWWLCRYAGAGPE
		1				ELDTSARNAGALTRRREIRDAA
1						TLLRLGLAYGPGGMSLREVTA
		l				WAQLHDVATLSDVALLKRLRN
İ						AADWFGILAAQTLAVRAAVTG
		1				CTSGKRLRLVDGTAISAPGGGS
		l		i		AEWRLHMGYDPHTCQFTDFEL
		l				TD\SRDGER\LARFAQPPDEIRIA
1						DGEFVWRPKCIRSLAFGEADYI
		l				VGVHWRGLRWLTAEGMRFDM
1		1				MGFLRGLDCGKNGETTVMIGN
l		l	i			SGNKKSP\GFPFRARFIAVSLPPE
l		1	1			KALISKTRL\LSENRRKGRVVO
		1				AETLEAAGHVLLLTSLPEDEYS
			1		i	AEOVADCYRLRWOIELAFKRL
l		ı	ĺ			KSLLHLDALRAKEPELAKAWIF
ļ		1	l			ANLLAAFLIDDII\SHRWISPPEV
ł					i	PDPKRRTNSLWRITKMVIWSLO
		1				VAIRGTVSLTAPSLCNSACCCC
		ı				VSTNSATTLNDFAFARSVIDLTI
25239	55607	A	25377	2	333	RLGVWQDILSRRASCYHGMEV
		Γ.		ľ		WDKDSFGHISFDDQSMGYSHL
		ĺ				GHIVENSVIHYA\ARLVIGADGV
		l				DSWLRNKADIPLTFWDYQHHA
		1				LVATIRTEEPHDAVARQVFHGE
		l				AFW
25240	55608	A	25378	3	235	VAVLEORVHEPLAANAPPOLR
23240	33008	ľ	23378	ľ	255	VS/ARLGVWODILSRRASCYHG
		1				MEVWDKDSFGHISFDDQSMGY
		1	l	1		MEV WDKDSFGHISFDDQSMG Y SHLGHIVENSVIHYA
25241	55609	A	25379	1	774	SHLURIVENSVIHTA
25241	55610	A	25380	1	1076	
23242	122010	Ι^	43300	11	1076	

			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		<u> </u>				
25243	55611	Α	25381	1138	1737	SVSTEPSVAAFSSIKLRQDPP/H
		1				DNLHHQYN*GDIAFC\FTPYFH
		1				NCLCQS*WARAFQ*RANEF*R
		1				MNCTQLARTSGSHHLIPLTLRF*
			ŀ			QICISSGQLIQYSVVCRFIHPPEH
						RLTIHPLAGQGVNLGFMDAAE
						LIAELKRLHRQGKDIGQYIYLR
		l				RYERSRKHSAALMLAGMQGFR
		l				DLFSGTNPAKKLLRDIGLKLAD
25244	55612	В	25382	1	735	
25245	55613	В	25383	1	1941	
25246	55614	В	25384	847	849	
25247	55615	Α	25385	1	1227	
25248	55616	A	25386	324	1533	EGFMEHQRKLFQQRGYSEDLL
		1				PKTQSQRTWKTFNYFTLWMGS
		1				VHNVPNYVMVGGFFILGLSTFS
						IMLAIILSAFFIAAVMVLNGAAG
			l			SKYGVPFAMILRASYGVRGAL
			ŀ		i	VPGLLRGGIAALMWFGLQRGS
	ĺ					PFYDLIQTALSSPHKVTIEQFYR
		l				EVGVFLGIALIAVVISVLNNFFV
						SHYVFRWRTAMNEYYMANWQ
	ĺ					OLRHIKGRTAFINAIMTLIAFLP
	İ					VLVTLSAHVPELPIIGHIPYGLVI
		1				AAIVWSLMGTGLLAVVGIKLP
				į.		GLEFKNORVEAAYRKELVYGE
		1		ŀ		DDATRATPPTVRELFSAVRKNY
ŀ		l	ł	ŀ		FRLYFHYMYFNIARILYLOVDN
			l	ŀ		VFGLFLLFPSIVAGTITLGLMTO
						ITNVFGOVRGAFOYLINSWTTL
					ŀ	VEL\MSIYKRLRSFEHELDGDKI
		1				OEVTHTLS
25249	55617	A	25387	1526	1683	20,11100
25250	55618	A	25388	2709	2918	CWCFWHRRSCCGSVRYALSAV
	[	1		Γ	I	PGCQCPET*RRRFPHSAF*RFRS
		1		l	1	SETGQTGAYVSGPDLQPERLQR
						LWC
25251	55619	A	25389	1	1812	· · · · · · · · · · · · · · · · · · ·
25252	55620	Α	25390	134	386	RLKPSAAIRRRVSSSRISTPLNPA
		1		1		STTAFVGTDCA\IPRLRATSGLA
l		1		ŀ	1	GSPLIQNRFCRARQPRWSAPVA
		ı	l	İ		RHAAVYARHRWNQII
					<u> </u>	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
25253	55621	A	25391	181	1630	RIRQFCFYHHCVLTLAICAFIVIT
		ŀ				LTIWVSFRVSVLVFAMADDIKV
1		1				AVVGAMSGPIAQWGDMEFNG
		1			ļ	ARQAIKDINAKGGIKGDKLVGV
		l				EYDDACDPKQAVAVANKIVND
		1				GIKYVIGHLCSSSTQPASDIYED
						EGILMISPGATNPELTQRGYQHI
		l				MRTAGLDSSQGPTAAKYILETV
	i	1				KPQRIAIIHDKQQYGEGLARSV
						QDGLKAANANGVFFDGITAGE
						KDFSALIARLKKENID\FVYYGG
1		l				YYPEMGQMLRQARSVGLKTQF
		ł				MGPEGVGNASLSNIAGDAA\EG
1						MLAPVLITVDQPFVQAGFQPLR
						RLLPAHETGRRTRAYGVGRLT
Ì		l				RQIRRQIATTFRHNAQAAESKD
						FQWYRCDPCQLFHLMNRQHAR
						QHHASNVKMAMIKVNRLFIGR
1		1				RSLHRYVALNMRITLGGVLHH
1		1				GEVGEDQRVGTQLRRHIHGAL
		1				PTGVTVRMRKSVNRDVKFAA
			1			MLMDKTHRFLQFFLGKVKAGE
25254	55622	A	25392	2	505	
25255	55623	Α	25393	1	2038	
25256	55624	Α	25394	188	1771	GKQTSTSPAGWENSLRMRYT\
	1	1				MSFSLIATGLLGVYLTTMPGY
1		l				WGILFVWALFGVTCDMMNWP
		1				VLLKSVSRLGNSEQQGRLFGFF
1		ı				ETGRGIVDTVVAFSALAVFTWF
l		l		i	ł	GSGLLGFKAGIWFYSLIVIAVGI
		1			1	HFFVLNDKEEAPSVEVKKEDG
1						ASKNTSMTSVLKDKTIWLIAFN
l					ł	VFFVYAVYCGLTFFIPFLKNIYL
1		1		l	1	LPVALVGAYGIINQYCLKMIGG
ŀ						PIVLEKVLPPVVSVRVKGTASQ
		1				GOKIPEEFKOFFGDDLPDQPAQ
		ı				PFEGLGSGVIINASKGYVLTNN
				1	Ì	HVINQAQKISIQLNDGREFDAK
1				1		LIGSDDOSDIALLOIONPSKLTOI
		1				AIADSDKLRVGRSGLNLEGLEN
		1		1		FIQTDASINRGNSGGALLNLNG
		1				ENPIDOLKVVGRPHDRIDGPLK
					1	TTGTARYAYEWHEEAPNAAYG
		1				YIVGSAIAKGRLTALDTDAAQK
		1		1		APGVLAVITASNAGALDKGDK
					1	NTARLLGGPTIEHYHOAIALVV
1		1		l		AETFEOARAAASLVQAHYRRN
		1		1		KGAYSLADEKQTVNQPPEDTP
1	L	1				NGA I SLADEKŲ I VNŲPPED IP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25257	55625	А	25395	356	849	GSACRVKEIPRPASQMP/HTLPA GSRPPGSEAEPGPEAAPPPARRE AHQIPRPRGHLPSSPGPRTHVA AHNIRVVTEAHADSHALLSDLG AAPFVVMSRILRVDGDEDPPHV DESIQPTTENAVYFRPVQLTSAI ETGGKEEPYGLSAASLGRAESS AASLAGRR
25258	55626	А	25396	154	379	LVPRLKLGDLPSEINPLSSCSLV REKDPPTTSCTHT\TNPRNISPIS NPDSTGNRTVQLTW*PLPEPLE LWPKAL
25259	55627	А	25397	4761	5127	LGSGDLPWEINPLSSCSLLREKD PPTTISGPQTITSPRNISPISNPHTR TSKRLNRSGQAFLQNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL
25260	55628	A	25398	I	753	MGSWLQGLRAMVFALNYMVT RVRNKKDPPTTSGPQTTSPRNI SPISNPRPRETEFICOPKTTAPL MDWEGSLPLMFNHCRDTSLIH PCFQGVRPCRDACLSPSLASP AFLGKGQVPLNPFTLSGKSRF SGGGASTPTFSFHVSTPSLLFW GRGKYPSTPSSPLVASPAFLGK GQVPLNPFTLSGKSRFSGEGA KAPETITDAELRVTLTVEAAVC STIALSLGWEILPRHWGKEEVT KTTYYPVIP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or peptide sequence	deterion, v-possible nacieotide insertion)
25261	55629	Α	25399	174	2238	LRSGDLPWEINPLSSCSLLHEKD
				1		PPTTSGPQT\TSPRNISPISNPRQR
				ļ		RHILSMDPKLRRRSWTWVGSLP
		ŀ				LVFNHCRDASLIIHPGFRGVRPR
						RDVCLGPSPLATITDAELYVTL
						TVEGKSIPFLIDTEATHSTLPSFK
						GPVALASIHVQNVQIKRDKEGH
	İ					YIMVKGSIQQEELTILNMYAPN
					1	TGAPRFIKQVLNDLQRDLDSHT
		l			i	IIMGDFNTPLSTLDRSTRQKVN
						KDIQDLNSALHQADLIDIYRTL
						HTKSTECTFFSAPHRTYSKIDHI
				1		VGSKALLSKCKRTEIINCLSDH
		1				SAIKLELRIKKLTQNHSTTWKL
		1		ì		NNLLLNDYWVHKEMKAEIKM
	i	1		l		FFEINENKNTTYQNLWDTFKAV
	1			ŀ		CRGKFIALNAYKRKQERSKIDT
	1			İ		LTSQLEELEKQEQTRSKASRRE
						EITKIRAELKEIETQKTLQKINES
						RSWFFEKINKIDILLARLIKKKR
	İ					EKNQIDAIKNDKGDIATDPTEIQ
				1		TTIREYYKHLCPNKLENLEEMD
				i		KFLDTYTLPRLNOEEDESLNRPI
				1	ŀ	TGSEIVAIINSLPTKKSPGPDGFT
				1		AKFYORYKEELVPFLOKYKEEL
						VPFLLKLFQSIEKEGILPNSFSEA
	1			1	l	SIILIPKPGRDTTKKENFRPISLM
			1	1		NIDAKILNKILANQIQQHIKKLI
				l		HHDQVGFIPGMQGWFNIRKSIN
	1	1				VIQHINRTKOKNHMIISIDAEKA
			1	l		FDKIQQPSC
25262	55630	Α	25400	3	267	EKDPLTTSGPQT\TSPRNISPISN
				1	ľ	LRLFAFTWTDPDTHQAQQITW
				İ	i .	AVLPQGFTDSPRYFSQAQISSLS
	İ					VTYLSIILIKTHVLSLPIMSD
25263	55631	A	25401	167	408	LGSRTFPWEINPPSSCSLLREKD
	1					PPTTSGPQT\TRPRNISPISNLVS
						GLFLLSSPTSLTIPQPLSSFNLDD
						TLQSLPSLNF
25264	55632	Α	25402	142	441	LRLGDLPWEINPLSSCSLLCEKD
						PPTTSGP\PRNISPISNPVSGLFLL
					İ	SSPTCLTIPQPLSPFNLGATLQSL
	1	1			1	PSLNFNSFHFLVETKETRFIRGP
	1	1	l		I	KTPAP
25265	55633	A	25403	79	381	LGSGDLPWEINPLSSCSLLREKE
	1	Ι		1	I	PPTTSGPQT\TRPRNISPISNPELA
		l	1	1		TLAGNLATGPRNARSPGFLLSH
		l				VLSVWDPTENQTVQLTWQPLP
	1	1	l .	i	I	OPLELWPKAL

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
25266	55634	IA	25404	1	511	MWKGPKGLDMYGKSSVSPKTS
23200	33034	^	23404	l'	311	DILGRDTLLLALKVQTVVLQTA
						CGEGHVAGNCGRPLETEGSLO
1		1				LTATKKLRDSVLQPKSPEFCQQ
				1		FTRAWNRTQVPDETEAPAGTY
1				1		AAQSGDLPWEINPLSSCSLLHE
		1				KDPPTASGPQT\TSPRNISPILNR
		<u> </u>				VSEVSDHAGTPALVLHP
25267	55635	A	25405	570	1182	LGSGDLPWEINPLSSCSLLHEK
l						DPPTTSGPQT\TSPRNTSPISNLH
1						ALKGLKPAITRLLQHGLLKPINS
1		1	1			PYNSPILPVLKPDKPYKLVQDL
l		1				CLINQIVFPIHPVVPNPYTLLSSI
		1				PPSTIHYSVLDLKLAFFTIPLHAS
1		1				SQPLSAFTWADPDTHQVQQIT
						WAVLPQSFTDSPHYFSQAQISS
						LSVTYLSIILIKTHVLSLPIVSD
25268	55636	A	25406	489	615	LRNTWNSPRLMACALHSGSPSC
						TWGPYS*SGLSENLASQRVCPP
ļ						YQNENVGRVRDTEIKEHCYEES
l			i			SYRAATQIQVRKVGIITEPYPFM
1		1	1			ASLRTHCIICETCYEMKISFSKS
1						LNPLEKNKKSQPANCAVKEVS
	ļ.					EQLRRRQAFSVAAGLKGKGSP
						AQSIRKNLQKPYQHFQTLQQLL
	į.					PLOWAPCYGPSNFATHGTHOG
						LWLVLSTVAAQAVPGALIAEA
	1					TALLAWIQGAVS
25269	55637	A	25407	579	715	LGSGDLPWEISPL\SCSLLHEKD
						PPMTSGPQT\TSPRNISPISNLR
25270	55638	Ā	25408	1553	1896	<u> </u>
2527I	55639	Α	25409	964	1332	SCRFIRIYQGACCNLHPGEINSH
1			1			VAHTKPVWWSLHTDTHENCHL
		1				NTAVFFYHWLALEFFLNPLRR/
		1				CSC*HSLPGQFPVSLCLRVLSVD
			i			CAHPWGKPEAPGS*HPGPWQFS
		1				SLPSPLWPLYQHP
25272	55640	В	25410	1	717	
25273	55641	A	25411	590	1142	PNSSWMRGEPKKDPPTTSGPQT
					ļ	TSPRNISPISNPR/PKETRFICGP
1	1		1			KTPAPLMDWEGSLPLMFNHCR
		l				DTSLIIHPCFQGVRPCRDACLSP
		l		1		SPLAASPAFLGKGQVPLNPFFTL
						SGKSRFSGGGASTPTPSFHVSTP
						SLLFWGRGKYPSTPSSPLVASP
				1		AFLGKGQVPLNPFFTLSGKSRF
1				1		SGEGA
		Ь.	L			London.

SEO ID	CEO ID NO.	1444	SEQ ID NO:	Mustentide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1			· ·	scquence		
25274	55642	A	25412	1	790	MGLVHLQRQSYWTVQRSSINH
						FLGCNPHTGKDKTLYMRWTKS
						FRKVEDPPTTSGPQTDQPKKHL
						TKFKSETKETRFIHGPKTPAPV
1						MDWEGSLPLVFNHCRDASLIIH
1						SHFKGVRPRRDACLGPSPLAAS
1						PAFLGKGQVPQPLISLCPDPLFP
						HPNLISLRPNPLCPHPDLVSLCP
1						DPFPAFLEAHKNFQTPEPQQPGI
ł						PPEPPPGACYKC/HEI*PPGQG
1						MPAAQDSS*AMS/LSVRDPTGN
						OTVOLTWOPLPEPLELWPKAL
25275	55643	Α	25413	1	736	MQAMEKWKREAKVETEKDQK
						NOYOQTWLSDSASGYRYTKLP
		l				FYFRHNNLIPALAHLLFLDSLYS
						DLLTAAFFMQFWLSAQMSSDQ
			ŀ			RGLPGYLLWAEEISLLEISELTS
						GKQDSSWPEVKAGLKKEANYL
i						SSDSARLHPGEINSLVAHTKPV
		l				WWSLHMDTHEIWCRDSNWGD
1						LPWEINPLSSCSLLHEKDPPTTS
						GPQT\TSPRNILPISNPPSSKHQE
1						KPPEAISTLPNAAATAAAAVGS
						LLWSL
25276	55644	Α	25414	1644	2010	LGSGDLPWEINPSSSCSLLREKD
ì						PPTTSGPQT\TSPRNISPISNPHTR
						TSKRLNRSGQAFLQNLLPQELA
				1		TSARNLTTRPRNACSPGFLLSR
			ļ			VPSVRDPTGNWTVQLTWQPLS
						EPLELWPKAL
25277	55645	Α	25415	1	1035	MGKEYSLDVKKSIKVFKDNRS
						QGNRLQKLGLEDTDREDAMGF
						GSHRAKLTVVAALGACHCPEN
			1			EGQTVLPSSTSGRSDKRERVSA
		1				GYTPPFFVKEGVPSPLFKLHVV
						RCCSIQSHHSRRSQNCAEDVIR
						KTKTDQAVSSMSSAPVTVQQL
		l				NIIPALLVALTCGWAFCLMVSO
						EQYDEASKQAASFSNNAVIPVY
		ŀ				MSHMSKTLYKSEVFPINTYAQK
						ICFIAHTKPVWWSLHMDAHEI
1		1				WCRGRRSTDLPWE\INPLSSCSL
1						LREKDPPMTSGPQT\TSPRNISPI
						LNQELATRAGNLATRPRNACSL
1		1	l			GFLLSRISSVWDPT*KFGLVQLT
1		1				LGKPLPEPLELWPKAL
25278	55646	Α	25416	174	393	LRSGDLPWEINPLSSCSLLHEKD
23270	22040	ľ	22-710	l,	J~~	PPTTSGPQT\TSPRNISPISNPGET
1		1	l			KETRFIRGPKTPAPVMDLGRQP
1		1	l			SLGV
				L	L	3LO 1

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25279	55647	A	25417	2	4574	WDVLGAVIGTECGTIESGLSMV FLKDGERKLCTPSMDTTGYGN
			ļ			LRFYFVMAKWIYIPENVVKGR
	l	l .	:		KEIILVLDFTWCMVHRGICDPG	
					NSHENDIILYAKIEGRKEHITLD	
	l				TLSYSS/L/SSLYWPVMSQILFW	
		ĺ			QRTVH*TWL\QL*DGIPDIPNVY	
				1	F*KLWQFQALLLP*LLLYPWC*	
	ľ		İ			SQLWLWCLGQW*GPGFQQRW
						AASANYIFP*QLTIQNNLRRTTR
						*CKAVWNSVQMVATVSFFPER
						RCMGY**DYHDICA
25280	55648	A	25418	I	363	
25281	55649	A	25419	1	301	
25282	55650	A	25420	2	309	
25283	55651	A	25421	3	512	YIGPSCLKFCSGRGQCTRHGCN
						CEMASQTFPMFISESFGSSRLSS
	1					YHNFYSIRGAEVSFGCGVLASG
						KALVFNKDGRRQLITSFLDSSQ
						SRIISVELPGDAKQFGIQFRWW
	1				ļ	QPYHSSQREDVWAIDEIIMTSV
	1				•	LFNSISLDFTNLVEVTQSLGFYL
						GNVQPYCGHDWTL
25284	55652	A	25422	2	878	
25285	55653	A	25423	1	750	
25286	55654	Α	25424	1	1404	

SEO ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
25287	55655	A	25425	I	2506	GCSRLLVTVDLNLTNAEFIOFY
		1	1			FMYGCLITPNNRNQGVLLEYSV
		l			1	NGGITWNLLMEIFYDQYSKPGF
						VNILLPPDAKEIATRFRWWOPR
						HDGLDQNDWAIDNVLISGSAD
						ORTVMLDTFSSAPVPOHERSPA
						DAGPVGRIAFDMFMEDKTSVN
		ĺ				EHWLFHDDCTVERFCDSPDGV
		1				MLCGSHDGREVYAVTHDLTPT
		1				EGWIMOFKISVGCKVSEKIAON
						QIHVQYSTDFGVSWNYLVPOC
		l				LPADPKCSGSVSQPSVFFPTKG
		l				WKRITYPLPESLVGNPVRFRFY
						QKYSDMQWAIDNFYLGPGCLD
		l				NCRGHGDCLREQCICDPGYSGP
						NCYLTHTLKTFLKERFDSEEIKP
				l		DLWMSLEGGSTCTECGILAEDT
						ALYFGGSTVROAVTODLDLRG
				l		AKHDYILLPEDALTNTTRLRW
						WQPFVISNGIVVSGVERAQWA
	İ			İ		LDNILIGGAEINPSOLVDTFDDE
				İ		GTSHEENWSFYPNAVRTAGFC
						GNPSFHLYWPNKKKDKTHNAL
						SSRELIIQPGYMMQFKPFGFCRS
						DSWQLVQTQCLPSSSNSIGCSPF
						OFHEATIYNSVNSSSWKRITIOL
						PDHVSSSATOFRWIOKGEETEK
						QSW\AIDHVYIGEACPKLCSGH
						GYCTTGAICICDESFOGDDCSV
						FSHDLPSYIKDNFESARVTEAN
		l				WETIOGGVIGSGCGOLARYAH
						GDSLYFNGCQIKRAATKPL\DL
25288			25126	146	10551	
25288	55656	A	25426	146	10561	GGGGGGGGGMERSGWARQT
						FLLALLLGATLRARAAAGYYP
						RFSPFFFLCTHHGELEGDGEQG
						EVLISLHIAGNPTYYVPGQEYH
						VTISTSTFFDGLLVTGLYTSTSV
						QASQSIGGSSAFGFGIMSDHQF
						GNQFMCSVVASHVSHLPTTNLS
						FIWIAPPAGTGCVNFMATATHR
						GQVIFKDALAQQLCEQGAPTD
						VTVHPHLAEIHSDSIILRDDFDS
						YHQLQLNPNIWVECNNCETGE
						QCGAIMHGNAVTFCEP
25289	55657	Α	25427	1	296	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
25290	55658	A	25428		557	MARSLGVLVALPFPLPVGFNAE EAHNIVKEFSPGKSHPRESLSQQ RETILVQAGAFHWFGWRGKEK LKPKFNTFGRLPNEMLEQWLSP TNQCVDGV/LKGGEDIYNHNNI NQWTASIVEQSL\THLVKLGKA YKYIVTCAVVQKSAYGFHTASS CFWDTTSDGTCTVRL/WENRT
25291	55639	A	25429	178	2270	MMCUNVFCHCLFVL  VRRLFCVOTGGSPVGRGSLHHL WLVFSHVLSLLCSPCLLAPGM GAERALKRWRWQOTQONK ESGLVYTEEBWEREWTELLKL SEPRTHSFNGGTGGGHURD EGKPLHGCSSLLRSGKGGHVK AESSERTHFSNGGTGGGHURD EGKPLHGCSSLLRSGKGGHVK AESSELQQSQAKFPLTSQIRALH PIPSQINEKPGAGHWSAKLHFP YWQLGEAGEEGGSSPDIMRCL LTCLSVPSTAVIPLTDSEHKLLP LHFAVDFGKDWEWGKDDNDN ARLAHLILSLEAKLNLLHSYMN VTWIRIFISTRAPLAQPESPTAS AGEDVGSLADSLDSDRDSVCS KNSNNNGKNGKDKEKEKQRE KDKTRADSVANKLOSFSKTLGI KLKKNMGGLGGLVHGKMGRA KSGKSEESGASASTSPSEKTTIS PTDKAAGASPAEKGGGPRGDA WKYSTDVKLSLNILRAAMOGE RKFIFAGLLLTSHRHQHEEMIG VYLTSAQERSFAEGGGRRDA ATAAAAAAPPPPPRPREPRPRE TEGPPVPERASPGPPTQVLK LERRSFGPAGRAAAAGG TACPGGGRAACERORTSAWPG VRAGRGGAAVRHVPAAEPLA VVAELQPGARRRPAHRQHGRW VAGRGRGGAAVRHVPAAEPLA VVAELQPGARRRPAHRQHGGW GAGRGRGGGGGGGGGAGGGGGGGGGGGGGGGGGGGG

SEQ ID			SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	delction, \=possible nucleotide inscrtion)
25292	55660	Α	25430	404	1116	SLGPLMLSGQKLQTSYTMEYY
						AAIKR/DKIVSLVGTWLELEAIIL
						KKLMQEQKTKYHMFLLDSLSH
						GMQQAERVLIADGTMLLSAQY
						QFENNLLVPILRVSFRKSLQRKE
						EPGRKAKKSQTSGEGIKKRRFW
		l				FEWKEPVALSSQGWYEAKGSE
						RPEKGHLGLLRAESFQDLRTAL
						ISKPYFSVPGKVGPAIKCPETLP
						ELKTYPQYGVTLGEPVRNEQQ
						QASSFPSLSNTHLSKKRNES
25293	55661	A	25432	1571	1782	WLLCRLPPRVPDQL*WCGCQPE
		1	ŀ			KCAGAEFQDGSAMPLPSRTCPH
		l				SPRMCTGWSTTCATTDSATTA
						CPLAL
25294	55662	В	25433	69	1160	
25295	55663	Α	25434	14	437	LQTSHPYPTTSKC/PPP/CEKPSP
						TSL/C*RRSAPHLQPPE
25296	55664	A	25435	782	997	MMLCQLQRPV/CGSHSCSRG/C
						PPAQ/CPSPVPVPSPQSAFPVPQS
		1			1	PSSTCPNPSHPIHPIPMVPSSWSG
						HWDSK
25297	55665	Α	25436	1117	1815	GDAHTEQCLQNLYPRGSRPPLP
						LESHPSSSKHSPKACPTGRS/CG
						PWK/CPGPEVRP*PPPSCTR*DP
		İ				HFRGLLEGLLEPRHVTCLALCG
			l		1	PQRVLYWPVYHERLGEGWDW
					l	CPSSWPGA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25298	55666	A	25437	1261	2757	ALGKDEKSQGPPIQTGGLGPRL
						FRLPSSOGOERRFAAAKAPSSL
	1	1				VPHNGSPLSCWRGLREEGGLSL
		1				ATLWTPCGVGSGVPAAPPSAW
		1				CDLGKLLVCWRGQNRGPRSTQ
		1		1		TDVRRHEARSRORRRKCVAAP
İ	1	1				VAPRSRRWRCPAALAAPAVAV
	1	1				PVVFALIFLLGTVGNGLVLAVL
						LOPGPSAWQEPGSTTDLFILNL
						AVADLCFILCCVPFQATIYTLD
1	ŀ					AWLFGALVCKAVHLLIYLTMY
	į.	1				ASSFTLAAVSVDRCAVPG\HPL
		1				GRAVGAGVGGGVLNVGLVWL
		1				LAALFSAPYLSYYGTVRYGALE
		1				LCVPAWEDARRRALDVATFAA
		1				GYLLPVAVVSLAYGRTLRFLW
		1				AAVGPAGAAAAEARRRATGRA
		1				GRAMLAVAALYALCWGPHHA
		1				LILCFWYGRFAFSPATYACRLA
		1				SHCLAYANSCLNPLVYALASR
						HFRARFRRLWPCGRRRRHRAR
		1				RALRRVRPASSGPPGCPGDARP
1		1				SGRLLAGGGOGPEPREGPVHG
l	i					GEAARGPE
25299	55667	Α	25438	1	1624	MKDKSKTLGLEASIFRNNWKC
						KSIFEGLKGHQEGYFSQMIISYE
		1				KIPSYRKSKSLTPHQRIHNTEKS
1						YVCKECGKACSHGSKLVQHER
						THTAEKHFECKECGKNYLSAY
		1				QLNVHQRFHTGEKPYECKECG
						KTFSWGSSLVKHERIHTGEKPY
						<b>ECKECGKAFSRGYHLTQHQKIH</b>
1		1				TGVKSYKCKECGKAFFWGSSL
	1	1		•		AKHEIIHTGEKPYKCKECGKAF
						SRGYQLTQHQKIHTGKKPYEC
		-				KICGKAFCWGYQLTRHQIFHTG
-				1		EKPYECKECGKAFNCGSSLIQH
		1				ERIHTGEKPYECKECGKAFSRG
		1				YHLSQHQKIHTGEKPFECKECG
						KAFSWGSSLVKHERVHTGEKS
1	1	1		1	1	HECKECGKTFCSGYQLTRHQV
1	1	1		1		FHTGEKPYECKECGKAFNCGSS
1	1	1			1	LVQHERIHTGEKPYE\CKECGK
1		1			1	GFS\GGYHLTOHOKIHTGEKPF
1	1	1				KCKE\CGKAFSWGSSLVKHERV
1	1	1			1	HTNEKSYECKDCGKAFGSGYQ
1		1			1	LSVHQRFHTGEKLYQRKEFGK
1	1	1	1		I	TFTHGSKLVHERTHSNDKPYK
l		İ			I	YNECGEAFLWTTYSNEKIDTDE
	1		1		L	THECOMILENTITISMERIDIDE

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
İ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25300	55668	Α	25439	32	447	VLGGSMMFREGQRGNRQKGP
						KKRRNLALSSALLASTA\PAGG
			İ		l	QPRHWRPG*CCLRQQL*PLQGN
						WAPVSPLQGHRSQLRAGYSISS
i		ı				FLQMFAP*VQGAARAQPAPGA
						AVPRGSGRQGGPRAVDLHGFR
		1				VGWNRLRAASM
25301	55669	Α	25440	1	858	
25302	55670	A	25441	147	1088	SRTTYKGKSSFQTYSDYLRWES
						FLQQQLQALPEGSVLRRGFQTC
		1				EHWKQIFMEIVGVQSALCGLVL
						SLLICVAAVAVFTTHILLLLPVL
	l	1				LSILGIVCLVVTIMYWSGWEMG
		1				AVEAISLSILVGSSVDYCVHLVE
		1				GYLLAGENLPPHQAEDARTQR
		1				QWRTLEAVRHVGVAIVSSALT
		l		l		TVIATVPLFFCIIAPFAKFGKIVA
		l				LNTGVSILYTLTVSTALLGIMAP
	l	l				SSFTRTRTS/CPQGPGCRAAGRG
		l				PGAGCLPRAPAERL*DSPARRG
		l		1		LPIARDGLWTLAPLVPWVGDR
		_				SCFPARLQLAVSPGLGPGRPAG
25303	55671	A	25442	1	1596	MGVSVRVDCGCARASEFLGRP
	1	l	İ			RGAVRGADPGSGLTETCAQSR
		l				TWARARSKGGFRLTLNFYGPR
						YPSEGTSRGQRSEALPFLDIQHP
	i	l				TPLGRPRMLQSRGEMVRSWGP
	i	l				VVEGKLGFCPPLTVFPGGLRGP
		l		ł		HPGLAGERENFARGAKQEACL
						LQGPGDAGLTHPCPATGYFPEA
						SCTSRSIRMFINSQERQLADMSL
		l				FIADSWLCYSGIICWKSLEHQR
		l				GASLSCVYMEGKGGNIWMKAS
		1	l	İ		NVLPLCQMLPTSGHSKSDLFGG
	İ		l			LAVEKQMRQDHHILLHDRSGF
						QLAVTSPLLTRLGKGHIIQVPV
l	i					YVLDAPSRWLGGLRLFRDSSCG
		1	1			LVLSLLICVAAVAVFTTHILLLL
	İ					PVLLSILGIVCLVVTIMYWSGW
	ł	1	1			EMGAVEAISLSILVGSSVDYCV
						HLVEGYLLAGENLPPHQAEDA
				1		RTQRQWRTLEAVRHVGVAIVS
l		l		l		SALTTVIATVPLFFCIIAPFAKFG
l		l	1	l		KIVALNTGVSILYTLTVSTALLG
l				l		IMAPSSFTRTRTS/CPQGPGCRA
	L	_	L	L		AGRGPGAGCLPRAPAERL*DSP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25304	55672	^	25443	1	2355	MDHPGFREFCWKPHEVLKDLP LGSYSYCSPPSSLMTYFFPTERG GKIYYYGGMGQDLADIRGSLEL MTHPEFFWYVDEGLSADNLK SSLRSEILFGAPLPNYYSVDDR WEEQRAKFQSFVYTYVAMLAK GSTSKVQVLYGGTDLEPDYEVR RTFNNDMLLAFISSSCIALLVYI LTSCSYFLSFFGIASIGLSCLVAL FLYHVVFGIQYLGILNGVAAFV IVGIGVDDVFVFINTYRQATHL EDPQLRMHTVQTAGKATFFTS LTTAAAYAANVFSQIPAVHDFG LEMSLIVSCCULAVLYTMPAA LGLWSLYLAPLESSCQTSCHON CSRKTSLHFPGDVFAAPEQVGG SPAQGPIPYLDDDIPLLEVEEP VSLELGDVSLVSVSPEGLQPAS TNGSRGHLIVQLQELLHWVL WSAVKSRWVIVGLEVSILLISLV FASRLRSASRAPLLFRPDISLV FASRLRSASRAPLLFREDTSLV FASRLRSASRAPLLFREDTSLV FASRLRSASRAPLLFREDTSLV VSAVSRWVIVGLEVSILLISLV KYKSGWVIVGLEVSILLISLV KYKSGWPMASRPEATLQDFFGTVYIS KVKSQGHPAVYRLSLNASLPAP GNFTKKLTACMSTVGLLQAAS PSRKWMLTTLACDAKGWFF GNFTKKLTACMSTVGLLQAAS PSRKWMLTTLACDAKGWFF DNFFYVATKEQQHTRKLYFAQS
						HKPPFHGRVCMAPPGCLLSSSP DGPTKGFFFVPSEKVPKARLSA TFGFNPCVNTGCGKPAVRPLVD

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \:-possible nucleotide insertion)
25305	55673	A	25444		1737	MLYAAECLENYMKLQVIPSAL NEALQAQSTWSDLGLASHUS STWCLHGESAAWSQPAVVECG QPRODQLQTHSEAWLCALVATF SQELEQFAVTAQQISDRQGHAV CTAPPRGRPSTLMTINLVCASSA DEGGGGKTETOTAGGRLGRAG TRSRGQLTRLITRTQAAEPRWF LQLLKRSANRSRALTRPPSGLSS DGARRLRISPSAVSSADTKFT VPVSSDSSGRDGGGETRAEAGF GGPHVAQPGVAPPAAAARDF RKPRGLNRQNVSPPGGEGGL GIPPRIORPPSFPGSPADFAS VSHTQGSPPDTGLPGTCQNRLP NPAAVDEGTCTRGSLNCRLS PRVSERRGPEGTFGGAAIRTPRA DPAAVDEGTCTRGSLNCRLS PVPRHGGGGPTAGAIRTPRA FCSRTAQPANOTTGNHERGLRS VAMFGDRASREATPALSLCESQ GGFEDEKEVFSPEPHVETSDEPL LSTGPAGCOWNLTSM WAFGDRASREATPALSLCESQ GGFEDEKEVFSPEPHVETSDEPL LSTGPAGCOWNLTTGGMWCAS VAMFGDRASREATPALSLCESQ GGFEDEKEVFSPEPHVETSDEPL LSTGPAGCOWNLTSM WEVTGEDW LSTGPAGCOWNLTTGGMWCAS LSTGPAGCOWNLTSM WEVETGEDW LSTGPAGCOWNLTSM WEVETGEDW LSTGPAGCOWNLTSM WEVETGEDW LSTGPAGCOWNLTTGGMWCAS LSTGPAGCOWNLTGMWCTGEDW LSTGPAGCOWNLTGMWCTGEDW LSTGPAGCOWNLTGMWCTGEDW LSTGPAGCOWNLTTGGMWCTGEDW LSTGPAGCOWNLTTGGEDW LSTGPAGCOWNLTTGGMWCTGEDW LSTGPAGCOWNLTGGMWCTGEDW LSTGPAGCOWNLTGGMWCTGEDW LSTGPAGCOWNLTGMWCTGMWCTGMWCTGMWCTGMWCTGMWCTGMWCTGMWC

SEQ 1D	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
25306	55674	A	25445	2	1642	LLSSISAWFGPPASTPAFTMSIR
		1				VTQKSYKVS\TSCPRAFSTRSYT
	Ì	1				SRPGSRISSSSFSRVGSSNFRGDL
		İ				GGGYGGASG\MGGITAVTVNQ
		1			1	SLLSPLVPEVDPNIQAVRTQEKE
						QIKTLNNKFASFI\DEVGFLEQQ
						NKMLGTKWSLLDQQKTA\RSN
						MDNMFESYINNLRRQLETLGQ
						EKLKLEAELGNMQPLVEDFKN
	l					KYEDEINKRTEMENEFVLIKKD
						ADEASMNKVELGSRLEGLTDEI
						NFLMQLYEEEIRELQSQISDTSV
						VLSMDKSRSLDMDSIIAEFKAQ
		1				YEDIANRSRAEAESMFQIMYEE
						LQSLAGKHGDDLRRTKTEISEM
		1		l		NRNISR\LQAEIEGLKGQR\ASL
		1				GGRPLQDAE\QRGKSWPIK\DA
				i		NAK\LSEAGSPPLQAGPKQDMG
	1	l				R\QLREY\QKLMNVKAGPWTIE\
l						IATYQESCLEGEEEPGWSLGCQ
		l		l		NMSNHT\KTTQRGYAGRPEPPP
						MGGFTSP\GFSYKPGAPGFGSG
		l				AGS\SSFNRHQLSPGAVVVKKIE
						TRDGKLVSES\SNVLPKVKQLR
						QPLPSLPLLRCPRGLGKEAPYP
25307	55675	Α	25446	1	1280	MAYLCNAICMTHMVTLDPVDQ
				l		ALPGATTATSVPGPQCDASCM
						MLFAVVPFNGIALAATQGAQS
						MLPPRVQGSLSSKPSTRRGRDA
						PGLQVSQAPPPRRGFAVGRRYS
						PPALAPGRCAAPHGGGRKELPT
						RRPGHGMAPKFPDSVEELRAA\
						GSESFRNGQYAEASALYGRAL
				l		RVLQAQGSSDPEEESVLYSNRA
						ACHLKDGNCRDCITDCTSALAL
						GPFSIKPLLRRASAYEALEKYP
						MAYVDYKTVLQIDDNVTSAVE
						GINRGPGLKEDTTQKRWNSLPS
						ENHKEMAKSKSKETTATKNRV
		1	1	I		PSAGDVEKARVLKEEGNELVK
		1			1	KGNHKKAIEKYSESLLCSNLES
				[		ATYSNRALCYLVLKQYTEAVK
	1	1		I		DCTEALKLDGKNVKAFYRRAQ
	1	1				AHKALKDYKSSFADISNLLQIEF
L			L	l	l	RNGPAQKLRQEVKQNLH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25308	55676	A	25447	1	1297	MHLLSAYFVPGSMLVGSGYM
						MVNITDVSPPSWSFLCSMLITTT
		1				QGAQSMLPPRVQGSLSSKPSTR
						RGRDAPGLOVSOAPPPRRGFAV
						GRRYSPPALAPGRCAAPHGGG
				1		RKELPTRRPGHGMAPKFPDSVE
		1				ELRAAGNESFRNGQYAEASAL
						YGCALRVLQAQGSSDPEEESVL
						YSNRAACHLKDGNCRDCIKDC
				1		TSALALVPFSIKPLLRRASAYEA
						LEKYPMAYVDYKTVLQIDDNV
		1			l .	TSAVEGINRMTRALMDSL\GPE
				i		W/RALKLPSFPLVPVSAQKRWN
		1		1		FLPSENHKEMAKSKSKETTATK
						NRVPSAGDVEKARVLKEEGNE
			1			LVKKGNHKIAIEKYSESLLCSN
						LESATYSNRALCYLVLKQYTEA
			ĺ	1		VKDCTEALKLDGKNVKAFYRR
	ŀ	i i	ļ	i		AQAHKALKDYKSSFADI\SNLL
			1	1		QIEPR\NGPAQEVAGREVKQNL
25309	55677	Α	25448	3	491	GITFTHSPAATGGGAQRVRRRD
		1	İ	i		PPPGVQLRNMAQETNHSQVPM
		1		1		LCSTGCGFYGNPRTNGMCSVC
		1		1		YKEHLQRQNSSNGRISPPATSV
		i i		1		SSLSESLPVQCTDGSVPEAQSAL
		1	i	1		DSTSSSMQPSPVSNQSLLSESV\
		1				ASSQLGQYICGTKAVPETEDVQ
1	1					ASVSDTAHV
25310	55678	Α	25449	1	860	HLLLLAIDYNLPIAGVLMESQY
		1			1	LGASPKRLVIPNLYAHRKSLAT
	1	l	1	İ	į.	LEPYAPRRPMPIARRYAIPYMS
						HHNGYIGDVYYRLTVEEKKSSF
			1			IARRSILTTEFTIRRTKKVPVPSI
		ı		1		NMSSASPLEDESRPSAGVQLRK
ŀ	1	1				GRYRLLRDRYRPGCNSVGESPR
1		1				KSSFSDDIMATESRESIFAEEPR
1		1	i			TGEHSVRGPVSNQSLLSESVAS
				l		SQLDSTSVDKAVPETEDVQDSL
		1				NASPTKQQCG/DVQTVDLYSNN
					1	KELFAQKCYRHRYISRLKKCCL
		1_				CHELVPRDTIKSPESLSVGS
25311	55679	Α	25450	880	1196	SPTTRRGTPGTCLKPTACAGAA
			1	1		*PGCSARRTCASAAPLSTCPPSS
		1	1	1		CAAPPPAPAAVPSTPRPTSPSPW
			l			AAPASPSRRRTQTASTPASTNR
		$\perp$				APSSCWAPTTRPLAP
25312	55680	Α	25451	254	579	IEKISLEPKNRPSPQIPNLVGP/R
		1	1	1		LFLVPGDFQSQVPNFLPFKPSSG
		1	ĺ			PHPAAGKGQPFSFLPAWRSTGP
		1	1			ERATPGPGRPAACSALEAPSLR
i		1	I			GPSGYSAQEPPRRPISARI

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
25313	55681	A	25452	6	1442	RSELIRHSWPRHAQLRGARART
						AVSIRECISVHVGQAGVQIGNA
						CWELFCLEHGIQADGTFDAQAS
						KINDDDSFTTFFSETGNGKHVP
1						RAAMIDLEPTVVDEVRAGTYR
			i		İ	QLFHPEQLITGKEDAANNYAPG
1			ļ			PPTPGGKESIDLV\LDRIRKLTD
						ACSGLQGFLIFHSFGGGTGSGFT
						SLLMERLSLDYGKKSKLEFAIY
i						PAPQVSTA V VEPYNSILTTHTTL
						EHSDCAFMVDNEAIYDICRRNL
		ļ	i		İ	DIERPTYTNLNRLISQIVSSITAS
		1				LRFDGALNVDLTEFQTNLVPYP
1		1				RIHFPLVTYAPIISAEKAYHEOL
						SVAEITSSCFEPNSOMVKCDPR
						HGKYMA\CCMLYRGDVVPKD
						VNVAIAAIKTKRTIOFVDWCPT
1						GF\KVGINYQPPTVVPGGDLAP
ì	ļ.	1			1	VORAVCMLSNTTAIAEAWARL
		1				DHKFDLMYAKRAF\VHWYVGR
l	ŀ	1				GDWKKGEFSEAREDLAALEKD
		i i				YEEVGVDSVEAEAEEGEEY
25314	55682	A	25453	3	618	SSAGREPDPSDLPRRLCFTHRLP
23314	33082	l^	25455	ľ	0.0	AARRWVOLCVHASPEPGGOGV
		1				CPGRSERMVIRVFIASSSGFVAI
1		1				KKKOODVVRFLEANKIEFEEVD
						ITMSEEQROWMYKNVPPDKKP
						TOGNPLPPOIF\NGDRYCGLLVS
1						FSVICIKNPNWHNLFLLIPWSGI
1						NPYCEQDSSFSENVGDEILKNS
						GVPRDFTSILIQKERKSEKVKG
						VDQGHR
25315	55683	A	25454	3	424	SWTMAATIQAMERKIESQAAH
		1		1		LLSLEGQTGMA*S*GTPPCCPG
		1				AAAGSRSSCCAAGSPRSPAASA
1		1				AARTPAAGSPARPTCPPAGSRT
		1				PRLSSRNQPASSRPSRFDLLGKA
						GEQPAIQSSSPWPESWLPSSTK
25316	55684	A	25456	268	445	
25317	55685	Α	25457	3	205	
25318	55686	Α	25458	27	272	AKCSGQGPGRVRAQGERADHE
		1		1		CPGAGAGGGGCNSAASAREES
		1		1		SRLISG\SLQMQNVSLASRRKEE
		1	1	1		EVRAAAAGGAAAGRPRV
25319	55687	Α	25459	1	253	
25320	55688	A	25460	2145	2399	
20020	1-3	100	1			

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	locatinn of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25321	55689	Α	25461	174	1309	HLLCCRAQRRPQTPPAARGLEA
						CSEGALKMPEAPP\LLLAAVLL
		l			1	GLVLLVVLLLLLRHWGWGLCL
		l				IGWNEFILQPIHNLLMGDTKEQ
		l				RI\LNHVLAACGSPGNAQSVLG
		i				GHLTPNCEQKEW/APLNVGDK
		1				KGQDSWDALISREQPALPCLLG
		1		i		NLGAYFGLLQLLRMAR\LLVNQ
		1				GARLIHHSRFNPDLCPPSPKRM\
						VDFAGVKDKALFQVTL\VCGAS
						PETFHPPSLKKKYDVGHNWTW
		l		1		VFLDHWKDRYL\PDTLLLE\EC
		1			1	G\LLPEGGQLLLAEQRLSSPGAP
		1				\DFL\AHVSREPACFG\CT\HYQI
		1				VPWKYRE\VVDGLGRRPI\YKG
						P\GSEAGALTAPPRPPSRALSPK
		l				PGTEGARPWLLLTLVRLRACVL
						NAKSHARAESLRA
25322	55690	Α	25462	2470	3460	SGPCPRCCAECRPYKTRPRSRV
						PGTHGPGPADHGQPPCCMAGA
1						HPPRPQAWMLLQTHSQDCEGK
		l				VGCGGIFCPCYHHCKHTHHHH
		1				ннрининүнүнинини
						ннинничничнын
	İ	l			1	нснин/нининирүрниүнин
		l				RGQDHHPHPHHHH/HHHYHHH
	l	l				НҮНННҮНРНННРННННОРОН
	1	ı		İ		нннонунннунниринр
1	1	1		1		РНННННҮНҮННННННҮ\НРҮ
		1		i		РННҮНННННННРНРНННН/
		1				нннүнниннинүнннн
		1				НННКРНННКНОНРННҮННН
						HPHPCHHHRLHHHHRHHHYHH
		L				TSSVQGPGSQPAGASLPGQACR
25323	55691	Α	25463	1	407	DAERQEALGIVRRIGTDTEAAT
		1		1		EPAGATVPAAAAAARIGTVGP
	1	1		1	1	QPPAMPRRKRNAGSSSDGTEDS
		1			1	DFSTDLEHTDSSESDGTSRRSA
1		1				RVTRSSARLSQSSSRISRSCSKS
	1					GSLLALRSLLTLPEE*PVVSSSL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nocleotide insertion)
				sequence		
25324	55692	A	25464	3	2539	RILYIPDGHRAPGASQSGNWEH
23324	33072	<u> </u> ^	2,5404	3	2339	PLLLLEPGNLASSPSMSLAYPHP
		1				CGLTIHQEHRRAHEELAYTPND
						RASSTGHPAFIEDGNPSPVLAFA
l						ASPRPNDSYILKREPPESCEKER
						VFEEATTRGKYGEGAKOETFTF
	İ					
		i				ALTLVFIQCVINAVFAKILIQFF
						DTARVDRTRSWLYAACSISYLG
						AMVSSNSALQFVNYPTQVLGK
						SCKPIPVMLLGVTLLKKKYPLA
						KYLCVLLIVAGVALFMYKPKK
						VVGIEEHTVGYGELLLLLSLTL
						DGLTGVSQDHMRAHYQTGSN
						HMMLNINLWSTLLLGMAVSCP
						DQGPELVPRCPFVQALEKPSWK
						NLHQQDLFATCYWHNEGESCV
1						SCHGKTLSSKTQGGILFTGELW
				ì		EFLSFAERYPAIIYNILLFGLTSA
						LGQSFIFMTVVYFGPLTCSIITTT
l	1					RKFFTILASVILFANPISPMQWV
						GTVLVFLGSTQIILDNLKILNTS
1						AKTLLYKTPLSWQELEGERASS
1						CAHKRSASWGSTDHRKEISKLK
				1		QQLQRTKLSRSGKEKERGSPLL
1						GDH/VSAGSTEGVPS/RASPQGP
1	1					LSCDSAPACT/VSLEGLNQELEE
1						VFVKEQGEEELLRILDIPDGHR
1			i			APAPPOSGSCDHPLLLLEPGNL
		l				ASSPSMSLASPOPCGLASHEEH
1						RGAAEELASTPNDKASSPGHPA
			i			FLEDGSPSPVLAFAASPRPNHSY
						IFKREPPEGCEKVRVFEEATHQ
25325	55693	A	25465	845	1316	LSLGDSAQCLLPHASWCQVAG
23323	33093	<u> </u> ^	23403	043	1310	HPAFLEDGSPSPVLAFAASPRPN
						HSYIFKREPPEGCEKVRVFEEAT
				i		S/RRVLTGPFLTSCPDK\NKVHF
l	1	l		1		
				1		QP\TGSAFCPVNLMKPLFPGMG
		l	l			FIFRNCPSNPGISSSPGQPQATTS
1	l	1		l		EGSGSLQGLPTAIRAMAAHPYH
	l	L_	l	l	1	Q

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25326	55694	A	25466	1077	1506	CDACGRRCRTCRTFCLGLQPAC LDGHHHRHPDCWFWSPRHR+ GMIIDVFSRYSGSEGSTOTLTKC EL, KVLMEKELPGFLQILTNEGE EL, VLYMEKELPGFLQILTNEGE EL, VLYMEKELPGFLQILTNEGE RVNALLKWLLKLGERWQMTE EGIKGQRSGHGPEQAENLGDS VPQDTTKDVPLTOHRLHQGLE AGVPKTSVPARPGI PVPALQHA QHGPGCERALHCHNGPQFL QMRTLKREVHAL PGGRAGGAA REGLGASICETGEHQMTNFQVP RWPPCFPGQAGPVLGTGTRHG LDLLSGRRGTVFKGSSVARH EEVTVTKQSAADLRHTGQGFT CCVLSGGRCGSQAGPVLGTGTRH NPLNDVMLVGDDAGPAGHFAS VYPPLAWTVTTVTLTVLTGFGV RVTDEAGHPVPSQVSGIGRCLQ GMKAPPVTVTVSGEKGSCLCA SCVLCLEHPYFPLVPWLPPVF DSVIPSSTSPGEAVLADVGFN NVPORAOLKPOKOLLPFY
25327	55695	В	25467	31	783	Quanqua ququum
25328	55696	A	25468	846	1392	PDPAAHRFGHPTLHPGSLRTSS GAGTWYQNPQHHNDHDYYHH HHIJHDDHHVYHHHHIHHHIH HHYHHHHHHHHHHHHHHHH HHQHHHHHHHHYHHHHHH HHHHHHHH
25329	55697	A	25469	181	412	LRSDQQTRKFVSRSSGACSPPTT TELSWPPSLLPSL*FHSPSSQP* MNHSASTTSPLPSFITERESILAT EWDTARN

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25330	55698	Α	25470	1	848	MPSLNTIVSPLGSPHTSLIPPML
						LSANLPFDTTIMIKLQTACSAPI
	l					HNLORPCGENLRTSTFVRRLDR
						NLVKSPOPGGGGOPSROWEAR
	ĺ					GAEPOGRRDPSEVO/RPAGRGF
	ł					GRISRAPRKPSRAPTPTQGLGPP
	l	l				LGAGGOGSLASCRPARKNARPI
						TRAAAHSAHPHSHWHSHARPO
						POSPSAAGOSGDPWPPARVPPP
	ĺ			l		PLLRLPORRTAGRTPVDAPARG
						IFTLSLSSSHSKSSGKHRGARKT
						PEMWPLFRGSLSKLSRRRKVSP
						SAALHWRLRRTOKRLCC
25331	55699	A	25471	92	1083	TMRTHGHRKGNITPWGLSGVG
						GL/ETGRALGEIPNVDEGLMGVI
						AAVAIVLVSLLFVMLRYMYRH
						KGTYHTNEAKGTEFAESADAA
						LQQRERALDSSRDSHLETLGAC
						PGRNGGGLALQEATPRDPGRR
						WPPORPPFAPRRWEKIWAHGPL
						GSAGQHQLTGRKVLVEGLGCI
						CMAHTDLONTSVAKMAINRPN
			ļ			EYAOVSLENDVSCKVKAVOAP
		l				ORLHWPSVDADTGGRGAVHIA
	İ					FPKHVEPETPFAHTIPARNSWT
						KWSSEHILETLSPOKPALPWAP
	l	l				RQQGRPLGLTAPISKRLGPGDG
	ŀ	1				PEGEAGERLAQAHFINTRPPST
		1				GPPGTPAAD
25332	55700	A	25472	73	424	RPGMWSTRSPNSTAWPLSLEPD
						PGMASACTTMHTTTIAEPDPG
	ŀ					MSGWPDGRMETSSPTIMDIVVI
						*CAIAAEAIVLVSLLFVMLRYM
	l					YRHMGTYHTNEAKGTGVADS
						ADACPAGDPA
25333	55701	Α	25473	139	546	RPGMWSTRSPNSTAWPLSLEPD
						PGMASASTTMHNYHHCRSLIPG
						M\SGWPDGRMETSTPTIMDIVVI
						AGVIAAV\AIV\LVSLLFVMVAL
			1			TCNRA/HRGTYHTNEAKG\TEF
		1				AESADAALQG\DPAL\QDAGDS
		1				SRK\EYFI
25334	55702	С	25474	142	408	

SEOID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
i i				sequence		
25335	55703	I.	25475	44	727	ARAGSRSRGLPFCGTAGPPPKA
25555	55/03	l <sup>A</sup>	23473	44	121	
						TLWGGLLRLGSLLSLSCLALSV LLLAOLSDAANNFEDVRCKCIC
		l			1	PPYKENSGHIYNKNISQKDCDC
		l				LHVV\DPMPVPGA\NVEAYCLR
		l				CECKYEE\RSS\STIKVTIIIYLSIL
		l				GLLLLYMVYLTLVEPILKRRLF
		ĺ				GHAQLIQSDDDIGDHQPFGKCT
		l				RCASPLPQFEPTCWNKVEYAQ
		l				QALESFQVQEQRKSV\FDRACC
		_				PQLNLGN
25336	55704	Α	25476	11	1323	VVLLVSVNTEAEESEKAATEQR
		l				/PLEGTDQTLDVEEEQEESKAA
		l				ACGSKKRVVPGIVYLGHIPPHF
		l				QPLHVRNLLSAYG/RSPSHYDL
		l				WNLKYLHHFTWSHHSEHLAFE
						RQVC\HRQHLRVEVTQAKCETI
						FYLQSVEWGQCFLAVDGDLAH
						PDGSWTFAQRPTEQELRARKA
						AQPVGKVLNYYPTQLSLECEVP
						SQPMGTGHSHRGLCQDVKVIN
						VPVSFVWCALVAGLLVVVPPPF
						PQAPEAEVSDISLKRGLQREIEQ
						CRRDIQNFPFPCASEELASQLFP
						LMEVPQGRGTTGFMNAPLTTS
						EVRGLKKELKPLLDDPERVAEQ
						IDQFLGSKLYTWTELMSILGILF
	1					SKEERNMICRAAMGAWERDYP
						AGQNIPAADVTFPARDPQWNN
						NNAAHQKNMRDLQELIIKGIKE
						SAPRPQNLTKAFDEQQEKDEGP
25337	55705	Α	25477	1	490	GTSGTRPLVSVNMEAEESEKA\
						ATEQEPLEGTEQTLYAEEEQEE
1		l				SEEAACGSKKRVVPGIVYLGHI
1		İ		l		PPRFRPLHVRNLLSAYGEVGRV
1		İ	1	1		FFQAEDRFVRRKKKAAAAAGG
1		İ		ĺ		KKRSYTKDYTEGWVEV\RDTR\
	1	l	l	i		IAKRVA\AALLK*PMGARRRSP
		l	ŀ			FRYDLWNLKYLHR
25338	55706	A	25478	2	574	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25339	55707	Α	25479	160	1548	KTSSQTLSLALTMFQRLNKMFV
		1			l	GEVSSSSNQEPEFNEKEDDEWI
						LVDFIDTCTGFSAEEEEEEEDIS
l		1				EESPTEHPSVFSCLPASLECLAD
l		1				TSDSCFLQFESCPMEESWFITPP
l						PCFTAGGLTTIKVETSPMENLLI
		l				EHPSMSVYAVHNSCPGLSEATR
i						GTDELHSPSSPSILPNKMLSVHV
						GTAIHNQAALCQSVESYWQCGI
	1					QLLTQFQSQSKLGQLLAATCKE
						LPGPKESRRTAKDLWEVVVQIC
						SVSSQHKRGNDGRVSLIKQRES
1		1	1			TLGIMYRYVLEPLVLTIILSLFV
1	ĺ	1	1		l	KLHNVREDIVNDITAEHISIWPS
		ļ	1			SIPKKQMSSRTFMSQEETVCRA
						AHTPSLPEEKWVEQLIYALVVA
		1		İ		AARIMAMWGPNAAWLVFLAA
		ı				AGPPPLTPPHSPP/PPPPPPALGR
						WMGPPLRDSASGLPRPPPGRISE
						DSGAWACGPALCPRPAIPSPAP
				ļ		ALRVPEALRLWGTCSV
25340	55708	A	25480	լլ	380	FTSPKTARNWGWLMQVRNQR
						LVLGKAGGKKGSPLEQRGGNG
						HHGGTRLICALV\LVS\MRPLAT
			İ			FAEPQTETCTVAPRERQNCGFP/
			ĺ			GVSRPPQCANKGCCFDDT\VRG VPWCFYPNTIDVPPEEECEF
25341	55709		25481	3	2367	VPWCFYPNTIDVPPEEECEF
25341	55710	A	25482	2	1230	WRRSRRRRPPAPOAGGGDFRA
23342	33/10	<u>۱</u> ^	23402	-	1230	GISPPTGKKSLGLMEPQGNHYR
				l		CRCLOVAGSOAWARCVSMPEL
				l		VVOKVVGHP/LVLLSVVDHFNR
	1		l	l	l	IGKVGIOKCVIGLFWGSWOKK
					1	VLDVLNSFAVPFDEDDKDNSM
l		1	l	l		WFLDHDYLENMYGMFKKVNA
1			l	l		RERIVGWYHTGLKIHKNGITIN
1				l		ELMKRYYPNSVLIIIDVNPKDL
1				l		GLPTEAYISVEEIODDGTPTLKT
1						FEHVTSEIGAESYLEKVATGKL
1	l		l	l		RINHOIIYELODVFNLLPDVSLO
1	i			l	1	EPIKAFYLRTNDOMVVVYLASL
l	1		l	l		IHSVGLTDPFC\VALHNLINNKI
			l			ANODGDKKEGQEKKES/KKDR
ĺ	l			l		KADKGKDKDKEKSDVKKEOK
1				l		NHCLKEKYRFRODSLPDDPRVL
l				l		GLELTPPVARQYSPQDLSEIPRH
				l		ADFRCDPAHFOLWWSQGETPS
		L	L	L		

AGSQAWRAGC VVVHPLVLLSV GROKENVELSV GROKENVELSV GROKENVELSV GROKENVELSV GROKENVELSV GROKENVELSV GROWHTGRELH KRYCPNSVLVIID SAYISVEEVHDD TTYSEIGAEBAU KLLDIRSYLEKV INVOLODYENK INVOLODYENK INVOLODYEN
AGSQAWRAGC CVVVHPLVLLSV GNQKRVVGVLL SNSFAVPFDED DHDYLENMYGM YGWYHTGPKLH ERYCPNSVLVIID EAYISVEEVHDD TISEIGAEEAEEV KLLDIRSYLEKV
CVVHPLVLLSV GNOKRVVGVLL V'SNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TYSEIGAEEAEEV VTTVGTLSQRITN KLLDIRSYLEKV
CVVHPLVLLSV GNOKRVVGVLL V'SNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TYSEIGAEEAEEV VTTVGTLSQRITN KLLDIRSYLEKV
CVVHPLVLLSV GNOKRVVGVLL V'SNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TYSEIGAEEAEEV VTTVGTLSQRITN KLLDIRSYLEKV
GNQKRVVGVLL /SNSFAVPFDED DHDYLENMYGM /GWYHTGPKLH KRYCPNSVLVIID TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
VSNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD VTSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD VTSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
KRYCPNSVLVIID EAYISVEEVHDD TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
EAYISVEEVHDD TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
TSEIGAEEAEEV OTTVGTLSQRITN KLLDIRSYLEKV
TTVGTLSQRITN KLLDIRSYLEKV
KLLDIRSYLEKV
GFYLKTNDQMV
VALHNLINNKI
QEKEESKKDRK
KSDVKKEEKKE
PLLFLRAMDST
ALNPRESPRSPE
AVQTLANVIRP
LVTMKGETVCT
ELEHPAAWLLRE
DGTAFVVLLTE
KFGLPRPQLR/EA
VGQL/AAAGIN
ETLTLADKYGI
IYLSEVLDTPLL
CQRVYRQELGD.
TGTPALTVVLR
EQAVYHSIDAYF
AGATEMALAK
GPNGPAFLAFAR
ENAGLAVSDVV
NLLMGVGAEGI
TLIVKAOGFRA
VDEIVVAKKSPT
KTKKRPPPVEK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide inscrtion)
ŀ				sequenec		
25345	55713	A	25485	145	1918	PLEYFORSVSGVPOLLFLEHLC
23343	33713	ľ`	25405	143	1710	NPRWPLLSLRAMDSTVPSALEL
						PORLALNPRESPRSPEEEEPHLL
ŀ						SSLAAVQTLASVIRPCYGPHGR
		ļ.				QKFLVTMKGETVCTGCATAILF
		İ				ALELEHPAAWLLREAGQTQAE
ł		ŀ	l	1		NSGDGTAFVVLLTEALLEQAEQ
			ŀ			LLKAGLPRPQLREAYATATAEN
						LATLPSLAIQSLGPLEDPSWALF
į.		ľ	ŀ			SVMNTHTLSPMDHLTKLVAHA
				ł		CWAIKELDGSFKPERVGVCALF
		ŀ				
İ		ŀ		İ		GGTLEDSCLLPGLAISGKLCGQ MATVLSGARVALFACPFGPAH
				ļ		PNAPATARLSSPADLAQFSKGS
ł						DQLLEKQVGQLAAAGINVAVV
		ļ.				LGEVDEETLTLADKYGIVVIQA
Į.						RSWMEIIYLSEVLDTPLLPRLLP
						PORPGKCORVYROELGDGLAV
ŀ						VFEWECTGTPALTVVLRGATT
1				i		QGLRSAEQAVYHGIDAYFQLC
						ODPRLIPGAGATEMALAKMLS
		١.				DKGSRLEGPSGPAFLAFAWAL
				l		KYLPKTLAENAGLAVSDVMAE
						MSGVHQGGNLLMGVGTEGIIN VAQEGVWDTLIVKAQGFRAVA
		1		ì		
		1				EVVLQLVTVDEIVVAKKSPTHQ EIWNPDSKKAK\KHPPPVETKKI
25346	55714	В	25486	1	642	EIWNPDSKKAKIKHPPPVEIKKI
25346	55715	A	25487	3	395	FLPVNLTHDWOGSSALATLERP
23347	33/13	^	23407	ľ	373	LSQVRLKRFVGTLIAFMVSAIVI
			1	1		LATASMAVASITESVQTAAFID
						NMARNVSNKLLLQQGIDQKIL
ŀ						ALLQSLEAALEYVGEQQDALA FQQQ*NCNWGHKHICIISLPWN
25348	55716	A	25488	3	358	HEPMCGETHQALQGAMEKLW
23348	33710	^	23400	ľ	330	SRFMELMQE/KKVDLKERVEEL
		l				EHCCI*LSGERQTPSGSGKPGHG
		1				KESCTLVRGAPASESCPPAGEYI
		1		1		ALYQSQRAVRKEEECISRLAQD
		1				KGEVKVKLLE
25349	55717	A	25489	I	250	
23349	133/1/	l^	23489	l'	230	VQCGGIPPGQNNKEEMEVLPEP
	l	ı				PPPINRKKDKSYATAMGPFLRQ
				1		EALSGELLACLVIQD*QGNWV YKPISFNIYKKLRKSIRG
25350	55718	A	25490	1	702	TAPISENITAALKKSIKG
25350	55719	A	25490	1	252	
25351	55720	A	25492	i	122	LAPLVTYFSSLSLGFFNLKGKL
23332	120	l^	25472	l <sup>*</sup>		APSSWRC*GLNEIIRGKH
25353	55721	A	25493	3	505	
20000		r		I*	545	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
25354	55722	A	25494	li .	3345	MRVGFRDIVGSLSEYSFGCPVN
		1				YEVFHSV WITILCCLMANDRKP
		1				QFLYFFQFFSFHGGRNLMSSFH
		1				PGNGHNDSRRSVFYANEKWEF
		1				LDPTPKDLEESIVOEEKKEPTPE
						GNKVSQRLKNLPHTSLKAKQL
		1			İ	LOTSSTNRGTVITATRLAFDLRT
					i	QSTKCSHPASGSSGHSTDFQLE
		1				GEWGLWDLGTKGFKLPYSLSI
						DIDNVKSPHFPHELKTLTVSLGS
		1				NRRMGLEKKECHQKQGALREQ
						LOVHIONVEILVSE
25355	55723	A	25495	296	1350	TLWLQGEQPSTQEIHEKV/LNE
23333	33723	ľ	25495	250	1550	AMGAMMYHTIILTREDLEKFK
		l			l	APRVIVQIGSGYDNVDIKAASE
		l				LGIAVCNIPSAAVEETPDSTICHI
						LNLYORNTWLYOALRGOAVA
		1				VRAKAFGFSVIFYDPYLODGIE
		ı			1	RSLGVORDLLYOSDCVSLHCN
						LNEHNHHLINDFTIKQMRQGAF
		ŀ			1	LVNAPHGGLVDKKALAQALKE
						GRIRGAALYVRESEPFSFAQGP
						LKDAPNLICTPHTAWYSKOASL
						EMREAAATEIRRAITGHIPESLR
					ł	NCVNKEFSVTSAPWSVIDOOAI
						HPELNGATYRYPPGIVGVAPGG
						LPAAVEGIIPGGIPVTHNLPTVA
						HPSQAPSPNQPTKHGDNREHSN
25356	55724	A	25496	694	1185	PKPFKEGTIRGAALDMHESEPF
23330	33724	A	23490	094	1103	SFAOGPLKNAPNLICTPHTAWY
						SEQASLEMREAAATEIRRAITG
		1				CIPESLRNCVNKEFFVTSAPWS
						VIDQQAIHPELNGATYRYPPGV
						VGVAPGGLSAAMEGIIPGGIPV
					i	THNLPTVAHPSQAPSPNQPTK*
						MK*KOMGEVA*GAARIRGETL
						GLNGFGCTGQA/VAVRAKAFG
						FSVIFYDPYLQDVVERSLGVQR
						VYTLQDLLYQSDCVPLHCNVN
		1		1	l	EHNNHLINDFTIKQMRQGAFLP
		1	l			PKPFKEGTIRGAALDMHESEPF
		l		1		SFAQGPLKNAPNLICTPHTAWY
		1			1	SEQASLEMREAAATEIRRAITG
1		1		1	1	CIPESLRNCVNKEFFVTSAPWS
1		1		1		VIDQQAIHPELNGATYRYPPGV
1		1		1		VGVAPGGLSAAMEGIIPGGIPV
L					l	THNLPTVAHPSQAPSPNQPTKH

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
<u></u>		_				
25357	55725	Α	25497	290	1251	PFMLYVSISTLYIAFCHILNLYR
						RNTWLYQALWEGTRVQSVEQ
					i	MGEVA*GAARIRGETLGLNGF
		1				GCTGQA/VAVRAKAFGFSVIFY
						DPYLQDVVERSLGVQRVYTLQ
						DLLYQSDCVPLHCNVNEHNNH
					ŀ	LINDFTIKQMRQGAFLVNAARG
i						GLVDEKALAQALKEGTIRGAA
						LDMHESEPFSFAQGPLKNAPNL
					l	ICTPHTAWYSEQASLEMREAA
1					ł	ATEIRRAITGCIPESLRNCVNKE
						FFVTSAPWSVIDQQAIHPELNG
			İ			ATYRYPPGVVGVAPGGLSAAM
						EGIIPGGIPVTHNLPTVAHPSQA
					1	PSPNQPTKHVDNREHPNEQ
25358	55726	l <sub>A</sub>	25498	1	1538	MLLQKTQFEYAFKKKRKLEES
23336	33720	1	25470	l'	1550	KKRGAGPASSDPRWRGSSQTA
1						PHASEVSGAPLGRSCETTRDTG
				1		VGPSPRQWLGAGAGTWQHRA
						RAASTPSSRGLRALOTWGGGE
			Ì			VMNGPLH\PPPPRVALLD/SRNC
		1				TVEMPIPKDLATMAFCDTHSTQ
						EIHEKILHEALGAMRYHTITLA
		1				RADLEKFKALGVIVRIGSGYDN
					1	VNIKAACELEIAVCNIPSAAVEE
						TANSTICHILSLYRRNTWLCQA
	1				l	WARKHVCYSMGQIREVALGG
1	i		:			AHIGGETQG\LIGFGSTGQAVPV
	1					RAEAFGFSVIFYDPYLQDGIERS
1						LGVQRMSQGAFLVNAARGALV
1	1					DEKALAQALNNGKIR/GAALDV
						PQSELFSFAQG\SLEMREAAATE
						IRRTITGCIPESLRNCVNKEFFVT
i						SAPWSVIDQQAIHPELNGATYR
						YLPGFVCVAPGGLPAATEGIIPG
						GIPVTHNLPTVAHPSOAPSPNOP
						TKHGDNPEHPNEQSRECRKVII
						QIHLRPRDSEKLMNSEKTNLTV
				İ		FLADSGHMHY
25359	55727	A	25500	1	2595	
25360	55728	A	25501	561	1023	SGHDAYREQIQEYRVISLLLNP
						N\DHVNKCQSTNDAYPTGFRIA
1		1	l			VYSSLIKLVDAINQLREGFERK
						AVEFQDILKMGRTQLQDAVPM
		1				TLGQEFRAFSILLKEEVKNIQRT
1	l	1		1		AELLLEVNLGATAIGTGLNTPK
		1	1			EYSPLAVKKLALKSLAFVGNLF
25361	55729	١,	25502	2	227	LISI LAVKALALASLAF VUNLF
25362	55730	A	25503	262	428	
23302	22/20	ΙΑ	23303	202	420	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25363	55731	A	25504	389	2310	ATSGPPGRSLGSACTIWVLVWT
25505	33731	^	23304	307	2510	GSIPIYSFHGKVEKYMCFHNMS
						DDTWSAKVFFPLEVFGFLLPMG
						IMGFCCSRSIHILLGRRDHTOD
						WVOOKACIYSIAASLAVFVVSF
		ŀ				LPVHLGFFLQFLVRNSFIVECRA
	ŀ					KOSISFFLOLSMCFSNVNCCLD
						VFCYYFVIKEFRMNIRAHRPSR
						ATEEVSKNLVAMKEILYGTNE
						KEPQTEAVAQLAQELYNSGLLS
1						TLVADLQLIDFEASLGLHGLEQ
l						AVDLALPIAQAQGEVLNNGKC
					j	MDQFPVDVYQGGAGT\YVNMS
						TNEVLANIGLGLMGHQKGEYQ
				1		YLNPNDHVNKCQSTNDAYPTG
						FRIAVYSSLIKLVDAINQLREGF
1		1				ERKAVEFQDILKMGRTQLQDA
l						VPMTLG\QEFRAFSILLKEEVKN
						IQRTAELLLEVNLGATAIGTGL
		l				NTPKEYSPLAVKKLAEVTGFPC
l		l				VPAEDLIEATSDCGAYVMVQG
		l				ALK\RLAVKMSQI\CNDLRLLSS
l					1	GPPG\SSIMPAKVNPVVPEVVN
1		1			İ	QVCFKVIGNDTTVTMAAEAGQ
		1			1	LQLNVMEPVIGQAMFESVHILT
ŀ		l		1		NACYNLLEKCINGITANKEVCE
		1			1	GYVYNSIGIVTYLNPFIGHHNG
		l				DIVGKICAETGKSVREVVLERG
						LLTEAELDDIFSVQNLMHPAYK
25364	55732	Α	25505	133	375	
25365	55733	A	25506	3	505	ARGREGVSRRERPLLSARRLGA
				l		EWDSAGAETASGLQVPRLGGS
						WPQTSVFSAAVKARGCRIATLP
		l		l	1	MDLIGFGYAALVTFGSIFGYKR
		l		1		RGGVPSLIAGLFVGCLAGYGAY
		l		I	Ì	RV\SNDKRECKKCHWFTAFLPG
				l	1	LPSMGVRFKRSKKIM\PAGLVA
		1		1		GL\SLM\MILRLVLLLL
25366	55734	Α	25507	244	696	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
				sequence		
		_				
25367	55735	Α	25508	1	1442	MGQLHQAQASADIATSRLQQT
						SLTDVTRHQQFFSTYNTDDFIQ
						FTATYREQTRTRRQRQYAVNH
	l					VTFFFGKCTFRDRHRHRVIGIVL
						NIGLTFPAHQTQDGIGSTRSQR
l						QSRLVANKVATRNLVKHFDDD
						REANRGIQEAQTEHHHRGVLV
						NESRQRFGCQQHNRHRNHYRR
						HHHRQMVNHPYCSNYRIQRED
						GVKDDNLCDDHPETGIQLYASL
i		l				LLQVFFFAANIYGWYAWSRQT
				1		SQNEAELKIRWLPLPKALSWLA
	į .					VCVVSIGLMTVFINPVFAFLTR
		l				VAVMIMQALG\LQGVMPELQA
		1				DAFPVWDSCMMVLSIVAMILM
1					ŀ	TRKYVENWLLWVIINVISVVIF
1						ALQGVYAMSLEYIILTFIALNGS
		ļ.				RMWINSALIHQVVLDLIQQGIVI
						VWRDHLHMQRLHRLLAYHPC
		1				MYLVHIADFRDFPAHTRLQVQ
l		l				RFPAIPVHLQVIHSRYLSTVATR
1		l				YAESEATPVSGALGLLCPTLPIV
25368	55736	A	25509	133	375	
25369	55737	A	25510	2	471	AFAORETAGRRVGORWCGDCF
		-				RTPGTALGGSWPOTSVFSAAV
1		l		1		KARGCRIATLPMDLIGFGYAAL
						VTFGSIFGYKRRGGVPSLIAGLF
		İ				VGCLAGYGAYRV\SNDKRECK
		i				KCHWFTAFLPGLPSMGVRFKRS
						KKIM\PAGLVAGL\SLM\MILRL
						VLLLL
25370	55738	Α	2551I	3	432	NSRVDDFVAAQDAKGKKVAP
23370	33730	^	23311	٢	132	APAVVKKQEAKKVVNPLFEKR
						PKNFGIGQ\QRLLARAEKKAAG
						KGDVPTKRPPVLRAGVNTVTT
						LVENKKAQLVVIAHDVDPIELV
						VFLPALCRKMGVPYCIIKGKAR
						LGRLVHRKTCTTVAFT
25371	55739	A	25512	59	882	SRLKNASIFVASPSGKKAKGKK
233/1	33/39	Ι^	23312	139	002	VAP/APAVVKKOEVKKVVNPLF
		1				EKRPKNFDIGQDIQPKRDLTSFV
		1				
		1				KWPPLYQRQRAILCKWLKVPP
	1				1	EINOFTQALDHQTAALLLQLAH
	1	1			1	KYRSETKQEKKQRLLALAKKK
		1	1		1	AAGKGGIPTKRPPVLRAGVNTI
1		l			1	TTLLENKKAQPVVIAHDVDPIE
1		1			1	LVVFLPALCHKMRVPYCIIKGE
1		1			I	ARLGRLVHRKTCTTVAFIQVNS
1		l	1		1	EDKGALAKLVGAIRTDYNDRY
		1				NEIRRHWGGNVLGPKSVACIG
1	I	1	l	1		KLEKAKAQELATKLG

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25372	55740	Α	25513	1	833	I GTRPKMPKGKKAKGKKVAPAP
23372	33740	ľ`	23313	ľ	055	AVVKKQEAKKVVNPLFEKRPK
						NFGIGODIOPKRDLTRFVKWPR
				1		YIRLORORAILYKRLKVPPAINQ
1						FTOALDROTATOLLKLAHKYR
1		1				PETKHEKKORLLARAEKKAAG
						KG\DVP\TKRPPV\LRAGVNTFT
		l				PL\VENKKAQLVVIAH\DVDPM
		İ				RGWLSFLPAL\CRKMGVPYCIIK
1				1		GK\ARLGRLV\HRKTCTTV\AFT
		l				
l				1		QVNSESQRRLWAKLVEAIRTN
						YND\RYDEIRRHWGGNDLRPK\
		<u> </u>				SVARI\AKLEKAKAK\ELATKLG
25373	55741	A	25514	1	1176	MEKELVDHTGLFLSAHASEAL
l		1				ALKLMIYSEVAHKLRAVRSQH
1		1				PDMGVSLPLTPANSCPKTIERM
		l				RRSRELEREKDQSIETDHLPWA
	1	1				FGSTFLKTPLSCKTLMKYICYA
1	ļ	i				FIINLSFVKGVSAVTLMMSEES
		l				NMQMQFSVSITSGFGPFKSHIIA
						AIPNAERKESQGEKMAPAPAVI
		ı				KKQEAKEVVNPLFEKRLKNFGI
		1		1		GQDIQPQRDLTRFVKWPHYIRL
		1				QRQRAILS\AHKYRPETKQEKK
İ	İ			1		QRLLAQAKKKATSK/EDIPTKR
		i		1		PPVLRAGVNMVTTLVENKKAQ
	ł	1		1		LVMTAHDVDPIELAVFCLPAPC
1		1		i		CKKGVPYCIIKGKARLGHLVHR
1						KTCTTVVFTKVNSEDKGALAK
						LVEAIRTNYDRYDEIHCHWGG
		_				NVLGLKSVAHIIKLEKAKVKEL
25374	55742	Α	25515	2	524	
25375	55743	Α	25516	144	412	AGSCPFAAGPGPLGSGRCFVLIR
						FILIQNRAGKTRLAKW\YMQFD
	ŀ			l .		DDEKQKLNEEVHAVVTVRDAK
		_				HTNFVGVSGTFKIILPPLWLASN
25376	55744	A	25517	38	476	
25377	55745	A	25518	235	892	RSRVGTNRLFGETYPRASPGPQ
1						STALLTAYKKMTDLVAVWDV
						ALSDGVHKIEFEHGTTSGK/REV
ı		1				VYVDGKEEIRKEWMFKLVGKE
	1	1				TFYVGAAKTKS/ATINIDAISGF
1		1	1			AYEYT\LEINGKSLKK\YMEDRF
	1	1	1			KNPPILWVLHM\DG\ENFRIVLE
			1	1		KDAMDVWCNGKKLETARDFC
	1	1				KMSDTISDDTKVDEQERALSRT
		1		1		PEDKWNFRPAVPMRGERGSPS
1						HCGQAH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25378	55746	ĪA	25519	li .	1233	MOLKFPGROKIHISKKWGFTKF
25510	55710			1		NADEFEDMVAEKRLIPDGCGV
				1		KYIPNRGPLDKCHHGKCVATG
		1				TSYMCKCAEGYGGDLCDNKN
	1	l	1			DSANACSAFKCHHGQCHISDQ
		1	ľ			GEPYCLCOPGFSGEHCOOGLLG
			1			GVREMLRCKVRSNIVTMKAKL
				i	i	SFRICMTLTILANMWPRPILGG
		1				VDQIPIKPKSKVLYLGAASGTT
			1	1		VSHVSDIIGPDGLVYAVEFSHR
		ļ	l .			AGRDLVNVAKKRTNIIPVLEDA
		1				RHP/HQPDQ\ARSVALNAHTFLR
ŀ		1				NGGHFLISIKANCIDSTASAEAV
		1				FASEVRKLQQENLKPQEQLTLE
		1				PYERDHAVVDYSSSSATEQRRT
						ENDSDKLTEVGFRKLVINFSKL
1			i			KEDVRTHHKEVKNLEKRLDEW
						LTRINSVEKTLNDLMEAENHGT
1	i					KKYVTQAQASVAYLIKWKKG
25379	55747	A	25520	78	978	AAGHSAKKSCLSLLPAWSFPLG
		1				STRAQWHVRRLQARISGGGRH
1		1		l	ŀ	RCGRRGQ\GKTRRRMGPMVVS
1		1		1		VEPHRHEGVFIYRGAEDALVTL
				ļ		NMVPGQSVYGERRVTVTEGGV
				1		KQEYRTWNPFRSKLAAAILGG
		1	}	1		VDQIHIKPKSKVLYLGAASGTT
		1		i		VSHVSDIIGPDGLVYAVEFSHR
l	1	1		1		AGRDLVNVAKKRTNIIPVLEDA
1		1		ŀ	1	RHPLKYRMLIGMVDVIFADVA
1		1		l		QPDQSRIVALNAHTFLRNGGHF LISIKANCIDSTASA\EAVFASEG
1		1		1		
1		1		ł		EKLQQENLKPQEQLTLEPYERD
		4.	25521	230	314	HACV/VGVYRPLPKSSSK OMPGNNPAFSA*CDAGASYQA
25380	55748	Α	25521	230	314	YVNSAIY
0.000	55749	١.	25522	1360	1848	RFRALV/TEGFSLRELFPVATVL
25381	55/49	A	25522	1360	1848	VASST\VTKRFIFLLAAD\VRLA
		1				LRRSI\THPFVRKQELTVYTLNN
	1			i	-00	ELENLLTNVVNQAQQGGKVMI
	1			1		DSVPVDPNMLNQFQSTMPQVK
1		1	1	1		EQMKAAGKDPVLLVPPQLRPL
						LARYARLFAPGLHVLSYNEVPE
						ELELKIMGALM
t	1		I			ELELKIMOALM

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25382	55750	Α	25523	91	1184	AAACSPPPPARLTYGSETLRGG
		1	i		1	DCSKMAAGCCGVKKQKLSSSP
						PSGSGGGGGASSSSHCSGESQC
l		l		1		RAGELGLGGAGTRLNGLGGLT
i		l			ł	GGGSGSGCTLSPPQGCGGGGG
		l				GIALSPPPSCGVGTL\LSTPAAA
						TSSSPSSSS/APASSSSPGSRK\M
		1				VVSTE\MC\CFCFDVLYCHLYGI
		1				\QQP\RPPRFTNEPYPLFVTWKIG
	İ					RDKRLRGCIGTFSAMNLHSGLR
	į .	1				EYTLTSALKDSRFPPMTRDELP
		1		ŀ		RLFCSVSLLTNFEDVCDYLDWE
				l		VGVH\GIRIEIHQCKKASKR\TA
	1					TYLPEV\AKEQGWDHIQTIDSLL
	1	i				RKGGYKAPITNEFRKTIKLTRY
						RSEKMTLSYAEYLAHRQHHHF
		1				QNGIGDPLPAYNHYS
25383	55751	Α	25524	3	154	
25384	55752	Α	25525	575	1707	TALLLTQSLFGGLFTQTHMKFG
		1				AVTRI*NRKTGNSKKQSTSPPPK
		1				ERSSSPATEKSWMENDFDELRE
	İ	ı				EGFRRSNYSELREDIQTKGKEV
	1	l			ļ	ENFERNLEECITRITNTEKCLKE
1		ı				LMELKTKARELCEECRSLRSRC
		1				DQLEDCLLKKLHSHQANPEFDL
		1				ITEHLTLCIRISIQIKAYLSLSKA
		ı				QSSLSHRPPTYLAYLFNGFRLF
		ı				KNLKAYLHPGEINSFIAHTKPV
		1				wwslhtdaheiwcrdsdlklv
		1				PTLPLIPLEAALRNITHSLSIPPP
						KNFRRPNTSTLFCVIFLINIRRQE
						YQASEPKPSHRIPCDLQRIKYLG
		1				IQLTRDVKDLFKENYKPLRNEI
	i					KEDTNKWKNIPCSWVGRINIVK
	1	l				MAILPKPLLVIPRQTGSGMDPQ
		İ				QTSGDLQKCLTVLRKTNKQKAI
		1				ASTSRKRMTMQKLHLKEKLINS
	1	1				KDQRTNDKNHMIISIDAEKAFN
	1	1		1		KTEHRFMLKTLNKLEINSRWIK
	i					DLNVKPKTIKTLEENLGNTIQDI
		1				VMDKDFMTKTPKAMATKAKI
1		I				DKWDLIKLKSFCTAKETIIRVY
		1				RQPTERESIFVIYPSDKGLISRIY
	1	1		I	1	KELAIPGKGNSSNVSKDSKMSK
1	1	ı	1		1	HQKMQGENKHD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence		
25385	55753	A	25526	110	569	TALLLTQSLFGGLFTRTRMKFG
	ł					AMTRIG\DLPWEINPLSSCSLLC
	i	l				EKHPPTTSGPQTDQPKKHLTNF
		ĺ				KSETKETCFIHEPKTLAPVTDW
						EGSLPLVFNHCRDGLSDHSATF
	ŀ					QGCQTMQGCLPWSFTLSGKSR
	İ			1		FSGEGANHHGHRASGNSHSGS
25386	55754	A	25527	2	464	LFGGLFTRRRMKFGAVTRIR\DF
						PWEINPLSSCSLL/CEKDPRTTS
1						GPQTDQPSKHLTNLKSASTPPP
	ł					YNPFITSPPHTRSGLQFRSTSSPP
<b>!</b>	l					APAQQFTLKKVAEAKGIVKVN
				1		APFSLSDLSQISVRLGSFIKYEKS
l		1				SPVHGSFGSNPETLYSPRP
25387	55755	A	25528	162	206	
25388	55756	A	25529	74	446	TAMLLTQSLFGGLFTWTRMKF
ļ		1				GAVTRIG\DLPWEINPLYSCSLL
	1	1				SRFKKIKACYHSPATSWPFKTY
	l					KLSLQLPHFTCPKTRQALQVSS
l		1				GAVPYQPNCFAYPPCGAQPVPS
						FVLNTFLHNSLCRA
25389	55757	A	25530	66	311	FGAVTRIG\DLPWEINPLSSCSLL
						REKEPPTTSGPQTNQAKKHLTN
						FKSGACYTCRKSGHWAKECPQ
						PGIPPKPRPICVGPH
25390	55758	A	25531	728	825	MKFGAVTRIG\DLPWEINPRSSC
						SLLHEKDPPM
25391	55759	A	25532	291	311	TALLLTQSLFGGLFTQTHMKFG
		_				AVTRI*NKKNNTK
25392	55760	A	25533	1	1056	
25393	55761	A	25534	245	487	TALLLTQSLFGGLFTQTRMKFG
		1			1	AVTRIG\DHPWEINPLSSCSLFQ
		1				EKDPPTT/SGPQTDQPKKHLTNF
					L	KSTSFVFSSCIPPP

SEQ ID NO:	SEQ 1D NO: of peptide sequence		SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25394	55762	A	25535	818	2391	TALLLTQSLFGGLFTQTRMKFG AVTRIGOIPWEINPPSSCSLEIP, RIPLLHFFGAGPSTQPELJUSPS AASPALGQGQDLINLVFKVYN NRKKLQFLASTVTGTATSPAH KNRQTREPQOPGVPEPPSIGAC YKCQKSGHQAKECPQLRIPHLS QWTGYPEPSIGAC YKCQKSGHQAKECPQLRIPHLS QWTGYPEPSIGAC YKCQKSGHQAKECPQLRIPHLS QWTGYPEPSIGAC GWTGYPEPSIGAC AIRKFSSILMRCNLCVOSPILVG EGVTGARCQGKSSTANPKLSL KSRTSNKKMKAFMSALQATFE EETLORVNSFHHNVLDNCLLP NGGTCLFETAPPEWEQKIQNTH LSIVDNLLWECKASGKPNPWY TWLKNGGRLNFEERIGIENGTLI ITMLNNSDSGYYQCAAENKYQI IYANAELRVLGSQLVHFRENGT ITMLNNSDSGYYQCAAENKYQI IYANAELRVLGSQLVHFRENGT
25395	55763	A	25536	425	749	TSGSQGTTTENQDELQIKFISAR HSQATEGINSTSAKFD IASLLTQSLFGGLFTWTHMKFG AVTRT/RGDLPWEINPLSSCSLL HEKDPPTTSGPQTDQPKKHLTN FKSAQLKASGK/DLQKPYQHFQ TLQQLLPLQWAPCYGPSSVSI

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25396	55764	A	25537	2	2204	I IDMIFTPGPPSTPKHKKSOKGSA
23390	33764	^	23337	<sup>2</sup>	2204	FTFPSQOSPRNEPYVARPSTSEI
						EDQSMMGKFVKVERQVQDMG
		1				
		ı				KKLDFLVDMHMQHMERLQVQ
	İ	i .			İ	VTEYYPTKGTSSPAEAEKKEDN
		l				RYSDLKTHCNYSETGPPEPPYSF
		ı			1	HQVTIDKVSPYGFFAHDPVNLP
						RGGPSSGKVQATPPSSATTYVE
		1				RPTVLPILTLLDSRVSCHSQADL
١,						QGPYSDRISPRQRRSITRDSDTP
		1				LSLMSVNHEELERSPSGFSISQD
		1				RDDYVFGPNGGSSWMREKRYL
		1				AEGETDTDTDPFTPSGSMPLSST
		1				GDGISDSTVPLFLSSEILQKQVG
		1				QSITSMLGFLSRGPSMKLCMGL
		1				ACVLSLWNTVSGIKGEAKKEK
						GMTFLPTTDSKKFFSLLSVTSYS
		1				SFAFHKFSVAVYNISNLKTVDP
		1				AKFPTRYCYCLNNRTNDLSDFT
		1				ALLVDIIGNSTSYLTEIFKSTSIL
		1				SVNQSNESDCIFICVMTGKSGR
		1				NLSDFWEIEEKYPIINYTFTSGL
		1				SGVLALLLTQSLFGGLFTRTRM
		1		1		KFGAVTRIG\DLPWEINP/LSSCS
		1		1		LLHEKDPPTTSGPQTDQPKKHL
						TNFKSAARPTFLGQGQVPLNPF
		1				SFTLSGKSCFPRRQEPPNRLFPH
		1				PNLLSLCPNPLFLCPNPFSTFLE
		1				GKNHHPHPFSVSQVFSLGLPPS
		1				LWEHSPMAHRLRVQPRQQPPDI
						HKQVISLQSGHSLLVKSQSWSQ
		<u> </u>				DPIKFQLPHHHKNTASVCINPSV
25397	55765	Α	25538	110	542	TALLLTQSLFGGLFTRTRMKFG
						AMTRIG\DLPWEINPLSSCSLLC
İ						EKHPPTTSGPQTDQPKKHLTNF
						KSETKETCFIHEPKTLAPVTDW
						EGSLPLVFNHCRDGLSDHSATF
						QGCQTMQGCLPWSFTLSGKSR
						FSGEGASCSLPG
25398	55766	Α	25539	1	781	MPLQPLATPFTSPGSPSVAQVT
						TNTGEPGFAQQEYAETPQTTAR
						PPHPHPALRALQASVHQTPRLG
						DCLGSSESATALHGSGEPNKLA
		1				PPGRPTERGGLFKCSVPLRTVR
		l				GCRAGLRGTETVPSSLQRQPAG
		1	l	I		DVGWINNKSTTALDRTPTDTQ
						RTRRPRPPKQKQRGRALKERPR
1		1		I		DSDSAREGPLKAVAGLFGGLFT
1		1	l	1		RTCMKFGAVTRIG\DLPWEINPL
			l			SSCSLLHEKDPPTTSGPQTDQPK
1	1	1	l			KHLTNFKSDLLSLATED

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25399	55767	A	25540	1571	1781	TALLLTQSLFGGLFTRTRMKFG
		1				AVTRIG\DLPWEINPSSSCSLLRE
		1			l	KDPPTTSGPOTDOPKKHLTNFK
		1				SA
25400	55768	A	25541	2150	3195	TVLLLTQSLFGGLFIWTRMKFG
						AVTRIG\DLPWEINPLSSCSLLH
1		1				EKDPPTTSGPQTDQPKEHLTNF
1						KSDED
25401	55769	Α	25542	4688	5149	TAMLLTQSLFGGLFTRTRMKFG
	İ	1				AVTR/IRGTDLPWE\INPLSSCSL
		1				LREKDPPMTSGPQTDQPKKH\L
						TNFKSGACYTCWKSGHWAKER
	i	1				PQPGIPPKPRPICVGPHLKIRTCS
		1				THLGQATPRAPGTLAQGSLTDS
		1				FPDLLGLAAEDSHCLIASEAP
25402	55770	A	25543	1	433	MAAFPAALNRPTRARARRRIS
		1				AHSAASAAAAVVVAGTARGM
1						VPGSEGP\CRA\GDEVADWEIVI
						EGTANLGPYFEGLRKHYLLPAI
		1				EYFNGGPPAETDFGGDYGGTO
		1				YSLVVFNTVDCAPESYVQCHA
						PTSSAYEFVTWLDGIK
25403	55771	Α	25544	1	235	
25404	55772	Α	25545	1	301	
25405	55773	A	25546	2	438	
25406	55774	Α	25547	1058	1494	KSVRLVVN/YLRTQKAVVRVSP
		1				EVPLQNILPVICAKCEVSPEHVV
		ı			İ	LLRDNIAGEELELSKSLNELGIK
		1			İ	ELYAWDNRRVPSAVPMQGPWP
		1			i .	AEHFLQVNEQPPAGSPSPCPSSS
		1				SSSSGLRGGMQTANGPACALTP
		1				TCAQTDCPCPTSH
25407	55775	A	25548	1	3965	RRFQPLPSAALRRCPPPARVGG
						RWVSAEKVNEGGSGGGGGQRL
		1		1		TRRARSTARVPAPGTMDAPRAS
		1				AAKPPTGRKMKARAPPPPGKA
		1	l	}		ATLHVHSDQKPPHDGALGSQQ
			1	1		NLVRMKEALRASTMDVTVVLP
		1	1	1		SGLEKRSVLNGSHAMMDLLVE
			1			LCLQNHLNPSHHALEIRSSETQ
		1	1			<b>OPLSFKPNTLIGTLNVHTVFLKE</b>
1		1	1	i		KVPEEKVKPGPPKVPEKSVRLV
		1	1			VNYLRTQKAVVRVSPEVPLQNI
		1		I		LPVICAKCEVSPEHVVL
25408	55776	A	25549	1	388	
	1	1	- 4 . 7			

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25409	55777	A	25550	1	1748	MVLARVARRPAGSAEAQASLA
23.10	153777	1.	23330	ľ		GKAALPERARKMSSPGIDGDPK
l						PPCLPRNGLVKLPGQPNGLGAA
		l				SITKGTPATKNRPCQPPPPPTLP
l .					1	PPSLAAPLSRAALAGGPCTPAG
1		1				GPASALAPGHPAERPPLATDEK
1		1				ILNGLFWYFSACEK\CVLAOVC
						KAWRRVLYQPKFWAGLTPVLH
		l		l		AKELYNVLPGGEKEFVNLQGF
1		l				TARGFEGFCLVGVSDLDICEFI
1						
ŀ						DNYALSKKGVKAMSLKRSTIT
						DAGLEVMLE\QMQGVVRLELS
		1			1	GCNDF\TEAGLWSSLSARITSLS
l						VSDCINVADDAIAAISQLLPNLA
						ELSLQAYHVTDTALAYFTARQ
						GHSTHTLRLLSCWEITNHGVVN
						VVHSLPNLTALSLSGCSKVTDD
1		1				GVELVAENLRKLRSLDLSWCP
1		1				RITDMALEYVACDLHRLEELVL
		l				DRCVRITDTGLSYLSTMSSLRSL
						YLRWCCQVQDFGLKHLLALGS
						LRLLSLAGETPVSALTLAVTTH PHLVHPPNLPGPCANSHPARTH
1						
						SPGSEAEEEGGAARPSPPEPWA
		1				ARTEPPSDPAAGCPLLTTTGLS
					ŀ	GLVQLQELEELELTNCPGATPE LFKYFSOHLPRCLVIE
25410	55778	١.	25551	1	377	MRRLTRRLVLPVFGVLWI/DGA
25410	33//8	A	25551	1	311	AVLLGNQEEVGGAD/WDLKCR
1						PL/EVNVSKSDDTLKINGVEDH
1						KTIFDGDGKTYQNVQQFIDEGN
						YTSGDNHTL/SRPSLR*RQRP*IP
						CIRSQHGNRKRIPRRRIFI
25411	55779	A	25552	222	287	CIRSQUONKKIIIIGGUT
25412	55780	A	25553	2	918	GHCEVNRDWLQPLLHRVKEDY
25412	33780	1	25555	1	/10	TRVVCPVIDIINLDTFTYIESASE
					ł	LRGGFDWSLHFQWEQLSPEQK
		1				ARRLDPTEPIRTPIIAGGLFVIDK
						AWFDYLGKYDMDMDIWGGEN
						FEISFRYWMCGGSLEIVPCSRV
						GHVFRKKHPYVFPDGNANT\YI
1						KNTKRTAEVWMDEYKQYYYA
1		1			1	ARPFALERPFGNVESRLDLRKN
1		1				LRCQSFKWYLENIYPELSIPKES
1		1				SIQKGNIRQRQKCLGISKGRTTK
1		1		1		KPQT*S*A\LCQGQRRRCQSPRV
		1		1		WGLSHYTQADSFQGELVALFSS
	1	1		1		FTFVSLGAPVVSCSFARMGD
	1	1_	L			LILASPOALA ASCSLAKMOD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25413	55781	A	25554	8.4	2804	PRGSWRCRRDLKCRPLSHSDA DWDDLWDQFDERRYLNAKKW RVGDDPYREVCESTGGRVSD AIRAIPDTRHLRKKATSNSLSRQ QLASPLEPRSSYGGYTPGPHAIGP LWTSGSLKTPNHIDTVFAPGLP QPWFHLNYLRAMPSLSSAPKCT LLVYCTDLPPTSIIITFHNEARST LLTHREPRAVSTSQMAMTAAA LTPAPLRTYSVHLSCRAHQLVP MPQRKKYDETWVREHTKHSKI SLFPSCRLHFSCLSRRMAVGS GKFQVMGDLGEPFLRVRWLRI WTLGPDFHGSALNSVLNRIPT HLIREIILVDDFSNDPDDCKQLI KLPKVKCLKNNERGGLVSSRIR GADIAQGTTLTFLDSHCEVNRD WLQPLLHRVKEDYTRVVCPVI DIINLDTFTYJESASELRGGFDW SLHFQWEQLSPEQKARLDPTE PIRTPIIAGGLFVIDKAWFDVLG KYDMDMDIWGGENFEMMTVQ VLQPRRSEALICTWKVHLTRL QSPCPAMLAPEYAPEASVLVCT STALLIALVQAFFTGPQAKKLQ QSPCPAMLAPEYAPEASVLVCT SLTYTTLGSEISFRVWCGG SLEIVPCSRVGHYFRKHPYVF PDGNANTYIKNTKRTAEVWMD ESKLDLRNINGRSGRPFANLEVER EYKQYYYAARPFALERPFGNV ESKLDLRNINGRSGRPF
						LAWSGEETDNDQLDEGFYVYQ

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25414	55782	A	25555	11	2439	MPLKKKGDEPQMEKYIQERSM
		l				LAPPSCSDHRDTHSRCIPHIQRL
-		1				FQCPLGPWFQGEQRNQARGEG
	Ì	1				GALHPLPVTAGTVALPGAAQPT
		1				PARGNVTESLQGATVKLVCKK
		1				TSFIFIYCQHPAQCLALACDHEC
				ł		IDLCTHVASTSLCLRGYQGMKR
						TIERALTATLAQGTAVPPFPSDV
						PSOKDAAVRGKGDGSEWERTL
		l				TMKRSNLNSEKILPAILLLTEFP
		ı			1	RHQSPCSFDKPHHPNTLGCWLP
		1				TVLETRGGTNGQSSGKREATLC
		1				PCPLLGLPISEEDCVPPALLLPPR
						G\LPPGLQLSWAPVPQFPPLGPS
		1				SLGIPA/LPLVLNLGCLPSLVCPP
						TSAHTSEVAPSLKSPAEPSPPAR
		l				LPRSHQPALSREMRHSDYSVSV
		l				HAICWDHDFYTLVTHYMNNTS
						PISSKRSSDKLNPHVLVVQDSM
						TILSLHNHLALAGQDMMVWEP
		1				RKTLQRRQQPDSSSHSPPPALV
						ECHPLEPEPLVAGIMYSFSGLQ
		1		1		GVGLRDRAVDETNKRNEKRTL
	1					EMSRVEALSSFENSEFGCPPSIN
		1				TREITGNSLEGNVKKGVSVPNC
		l				TAPGKRTEKKYSKIHEMVKHS
		l				GNCKRTDGIWEEYGWSWRLH
	ļ	l				MKKVFPGFMLVKGGEDAAPGT
		l				KEIKSVSGIFQRGKKKPRGRKE
		l				KNRKKRGFAFSKETNFVYLLIL
		l				VCLIGKVVVWLTSACAEKPKP
		乚				HGEATCRHSGPSAPLNFQPTRV
25415	55783	Α	25556	2	1178	AKCVEVCGKREPPSMSPLNQSA
	İ	1				EGLPQEASNRSLNATETSEAWD
	1	1				PRTLQALKISLAVVLSVITLATV
		l				LSNAFVLTTILLTRKLHTPANYL
		İ				IGSLATTDLLVSILVMPISIAYTI
						THTWNFGQILCDIWLSSDITCCT
		ı				ASILHLCVIALDRYWAITDALE
		İ			1	YSKRRTAGHAATMIAIVWAISI
		1				CISIPPLFWRQAKAQEEMSDCL
		I			i	VNTSQISYTIYSTCGAFYIPSVLL
		ł				IILYGRIYRAARNRILNPPSLYG
		1		l	1	KRFTTAHLITGSAGSSLCSLNSS
		1		1	1	LHEGHSHSAGSPLFFNH\VKIKL
		1		1	1	VTVALKRKEDSAARERKATKIL
						GIILGAFIICWLPFFVVSLVLPIC
		1			1	RDSWWIHPALFDFFTWVGYLN
						SLINPIIYTVFNEEFRQAFQKIVP
		Ļ	L	ļ		FRKAS
25416	55784	Α	25557	3	146	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25417	55785	A	25558	45	592	PSPPPPARAPSARTRRAPIPAAG
23417	33703	Γ.	22550	1.5		OGRARPPRTVSRCGSAAMATKI
		1		1	\	DKEACRAAYNLVRDDGSAVIW
	l					VTIKYDGSTIVPGEOGAEYOHFI
		1		}		QQCTDDVRLFAFVRFTTGDAM
		1		ł		SKRSKFALITWIGENVSELORA
						KTGTDETLVKEVVQNFANEYVI
l		1				SDRKELEEEFIKS\ELKKAVGAN
		1				YDAQTE
25418	55786	A	25559	249	1808	INGGTLTVTLSVTNOGAETLPF
230	33,00	١.	20000	1 '		GTGWHPYFPLSPOTRIOAOASG
1	1	1				YWLEREQWLAGEFCEQLPQEL
		1		1		DFNQPAPLPRQWVNNGFAGWN
		1		1		GOARIEOPOEGYAIIMETTPPAP
	l					CYFIFVSDPAFDKGYAFDFFCLE
İ		1				PMSHAPDDHHRPEGGDLIALAP
				1		GESTTSEMSLRAYNDTNRRSDK
				1		AFTPHPTCFPSNQNNSASPPTIT
1				i		PDTATIAPVSHKAFAGNALRSII
						SDGKLTAGSVINNASAGAVPIP
						ASIIVCTIGISAAVGMTNKHPAT
						AIDTTHIMLLSTAPSAWGNNQT
				1		RAAPNTSLLAAYRFLIDSRDTE
		1		İ		TDSRLDGLSDAFSVFRCHSIMN
		1				CVSVCPKGLNPTRAIGHIKSML
		1			ŀ	LQLPPNVEKFAGAYLIQFALFQ
		1		1	ł	PLTHNRLMFFGAFADFLHADQ
	1	1		1		TFPGQITAAVKGQFVRRRLRFF
		1		1		AIISPSRTLS/YHTP*PRR*PR*SN
		1				FVTGRDAGRGLYNRQ*KTS/PS
		1		I		SICSA*GANPVVHHAMTVKFA*
		1			l	WQPIMKISSTSFPSMRPLSHMK
1						TINGLTTFVAW
25419	55787	В	25560	1	567	
25420	55788	Α	25561	1	741	MLILISPAKTLDYQSPLTTTRYT
		1				LPELLDNSQQLIHEARKLTPPQI
			1	1		STLMRISDKLAGINAARFHDWQ
1		1		1		PDFTPANARQAILAFKGDVYTG
		1		1		LQAETFSEDDFDFAQQHLRMLS
				1		/GLPYRLEMGIRLENA\RGKDLY
						QFWGDIITNKLNEALAAQGDN
						VVINLASDEYFKSVKPKKLNAE
				1		IIKPVFLDEKNGKFKIISFYAKK
	1		1	1		ARGLMSRFIIENRLTKPEQLTGF
						NSEGYFFDEDSSSNGELVFKRY
		L	L			EQR
25421	55789	Α	25562	3	320	IGLVLPISVRKRHAASARCLVN
				1	1	RRPMPRLHGLPGIPMRPPSLPRV
	1	1	1	1	1	RHAGTVFRRHRKRGSPMAY*Y
[	1	1	1	1	1	GHSDVVKHREALVADLCHKAA
		1			L	FQLCRGQRHCRPALWRHR

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25422	55790	IA	25563	1600	1908	
25423	55791	A	25564	142	326	TRRAPSAISSRCCCNSHOTSKSS
25425	33771		23301	1''-	520	LVRTSSSLRSSSHLRTIA*CSSV
		1				HLPISCMQIRPSQAR
25424	55792	A	25565	1	1599	TIET ISCMOTO SOAR
25425	55793	Ā	25566	393	611	HSRAVCRFYPAKTSPFPVRRCR
23423	33793	l^	23300	1393	011	YROFVPR*HONE*AGRE*OPCSI
		1		1		ATVLPYRALPSLAHPRLSADOL
				1		PAAHL
25426	55794	A	25567	971	1628	TAKIL
25427	55795	Ā	25568	3	1895	
25428	55796	c	25569	1	2505	
25429	55797	A	25570	1	3345	
25429	55798	A	25571	457	790	PSFRRRYRQVVVISVRKRHAAS
25430	22/98	l <sup>A</sup>	255/1	437	790	ARCLVNRRPMPRLHGLPGIPMR
1					i	
1		1				PPSLPRVRHAGTVFRRHRKRGS
1						PMAY*YGHSDVVKHREALVAD
						LCHKAAFQLCRGQRHCRPALW
		_				RHR
25431	55799	Α	25572	1662	1767	
25432	55800	Α	25573	3	603	RLRSLFFLPDKMKLKDCVMIKK
						IFALPVIEQISPVLSRRKLDELDL
1						IVVDHPQPPSGDYTLHPLPPIIR
				1		ANRPNRFRINAGCTRTFTLSTPI
						NVFRHKILRTQEFPSLTHHAYSP
						LLVVINKAKFDGLSPEFQQALV
1						SSAQEAGNYQRKLVAED/LAK
					l	NHRRHERSGRGS/LSPISTAKPL
						ATHWGIRFATCLLKMCRRELIC
25433	55801	Α	25574	2271	2519	HRQLVIVFQQPLVSGFHEAELS
	i				l	LDDAKWVLHP\ARMLAFMYSM
					l	LMAVLFLRGCCFKVLTLPGRSA
					1	ISQSTSTSASSSRCGAPW
25434	55802	Α	25575	931	1213	
25435	55803	Α	25576	1	2767	MIAILSGLRCSIVANYIYAENNL
						FWLRLNNPKAIWCLRICTFATV
					1	IGGTLLSLPLMWQLADIIMACM
						AITNLTAILLLSPVVHTIASDYL
					i	RQRKLGVRPVFDPLRYPDIGRQ
					I	LSPDAPLTTTRYTLPELLDNSQ
						OLIHEARKLTPPOISTLMRISDK
						LAGINAARFHDWQPDFTPANA
	1	1		1	I	ROAILAFKGDVYTGLQAETFSE
	1		1		1	DDFDFAOOHLRMLSGLYGVLR
		1				PLDLMQPYRLEMGIRLENARG
1		1			1	KDLY\QF\WGDII
25436	55804	A	25577	395	467	
25437	55805	A	25578	1	675	
25438	55806	A	25579	<del> </del>	4014	
-5455	122000	٠.		J	Little	L

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
i	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
25 420	55007	<del> -</del>	25580	1802	2385	I IRKISAPALIKSRTG*EMASLPTS/
25439	55807	A	23380	1802	2383	
						HDKQIEQALADVDVPIVGVGGS
						YHLAESYPPVHYIATDNYALVE
						SAFLHLKEKGVNRFAFYGLPES
						SGKRWATEREYAFRQLVAEEK
						YRGVVYQGLETAPENWQHAQ
1						NRLADWLQTLPPQTGIIAVTDA
l		i		1		RARHILQVCEHLHIPVPEKLCVI
		ـــ				GVMNRRTVRSPFRESLKISP
25440	55808	Α	25581	1	1568	MVKQLKLVSFLLRPGDSKQGY
İ		1				DKHSSLQVGLMIPVCSCIRFRKF
		ł				SEQSFKFEEGTDAAFHGFWLW
		1				PCTMLNVTPIKGMMTVIYEFPV
1						DSETTLQNYDIYFTNEELTDEQ
l						KSLIEWYRDVFRPEDLRLVESV
		ŀ				QKGLKSRGYRGQGRIMADSSG
		1				SGISEHAWCMSRGAQGRQFCK
		1				GAKMSQVLITGATGLVGGHLL
		1				RMLINEPKVNAIAAPTRRPLGD
		1				MPGVFNPHDPQLSDALAQVTD
ļ.		1				PIDIVFCCLGTTRREAGSKEAFI
					i	HADYTLVVDTALTGRRLGAQH
		1				MLVVSAMGANAHSPFFYNRVK
						GEMEEALIAQNWPKLTIARPSM
		1				LLGDRSKQRMNETLFAP\LFRL
						LPGIILLEELNWKTWAERWNS
1		1				MLGPRAVKVFFSLAFLPGTLEP
	ł	ı				AQILFPTQRQGKKAALLLGLW
1		1				KLEIYSDNRRSPEVSTAWNSPP
		1				TGKLDNKQYMIMIPRKRETNTT
		1				TRGASNARLDPPSRKGYKGHY
1		1				ETIGHALEHDKOSOGSYNVEHT
		1				IKROTPRVRRCTSIIAGIYQELG
25441	55809	В	25582	I	1560	
25442	55810	Α	25583	1	2115	
25443	5581I	A	25584	3036	3957	RIYDAVSEPAEPVDCPRNPVCR
						FY*QYRDHRGKTVYDVASGDA
					l .	LFISELG/PLPENVTWLSPEGEFQ
1		1				KWN/GTAWVKDTEAEKLFRIRE
1						AEETKNNLMQVASEHIAPLQD
1		1				AADLEIATEEEISLLEAWKKYR
1						VLNSRAMALILTPDLIRSNTACE
	1				l	CSSFVLAGOTAKAAADDGLFPF
		1	l			IFARVNKAGSPVAGLIIVGILMT
	1	1	l		I	IFQLSSISPNATKEFGLVSSVSVI
	1	1	1		I	FTLVPYLYTCAALLLLGHGHFG
	1	1	l		I	KARPAYLAVTTIAFLYCIWAVV
		1	l		I	GSGAKEVMWSFVTLMVITAMY
		1	1		1	ALNYNRLHKNPYPLDAPISKD
25444	55012	+	25505	ļ, —	2490	MEN LINKLININY TYLDAPISKU
25444	55812	A	25585	1	2490	

SEO ID	SEQ ID NO:	111.4	SEO ID NO:	Nuclcotide	Nortestide Innetion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25445	55813	Α	25586	368	761	LYCEACIMAFRMSEQPRTIKIY
						NLLAGTNEFIGEGDAYIPPHTGL
					i	PANSTDIAPPDIPAGFVAVFNSD
i			ŀ			ESSWHLVEDHRGKTVYDVASG
	l				i	DALFISELGPLPENVTWLSPEGE
		l				FQKCSGTTRVKNAKA*TLF
25446	55814	A	25587	1	809	MPVSSYERGHAEKRVVQECCG
					\	INLTSSANTILSDCERVNGYCVL
					l	CHTTRALVTGNHHRNAVYAET
						PSNSRINYIVSSHNAFRMSEQPR
						TIKVYNLLAGTNEFIGEGDAYIP
					i .	PHTGLPANSTDIAPPDIPAGFVA
ļ						VFNSDESSWHLVEDHRGKTVY
						DVASGNALFISELGSLPENVTW
						LSPEGEFOKWNGTAWVKDTEA
				1		EKLFRIREAEETKNNLMQVASE
				1		HIAPL\QDAADLEIATEEEISLLE
						AWKKYRVLLNRVDTSTAODIE
						WPALP
25447	55815	A	25588	1	2301	
25448	55816	Α	25589	718	1131	
25449	55817	Α	25590	279	513	CRRIDTWQPIYQTCGRLMAVEL
					ļ.	LTVVTHPLNPSQRLPPDRYFTEI
						TV/SHRMEVVKEQIDLLAQKAF
						SLAYLSPCESGL
25450	55818	A	25591	1	407	PQDNAKKLRPHQLSSDEGHTG
1	İ					MGGTAKDVGFVSMRTYSWISS
1						ALPKRLGGGVMPIGATIATEEV
1	ŀ	l				FSVLLGNPFLHTTTFGGNPLAC
l						AAALATINVLL\GRTYRLRLSK
l						KAICCWTVSVNWRGNIPIWYR
1						KRVVKGC
25451	55819	Α	25592	1	2079	
25452	55820	В	25593	1	700	
25453	55821	Α	25594	1427	1845	ACISGFSTETSASGRVSVITDAS
1	1		l			LFRVLPRVCGMAVAATKRSGRI
						TTSEALCCANQLRRRPCVSPTR
1			1			STPSWLSCAV*ICTSGTT*MKR
l						VPNARHCWICSSLIPHSGLHPQP
1	1		1			ITAKFAPIALSSSVTSPFSSVTFG
		L				*IN
25454	55822	Α	25595	2	295	
25455	55823	Α	25596	1	900	
25456	55824	A	25597	1	1422	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	i			sequence		
25457	55825	A	25598	2	535	I IYGNREORAVSSHTNTWVNRAL
				Ī		ARGWSSLGYRWWVSAWTPSR
	l			ŀ		RFISOLMSRPVDASAAKVKRSA
	l	l				SVPCGSIPFGNCFSVRLRILSASC
	i	1		İ		GCIILPVRFSSSSGSEIPSTISSGSI
	l	ı				TLPLDLDIFWPSSSRIRPVM*TV
		l		l		WNGTCGLPFSSLMKCMVIMIM
						RAIOKKMMSKPDTITLVGWN
25458	55826	A	25599	442	1368	RRTMAAFACGVVRDASEVIRPS
		ľ.				STLVPLVGEKHAKGLFGTIVDN
		l				FYLVALIFAMGTSLGLATPLVT
	i	l				ECMOWLFGIPHTLLGFI/LYNAI
		l				CVACGLQKGVRIASDVRSYLSF
	l					LMLGWVF\IVSGASFIMNYFTD
İ				i		SVGMLLMYLPRMLFYTDPIAK
		1				GGFPQGWTVFYWAWWVIYAI
		1				OMSIFLARISRGRTVRELCWIL
	ì	l				WTVLGSNTLLLIDKNIINIPNLIE
1	i .					OYGVARAIIETWAALALNNGN
		1				MWGFFILWFIGPGTLVNAWON
1	i	ļ	i	Ì		RAQFVHHILRRNGIADGFRHLA
		1	i		1	ALTIHGKAVGOYLTIRRFTLHR
25459	55827	Α	25600	2468	3907	
25460	55828	Α	2560 I	3	3738	YKTNYTDNSEYYANVGFNVKP
		l				VKRDGKMSVMSDPDTAIYPFPP
		l				KPTPLSIDEKAYYREKIKRLLTE
						RNAVMVAHYYTDPEIQQLAEE
		l				TGGCISDSLAMARFGAKDPASN
		l				LLVAGGGTCRSVVINAVFSYVT
		1				NVWGWAFEWYMVVMLFGWF
						WLVFGPYAKKRLGNEPPEFSTA
		1				SWIFMMFASCTSAAVLFWGSIE
					I	IYYYISTPPFGLEPNSTGAKELG
		1	[			LAYSLFHWGPLPWATYSFLSV
l	L			l		AFAYFFFVRKMEVIRPS
25461	55829	Α	25602	1331	1456	
25462	55830	A	25603	549	588	
25463	5583 I	Α	25604	19	1629	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
					L	
25464	55832	Α	25605	1	1995	MVGVRFALGLMWLTLIVAETIS
						ANSGIGYLAMNAREFLQTDVV
	l	l	1			VVAIILYALLGKLADVSAQLLE
		ı				RLWLRWNPAYHLKEATLSAEQ
		ı				AARIREMTVITSSLMMSLTVDE
		1				SDLSVHLVGRKINKREWAGNA
		ı				SAWHDTPAVARDLSHGLSFAE
		l				QVVSEAHSAIVILDSRGNIQRFN
		1				RLCEDYTGLKEHDVIGQSVFKL
		l				FMSRREAAASRRNNRVFFRSGN
						AYEVENVPDPGVEQADDIILRIT
		1			1	ATAICGSDLHLYRGKIPOVKHG
		ı				DIFGHEFMGEVVETGKDVKNL
		l				OKGDRVVIPFVIACGDCFFCRL
		1				QQYAACENTNAGKGAALNKK
		l				QIPAPAALFGYSHLYGGVPGGQ
		l				AEYVRVLKGMWGRLNDAOPG
		l				FRSSRPLRYGAGIMTLLNISGLS
		1			1	HHYAHGGFNGKHQHQAVLNN
		l				VSLTLKSGETVALLGRSGCGKS
		l				TLARLLVGLESPAQGNISWRGE
		l	1			PLAKLNRAQRKAFRRDIQMVF
		l	i		ł	ODSIST\VNPOPNRLHIV/RFPLT
		l				
		l	i			RLNQYQPSFSTDLYHGTLKPAS
		l				LTMSGVVLLGRM/PRKTSQQV
	1	l				QWA\CIARTDKASMPTVYSESL
		l				FVEPLERVLYVAVILTQIIRGLR
		l			1	DTEIETINPDIAVHFALCFHGLG
		l				SIPTKGAEKSPFLTIHKVRVKPD
		l				IPSPVSIMAPCRAHPTCEALFNN
		ᆫ				STALHSPWFCDSL
25465	55833	A	25606	179	371	CVLQYTHWPACSTVA\HSRRW*
		l				NRRRLRLAVTKTGSLFSHRCAG
						ARLAFSKKLRCRDALPASRS
25466	55834	Α	25607	544	983	SVQNPRVNWIHAALQRTGRGR
		l				RRHEQHGEDHFVNGAAGVHQ
		1				AANGLVNPPRHQVFGAHQAKG
		ı			l	DGENHRQRGAPDGDLQRDGHF
		1	ļ			GEVILPLAEIGREEVGGERRHV
		1				AAVFDQ/S*AGPFPRPATRRPTR
		1				RVQRPSSEARTSCAWVGRW
25467	55835	В	25608	1	1746	
25468	55836	Α	25609	1	858	
25469	55837	Α	25610	98	288	LCRNNGEPLARSGAAMGALLD
ļ		1				REHSRHP\PDLEG\GSQQQVCDS
	i	l				GGSVTAANTSGGQQVKAQLEL
	L	Ь			·	

SEQ ID	SEO ID NO:	Mes	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
25470	55838	Α	25611	1934	2812	RPQTYSDAQPGFRSSRPLRYGA
		1				GIMTLLNISGLSHHYAHGGFNG
					1	KHQHQAGLNNVSLTLKSGETV
		1				ALLGRSGCGKSTLSRVLVGLES
						PAQGNISWRGEPLAKLNRAQR
		1			i	KAFRRDIQMVFQDSISAVNPRK
		1				TVREILREPMRHLLSLKKSEQL
		1				ARASEMLKAVDLDDSVLDKRP
		l				PQLSGGQLQRVCLARALAVEP
		l				KLLILDEAVSNLDLVLQAGVIR
						LLKKLQQQFGT\ASLFITHDLRL
		l				VERFCQRVMVMDNGQIVETQV
						VGEKLTFSSDAGRVLQNAVLP
		l				AFPVRRRTTEKV
25471	55839	Α	25612	1	515	MLAVECRSLPFPPLVQPVRYTD
						VTVKDDYNPETEQYTLTISQRT
						PATPDQAEKQPLHIPFAIELYDN
						EGKVIPLQKGGHPVNSVLNVTQ
						AEQTFVFDNVYFQPVPALLCEF
						SAPVKLEYKWSDQQLTFLMRH
		l				ARNDFSRWDAAQSLLA/ILHQA
		<u> </u>				ERRASSARSAAVSAGACG
25472	55840	Α	25613	1	1053	
25473	55841	Α	25614	1	1521	
25474	55842	A	25615	430	1120	QTASTFLKRGKCASRQSKLCGN
	İ	1		l		RRRKRRQRISSYCLLRGTACSP
		1				AHQPDAFHQKRGNAGRHYAEC
1		Į.				VLQYSSCSTRYS\PGR\TQLINLF
		1				EVADGKRLVDLPGYGYAEVPE
		1				EMKRKWQRALGEYLEKRQSLQ
1						GLVVLMDIRHPLKDLDQQMIE
1						WAVDSNIAVLVLLTKADKLAS
						GARKAQLNMVREAVLAFNGD
l .						VQVETFSSLKKQGVDKLRQKL
		<del> </del> —		ļ		DTWFSEMQPVEETQDGE
25475	55843	Α	25616	407	1176	AYSTSLRVKICRKTSTLLLRSRV
						TQIRSNTKSTKRAAHCSLTASC
						PPRCSIHATTVTSTTPCLWRRIA
			İ			TMLRALARLLLRICFSGRTLKIA
					l	CLLLLVAGATILIADR/AALYHA
						GKVKWLLVSGDNGRKNYDEA
						SGMQQALIAKGVPAKVIFCDY
					I	AGFSTLDSVVRAKKVFGENHIT
					1	IISQEFHNQRAIWLAKQYGIDAI
		1				GFNAPDLNMKHGFYTQLREKL
				1		VIAKGHGSLLTDLPVAKAGTM
		L				WAIEIDDVARHSRSHL
25476	55844	A	25617	3	168	NPFYSAMR\KSAGIRHILARHVE
		l				GASHMAEGYTRATAGNIGVCL
						GTSGRCCFRLCW
25477	55845	В	25618	169	1227	

SEQ ID SEQ ID NO: NO: of peptide h					Amino acid sequence ( X=Unknown,
sequence	lou	in USSN	location of first	codon fur last amino acid	*=Stop cudun, /=possible nucleotide
		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			sequence		
25478   55846   /	۸.	25619	489	740	AIARSCADYHPANFRHHRAAA
					RAGDDYLSRRAERQPGAKAGG
					SRLRAGKRPCSAFRYW*CAAG
			ļ		E*SVGEKIMAGDVISPKRRL
25479 55847 A		25620	146	475	
25480 55848 E		25621 25622	662	191 4568	
25481 55849 A 25482 55850 A		25622	20	2661	AGHIHRPRYOHGVGTESTSIMS
25482 55850 7	٩.	25623	20	2001	VASRSAERVFLTKFESWKNFPI
					NRGRNKMAKMRAVDAAMYV
					LKKEGI\TPAFG\VPGAA\INPFY
1 1 1					
					SPMRKHG\GIRHILARHVEGAS
					HMAEGYTRATAGNIGVCLGTS
					GPAGTDMITALYSASADSIPILC
					ITGQAPRARLHKEDFQAVDIEA
					AKPVSKMAVTVREAALVPRVL
					QQAFHLMRSGRPGPVLVDLPF
1 1 1					DVQVAEIEFDPDMYEPLPVYKP
					AASRMQIEKAVEMLIQAERPVI
					VAGGGVINADAAALLQQFAEL
					TSVPVIPTLMGWGCIPDDHELM
					AGMVGLQTGHRYEKYTEGRKI
					VHIDIEPTQIGRVLCPDLGIVSD
					AKAALTLLVEVAQEMQKAGRL
			l		PCRKEWVADCQQRKRTLLRKT
					HFDNVPVKPQRVYEEMNKAFG
			l		RDVCYVTTIGLSQIAAAQMLHV
			l		FKDRHWINCGQAGPLGWTIPA
			l		ALGVCAADPKRNVVAISGDFD
l.			1		FQFLIEELAVGAQFNIPYIHVLV
			1		NRPAANGAQGSCHPDAPAVFR
					SSIFIRKSEEKLVVTMNELSASR
					ALPEETMPGRFELKPTLEKVLH
				1	APDNFLFMDPLPPMHRRGIIIAA
			l		IVLAVGFLLPSDDTPNAPVVTR
					EAQLDIQSQSQPPTEEQLRAQL
			-		VTPQNDPDQNLYRKASQKSSR
					KLPKRDLPHILTPFRAPMASVC
					AKRKGQVLHQQYSLKKYRYK
25483 55851 A		25624	1	570	
25484 55852	4	25625	312	873	APRSRVQAKIAASNTGELNALQ
			l		QLGFS\LVEGEVDLAL\PVNNA\
1 1 1					SDSGAVVA\QETDIPA*RQLASA
1 1 1			1		AFAQSRFRAPWYAPDASSRFYA
			1		QWIENAVRGTFDHQCLILRAAS
			l		GDIRGYVSLRELNATDARIGLL
					AGRGAGAELMQTALNWAYAR
					GKTTLRVATQMGNTAALKRYI
			l		QSGANVESTAYWLYR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25485	55853	A	25626	2	922	FSPPGLHDAGEAVFWRVNKSA
25405	33033	ľ.	25020	[		NYGVLDKLARGYADLSKAESO
					•	WDEMMRTAGSLKLGTIHASINS
					1	LFENITAAPADPILGLADLFRAD
						ERPGKINLGIGENPSCCRTSSSP
						VFDAAIWPAPVNNASDSGAVV
	İ				l	AQETDIPALRQLASAAFAQSRF
				ł		RAPWYAPDASSRFYAQWIENA
				ł		VRGTFDHQCLILRAASGDIRGY
					1	VSLRELNATDARIGLLAGRGAG
				•	1	AELMOTALNWAYARGDHMI/R
1						I*RTAGGGNRTRLYAVGNG*RQ
						TVWRWRFYPSLPAVAGATFWO
						RQSVTDAVLHRFAGDGGAAAR
						YPAWR
25486	55854	Α	25627	911	1441	AIPSISCFLLAIKALILSAIWLNA
				i		TPSRSKLEPSSKWIRSLRCPSPN
	l	l			1	RCAAASSFNISCQWFLSEYGPP
						NQVASGKTSPFVIVFKQPRYRA
						VTKPNCRLMMRNGCSTLARML
						PVMYAMLMPVLFLRGCCFKVL
						TLPGRSAISQSTSTSASSSRCGA
						PW*PASAETNCSSPCSRLPS
25487	55855	Α	25628	I	1247	MERVLDNLLNNALRYCHSTVE
						TSLLLSGNRATLIVEDDGPGIAP
						ENREHIFEPFVRLDPSRDRSTGG
						CGLGLAIVHSIALAMGVNAQA
						DFMKLTGADEQIAAYCFKMPF
						VFHLIEEVSRNFGYALCLINIDH
				l	1	KAALNITQRTAANILLDGQMQ
						HAVDQAFTQRTARQGSTFVQY
				l		ARLARKLATANICWSYFVPVR
1				l		ASIEPLTWENAFFGVNSAIVRIT
		i				SEAPLLTPDALAPWSRVQAKIA
				l		ASNTGELDALQQLGFSLVEGEV
1						DLALPVNNASDSG\AVVAQETD
		1				IPALRQLASAAFAQSRFRAPWY
				i		APDASSRFYAQWIENAVRGTFD
			1			HQCLILRAASGDIRGYVSLREL
		1	l	I		NATDARIGLLAGRGAGAELMQ
l						TALNWAYARGKTTLRVATQM
		1	1	1		GYTAALKRYIQSGANVESTAY
L		L.		l.	100.5	WLYR
25488	55856	A	25629	1	1925	
25489	55857	A	25630	402	664	TARRLLFFRD/RTARVAVPNAA
		1	1	l		VVLPFPLPVKTMIPRSLGRRRS
						GGICRPLGYLVAMDAIDGLQN
L				l	L	ADNSNGESRIATSSFRSRSARR

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nuelcotide insertion)
25490	55858	Α	25631	920	1237	IARPGCHLSHCHSEPSGRLSK*P
						FSCNSLKTGDF*PI*GLIQTQIFS
					İ	PFAFRRIIPSGSGKVSGSHSKS
		1				HHWKAFIQKQSKWKTCSGRLR
		l				SAIPSIKLFTVASS
25491	55859	Α	25632	1	1341	MVHRFGIRVRFVALGFYQDVIL
		1				PVRAHRHEWGHYVHLCASIQR
					1	QIDVSFARDATSHSSCPVTGVR
			1			FWGYPFAANKVVIAGFELEGET
						MTRPGLICAEGGLLVMIVSLRS
		ļ				ELYDSYHEFTRQRVTEIVEKAA
		l				NHLPAVVEMMTLHRCAINRHN
		l				FVRRVGPAGISTFFASSPDGVN
		l				AGFSTFRVVFTCQRSRPLQRHS
						HADVQTATLLLNTVNLEQKQA
		1				NAILSGLSDMIPNSSPESAPEIQL
		l				LQSRMILGKTIAELNLRDIVEQK
		l				YFPIVGRGWARLTKEKPGELAI
		l			1	SWMHIP*TLSKNRPTPFS/DGLS
		l				DMIPNSSPESAPEIQLLQSRMIL
		1				GKTIAELNLRDIVEQKYFPIVGR
		1				GWARLTKEKPGELAISWMHIP
		1				QLNGQDQQLTLTVGENGHYTL
		ļ				EGEEFTVNGMVGQRLEKDGVA
						LTIADIKAKPGTQFVLSQRTELE
		1				AINALQETFTVSERSKESGMLE
		1				LTMTGDDPQLITRILNSIANNYL
		l		1		QQNIARQAAQDSQSLEFLQRQL
	1	l		1		PEVRSELDQRKKNSTFIASSAIR
25492	55860	Α	25633	170	935	LTQEDTRINLIPMAVESLHLPTQ
		l				MLINGGETYA WRNWKRGGQY
						KSATLNTGQPHVRARELVDSD
					į.	TLASDAARLTCRHGLALPALFT
	1	1			1	LIAVVTSLLSPQFIRQILWSRLT
	1	1			l	KTR*AGDQLDAYSTTEWSGSA
	1				I	TDTHGWGKRPLYTGR*RVHRQ
					1	WYGRPASGKRWRCADYRGH*
						GQTRNTVCPEPA YRTGSD
25493	55861	В	25634	42	755	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of loca	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
	1	<u> </u>				
25494	55862	Α	25635	793	2127	RYCKGTVMDQIRLTHLRQLEA
		1				ESIHIIREVAAEYSNPVMLYSIG
						KDSSVMLHLARKAYYPGTLPFF
						LLHVDTGWKFREMYEFRDRTA
1						KAYGCELLVHKNPEGVAMGIN
	1					PFVHGSAKHTDIMKTEGLKQA
	1					LNK/YTTSRAKERIYSFRDRFHR
						WDPKNQRPELWHNYNGQIN\K
				i		GESIRVFPLSNWTEQDIWQYIW
	1					LENIDIVPLYLAAERPVLERDG
	1			ľ		MLMMIDDNRIDLQPGEVIKKR
	ì	1				MVRFRTLGCWPLTGAVESNAQ
		1				TLPEIIEEMLVSTTSERQGRVID
		1				RDQAGSMELKKRQLIELIINVH
	l	i				NLLKNGFGFQVKVNRIALLAIN
	ľ		ì			VEFFFRLVQLAAHFSSGTLAQD
						KLCSWFGLNVRDSQRNAIFFQT
		1				LADHTIDGELFTFQCIVAVFPNL
		1				PIYSYATIYVSSSSIPISSEESPSIR
1	1					FACSQTSRQPPVSDSRFCVSQV
25495	55863	Α	25636	360	566	GAETMGDLLWVVGILLMCSLS
1		1				TLVLVWLDPRLKS*RT*A*CGA
		1		ŀ		LTSHQAINNGRNEKRKPIRESDF
		1				LKA
25496	55864	Α	25637	1	312	LLRKSVSVIIKGTIKTIIGFMLLQ
		1				AGSGILTSTFKPVVAKMSEVYG
		1				INGAISDTYVMQDG*APELGLS
		1		1		PGRFLRHDTDFVLQLGIVMVRL
		1				AGDGSLNINAQANN
25497	55865	Α	25638	517	796	PTARFGWVKGVDLPAD/CNRQ
	1			1		DRFAIDVRVQGS*\WGCVLPLF
1	1	1				RVLLFVSCALLLVSVSCVLRLL
	1					FCCSS\LSLFLSGLGGGRSPKAG
				l		DVFRDRR
25498	55866	Α	25639	47	411	AIKVRELSIKLKMC/YSLIKTLH
	1					G*KYRNFMVIGSMVFGKKAITH
						VAGVKRRTAVVVGFKVFDIQR
1						SQFRIVVTGDLAQLLYRVIKVIT
				1		CGHFVRQHGIVLCAGVLHVGD
		_				RYQAHVKTLGGLI
25499	55867	Α	25640	I	1488	
25500	55868	Α	25641	2	298	CCICL/YSYAPIDVW/WG/WNTA
		1		1		GQVQAA*TLKAASSSIVTIPLRN
		1				TFIFNYSLSGLRRRRLIIRSRRHS
	1	1		1		THASNITLIAASTASRIGWFASA
		_				YHTRSNHGR
25501	55869	С	25642	I	2064	
25502	55870	В	25643	1	1116	1

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25503	55871	Α	25644	312	620	SACRCCLVVVPLFVCL/GSSLSL
		1				APTFPLLASFSSSRASRVVAFGL
						GSLRAGSALCLPCAAVVLALRS
						AGTCLEWWWWHSVVLPPETK
						RLPSTSLIPYPASVSI
25504	55872	Α	25645	2	2237	
25505	55873	Α	25646	692	6383	RMSRSSDYDQYRSRNALIRRHI
		1				EKMDASLHVGTKEFDISKVSEV
	1	1				DSVDDLLIDNAARYLLKDWKG
1		1				VGELVNGVEVALEYTAERGIAL
		1				LKQNPELYWQILAEAASIAQVG
		1				GEVWIAPKFERNGLRLLANSEI
		1				GAASQLQTYHRVDPGRPCKLD
	1					LSGGMSQRVMIAMAIACRPKL
l						LIADEPTTALDVTIQAQIIELLLE
l						LQQKENMALVLITHDLALVAE
						AAHKIIVMYAGQVVETGDAHA
				l		IFHAPRHPYTQALLRA
25506	55874	Α	25647	856	1467	
25507	55875	Α	25648	1823	2014	SQEIALMQFRPRLTGASGSP*RP
1		1				PHRTLLRSDQNAATIPQKRASA
						LIPLMRILPVRYGHLLLC
25508	55876	Α	25649	1	218	
25509	55877	A	25650	2740	3293	IFA VNLILQCHVGGTHHQRFLL
		1				FAGNGDAGNQIRERFPNAGG/E
		İ				LQSPDVALLLRPAFWRRPQSSA
						AAAHGE*SRGSVPEAPYTRRQF
						ALPAPPIKCAPLPERQRPSVPSR
	1					HLRLPACPGYKNRASSAKPSYS
	1		l			FLAQRQHLQRLSPLPQNQNLPQ
			1			RRRDQRQRAGAMSARVPDLISS
						SRSMRRTS
25510	55878	В	25651	I	1875	
25511	55879	В	25652	1	2981	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25512	55880	Α	25653	I	1649	MTFRNCVAVDLGASSGRVMLA
		l				RYERECRSLTLREIHRFNNGLH
		1				SQNGYVTWDVDSLESAIRLGL
		1				NKVCEEGIRIDSIGIDTWGVDFV
		1				LLDQQGQRVGLPVAYRDSRTN
		1				GLMAQAQQQLGKRDIYQRSGI
		İ				QFLPFNTLYQLRALTEQQPELIP
		l				HIAHALLMPDYFSYRLTGKMN
		ĺ				WEYTNATTTQLVNINSDDWDE
		l				SLLAWSGGQQSLVWVAEASGE
1						WGVLACTLFAWNRNYFVLLFV
						GVFLSSFGSTANPQMFALAREH
						ADKTGREAVMFSSFLRAQVSL
						AWVIGPPLAYALAMGFSFTVM
		1				YLSAAVAFIVCGVMVWLFLPS
		1			i	MRKELPLATGTIEAPRRNRRDT
						LLLFVICTLMWGSNSLYIINMPL
		l				FIINELHLPEKLAGVMMGTAAG
						LEIPTMLIAGYFRQTSGPTAYGR
		l				SVGRIRRSRRIRQSCYYQRIFSL
		1				LACELANALERPENFCGMHFFN
		1				PVHRMPLVEIIRGEKSSDETIAK
1						VVAWASKMGKTPIVVNDCPGF
						FVNRVLFPYFAGFSQLLR/ERRG
		1				FPQDRQSDGKTVWLADGPGIS
						AGRCGH
25513	55881	A	25654	1590	2855	RNLLGEAADPVSGPHSAIYRPD
120010		ľ.		1.070		WPKSGDCACQGPIKGSANRPA
		1				VVPHVHGP\SEDLEVFLNVFGE
		ı				LPOPLIDTOILAAFCGRPMSWG
i		l				FASMVEEYSGVTLDKSESRTD
		l				WLARPLPERQWEYASPNVWY
		l				LLPITAKLMVETEASGWLPAAL
		l				DECRLMQMRRQEVVAPEDAW
		l				RDITNAWQLRTRQLACLQLLA
ŀ		l				DWRLRKARERDLAVNFVVREE
						HLWSVARYMPGSLGELDSLGL
		l				
						SGSEIRFHGKTLLALVEKAQTL
		1		1		PEDALPQPMLNLMDMPGYRKA
		1		l		FKAIKSLITDVSETHKISAELLAS
1		l		l		RRQINQLLNWHWKLKPQNNLP
1			l	1		ELISGWRGISAVKSSEAGLGAL
1		Ì	l	l		SATSGFGKLQIQHQAFTLRTRT
1		l	1	l		TDQHTLLAGTLFIAKILIPMVSF
		I		l		TFQYCCFAVPQATYCHRIAPIL
L		L	l	L		GNGAMKPGRKIS

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25514	55882	Α	25655	I	3315	MDELRLVLMTIIHIKLPPIRRAD
						GSFGNDLTTGAGFNDRKTVPR
	l .	1				YARVHVYRCRKVICIFTKRIPFC
		1				LDVPAHRALVVMKGTLYGMP
	ŀ	l				VVAAAFEFAFMGGSMGSVVGA
				l		RFVRAVEQALEDNCPLICFSAS
	1					GGARMQEALMSLMQMAKTSA
	1					ALAKMQERGLPYISVLTDPTM
	1					GGVSASFAMLGDLNIAEPKALI
		ĺ				GFAGPRVIEQTVREKLPPGFQR
		ŀ				SEFLIEKGAIDMIVRRPEMRLKL
						ASILAKLMNLPAPNPEA
25515	55883	Α	25656	246	422	RHADTDLRR*ISDRFSPAPPADP
İ	1					ANGGR*TPRHAAKRRDPGTPV
				1		QPARKPSKPTRLLR
25516	55884	Α	25657	884	1276	LVTRQLSPGNRCNVFAFSSAVE
						TSLTCQGWLSPVCAVCQAISSS
		l		l		HNASIQVRSPAASCGSPFCSKRP
	1					SALWWTSVSPFLSPRRRTSGAN
						AESVSAT*SKRRSSARRSASARS
						TLSGAALRSRTASNEWRS
25517	55885	Α	25658	649	1427	LPLLGWSMSPRMTAQLACDAL
						QMALWRRKRPRNVIVHTDRGG
		1				QSVQQFRALKRHITASRETERF
	1	1				YLDVQKQFPKVTAQKVIVSEA
		1				GASVYSASELAAQEFPDLDVSL
	1	l				RGAVSIARRLQDPLAELVKIDP
		l				KSIGVGQYQHDVSQTQLARKL
		l				DAVVEDCVNAVGVDLNTASVP
						LLTRVAGLTRMMAQNIVAWR
1		l				DENGQFQNRQQLLKVSRLGPK
İ		l				AFEQCAGFLRINHGDNPLDAST
		l				VHPEAYPVVERILAATQQALKD
		l				LMGNSSELRNLKASFLDNEEN
		l				WPLLLDALIPVANTCEMILMPA
		1				CFGLADDKLWRWLNEKLPCSL
		l				MLLPTLPPSVLGIRLQNQLQRQ
		I				FVRQGGVWIECGDGGDTTTITI
		l				TQR**PAGRVYRSPGSLSGGGT
		L				HSGSNTAGTERSDG
25518	55886	Α	25659	I	1878	
25519	55887	A	25660	1	4329	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25520	55888	A	25661	2514	4173	PISCLPDDYYGHCRGVSAHF GASVSCVELLSACARPLWRHL GLALLRVWCRTFILLSALASVF CPCSVVWGRLLFSASLSVVVW GGYFLSPLGSLSPRGTARLGAA CRSREDJRRR*WRGIFTSRTIFAS AVPASVNDBYCAZPAACIRFTS TSAY*VGCSDRNA/DAEASGEG WRRAFGDATLSTGQFGGEAREE VILGLIGSQAKTGGNTPKASAV RKITLVAWPALETGLTMLSM** IG*ETRYSEVEPSSKSIVPSASPDSL IVFA*QPPSKLNTPSSSQCSSSP RIRRRGSVERVLPVPSFRNT ATSPPSTLAEQCIEAJPSAVFA APVRVAASMISGFCALASIRS ASTRRPSASVFITSTFLPLR*VMI SPSLNALPLIRLSAQQRNSFTRL SPRVMANBASPVTVAAPPMS DFIESINAVCLMQARVHWRFI ASWVVIQPSPLENNLRVSLC AAPGTLCLTTFVSSSGDR*NAL CNRCNRPAPCFRSSAIRFATVLA ARRHDWVWIPSPLIPRISS

SEQ ID	SEQ ID NO:	IMa-	SEQ ID NO:	Nueleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25521	55889	A	25662	2221	4400	I IRGCVVSGKSSCSKTNLPSDDKR
20021	33003	ľ	25002	1222		TGASCPLRDLFLRYLRAHALVT
						AEQLAHEFSLGIAIVEEOLOOLE
						EQGLVMNLQQDIWVSDEVFRR
	1	1				LRLRSLQAAREATRPVAATTYA
		1				RLLLEROGVLPATDGSPALFAS
		1				TSPGVYEGVDGVMRVIEQLAA
		1				SAINASLWESOEFVYGKPVYAV
1						GENYSQGQYYLASFANKIWLSI
						OGVVDLHGFATNGLYYKSLLD
						KLKVSTHVFRVGTYKSAVEPFI
		1				RDDMSPAAREADSRWIGELWQ
		i				NYLNTVAANRQIPAEQVFPGA
		1		1		OGLLEGLTKTGGDTAKYALEN
1		1				KLVDALASSAEIEKALTKEFGW
1		1				SKTDKNYRAISYYDYALKTPA
		1				DTGDSIGVVFANGAIMDGEETO
1						GNVGGDTTAAQIRDARLDPKV
1		1				KAIVLRVNSPGGSVTASEVIRA
		1	l			ELAAARAAGKPVVVSMGGMA
						ASGGYWISTPANYIVANPSTLT
1		1				GSIGIFGVITTVENSLDSIGVHTD
				i	1	GVSTSPLADVSITRALPPEAQL
İ						MMQLSIENGYKRFITLVADARH
						STPEQ/IDKIAQGHVWT/GLGDF
						DDAVAKAAELAKVKQWHLEY
		1	ĺ			YVDEPTFFDKVMDNMSGSVRA
	1					MLPDAFQAMLPAPLASYQVRS
	1	1				PCLTYILLLFRYHSYQYHAKEIN
		1				LRCLHGRDHRDAAFRAGLYTG
		1				VRSSTTPTGADAGIPSPGDARF
		1				AIHEYIPRNGSSRFNPGKLAPHA
25522	55890	A	25663	1	1665	AME I I I COSSIG I G CICE II III
25523	55891	A	25664	475	1182	
25524	55892	Α	25665	242	3059	
25525	55893	Α	25666	1761	1970	
25526	55894	Α	25667	455	I137	GTKPRDIDHILGTFITPGMPKGG
				İ		KLDVYAAPELPLKLLGRPTEGE
					ŀ	YNEEF/SLLPVVNYLKDKLSNP
				ĺ		V/RLDGVDVAEGEL/VVLENVR
						FNKGEKKDDE/HRAQASTHGIG
						K/FADVACAGPLLA/AVLDSLSK
						/IADQLIVGGGIANTFI/AAQGHD
		1	l		I	VGKSLYEADLV/DEAKRLLTTC
		1				NIPVPSD/VRVATEFSETAPATL
		1	1		I	KSVRHSDKISYISTGGGAFLEL
						WKVKYLPAVAMLEERG
25527	55895	Α	25668	1108	1932	
25528	55896	Α	25669	1496	1631	
25529	55897	Α	25670	462	1152	
25530	55898	A	25671	545	598	l

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		1		scquence		
0.550.1	55899	+-	0.000	I	1761	MACURINIDADO A DOCUMENTO
25531	33899	A	25672	1	1701	MRGHNWIDMDQARQQSTPHT
		1				DRKICHKNDRPRTTPLRKIDAH
		1				PHTLIILPAESTLSTTKYKLRAL
1		1				LVENTNKDKSAVSVVFRGSVL
		i				HQQAANFPNLMLCFQLKNGVN
		1				ACNDFIMLFVDDNAAGSIERAA
		1				SPCINEKQHAFSESVPAIAAVRO
		1				LGSMIAVEFNDPQTGEPSAAIA
		1				QKIQQRALAQGLLLLTCGAYG
		1				NACKRRIDYVCRIKHSRRIRQV
		1				VLLNFAKSGAFSTTRGTDDKLT
		1				PVIQPRASGEYNEEFSLLPVVN
		1				YLKDKLSNPVRLVKDYLDGVD
		ı				VAEGELVVLENVRFNKGEKKD
		ı				DETLSKKYAALCDVFVMDAFG
						TAHLRAGFLLTGI\GKLRCSLRC
		1				AGPLLAAELDALGKALKEPARI
			1		1	MVAIVGGSKVSTKLTVLDSLSK
		1				IADQLIVGGGIANTFIAAQGHD
						VGKSLYEADLVDEAKRLLTTC
						NIPVPSDVRVATEFSETAPANL
						KSVNDVKADEQILDIVRDLDAA
						NVVINAVFSYVTNVWGWAFE
		1				WYMVVMLFGWFWLVFGPYAK
		1				KRLGNEPPEFSTASWIFMMFAL
		1	1			LYVCCRTVRLGREIHRRAQIVH
						IDIEPTQIGRVLCRISVLSLMLKR
25532	55900	A	25673	1	984	
25533	55901	A	25674	1	1181	MMAVSAPYVGDNIDDGGIYTQ
		1				SETHTISSDCVLDTAAMWTPLS
		1				AVIGCTTNPAQYPANAAEVYN
		1				KDGNKLDLYGKVDGLHYFSDN
1						KDVDGDQTYMRLGFKGETQV1
						DQLTGYGQWEYQIQGNSAENE
						NNSWTRVAFAGLKFQDVGSFD
						YGRNYGVVYDVTSWTDVLPEF
-	1		l			GGDTYGSDNFMQQRGNGFATY
						RNTDFFGLVDGLNFAVQYQGK
1						NGNPSGESFTSGVTNNGRDALR
1	1					QNGDGVGGSITYDYEGFGIG\Y
						TQTYNATRVGSLGWANKAQNF
1		1	l		1	EAVAQYQFDFGLRPSLAYLQSK
		1			I	GKNLGRGYDDEDILQICCMSDP
		1	1		1	TQNRQASAKLALPCQVALLSSA
		1		1	l	SPHHAFTPSTSIIQPAHIIIHSSPP
		1			1	PWASSHSISTHQQHTQCSSSSNT
		1		ŀ	1	LAVH
25534	55902	Α	25675	1	147	

SEO ID	SEO ID NO:	Mat	SEQ ID NO:	Nueleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25535	55903	A	25676	683	947	QVRDSLQQGRERRIALSIGWLV
12333	33703		23070	003	j	WREGCODOCELEAGGASALTR
						RGSCRELDPAPFATMLLFCPGC
	1					GNGLIVEDG\QRCHASTDAVPP
25536	55904	A	25677	12	393	RGSCRELEPAEFETMLLFCPGC
23330	33704	,,	23077	1.2	177	GNGLIVEEGORCH/RAVACNT\
	Į.	1		l	i	CPYVHNITPQGNTIWKYPKLKE
1				ĺ		CGSDVLGGAAAWENVDSTAE
				l		SC\PKCEHPRAYFMQLOTRSAD
				l		EPMTTFYKCC\NAQCGHRWRD
25537	55905	A	25678	234	567	YVDETDDCFENNRCGOPVNGA
2555,	33703	^	230.0		100	YSPAGLSRVAADASLTTPHAK*
		1				TLRSLTLHQHDKTRTELLNDVA
1		1		i		GALALDDKLGRSTNQLSGGEW
1		1				TPSLARPFLLLGPRKMRLLPLH
						I.PP
25538	55906	A	25679	1	794	HCDGKHFTGVGKIMSIGMQLQ
25550	33700	ļ.,	20017	ľ		DVAESTRLGPLSGEVRAGEILH
		1				LVGPNGAGKESLTGREWPEMP
		i				TVKGTIOFPGHPLEAWSAKK\L
1		i .				ALLRAYL\SOOOTPPFPPPVWH
1						YLTLHQPDKTRPELLNDVAGA
1						LALDDKLGRSTNQLSGGEWOR
						VRLAAVVLOITPOANPAGOLLL
		1				LDEPMNSLDVAQOSALDKILSA
	1	ı				LCQQGLAIVMSSHDLNHTLRH
						AHRAWLLKGGKMLASGRREE
		1				VLTPPNLAQAYGMNFRRLDIEG
		1				HRMLISTI
25539	55907	Α	25680	12	414	RAAPSRNLPPRMPIPIAAPIAAR
-		1				PIITAAAMYSRSIFRFSMTVSSLF
		1				QLKRSSVGKLMFFRRHRQIDDR
		1	1	1		QNHEDEGLQRNDQDVENGPRH
		İ				IQDPL*PPRQETSNQNEDQLSGV
		1				HVTEQSQTEGSWFGQHAYPF
25540	55908	Α	25681	568	724	RFSLGTVLDGIYPHQYDGYSR
						WSAKRYL*WRNL*SGTHRSC*
1		1	1	l		VNNFTRSNKK
		_			1	

SEO ID	ICEO ID NO:	Met	SEQ ID NO:	Nuelcotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25541	55909	ĪA.	25682	1	974	MNGKLQSSDVKNETPYNIPLLI
23341	33909	l^	23082	1'	274	NENVISSGISLISLWHTYADEHY
	i .	1		1		RVIWPRDKKKPLIANSWVAVY
	1	1				TVTGCGNSDRLNNIRTLRA\MA
	1	1		1		
		1		ì		REFSIDVLDEMLQQFRVVTPDR
	1			1		PEHKQLPQHELAERQEKISTWL
	1		l	l		ELMKADGINPEELLGN\SSAAA
	l			1		PR\AGKKRQPGSAKYLFT\DVN
	ŀ					GETKTWTGQGRTPKPIAQALAE
		1	ł			DCHGKPEYGSAVHGCRCDDGS
		ı				AGNLCFDLNRHCGLGVRLRPR
		1	1	!		KINGDYRSRFCHAGETGVCAG
		1		1		AETTQMAESGVSGAGLAVRGE
		1				RDGKRSPLQIAIMMNGSSGQAI
		_				SSNVIILQLFLVEVIKSLRMLYM
25542	55910	A	25683	1	1359	
25543	55911	A	25684		918	DADVACALICRI CI UDOCCIIOED
25544	55912	Α	25685	72	690	PAPVAGAHCPLGLHRSSEHQEP
		1				QLRHVARWPSS*SWLCHGTFR
1		1				KLLPGKKRRGGNKKF*GRRAR
		1				GVGCVVSRVWCGPACACSLRR
	1					WLAHTVHWVFTEAQSIKSHSS
1	İ	1	ł	1		DMWPDGLALSPGCAMGPSGSC
1	İ	1				SRGKNVGGATKNFRGVHNIYC
1		1		1		HKPIPTTQHESKYARQTTTEEC
1	1	1	ł			TQTSSHDFRTTFSAVMQQRLQI
		1		1		ARNLVTHPKLVFMDEPTGGLD
	i	1		1		VSVQARLLDLLRGLVVELNLA
	1	1				VVIVTHDLGVARLLADRLLVM
		1		l .		KQGQVVESGLTDRVLDDPHHP
l .						YTQLLVSSVLQN
25545	55913	Α	25686	1334	1545	RSQSRLERSCSVTGSM*RVSPA
1		1				RSFRRITKRVLAAARLAT*LPAS
		1				GRRTGVGVSVDSEFPSELLSSSF
1	i	L	L	l		TD
25546	55914	Α	25687	1784	2125	WLQHIHPQLLRCPVLRAQNVW
		1				IRTLYDRH/RFVTRGTLGWIETG
1	1	1	1	1		DF/DKVPPDLRFFAGGDRSI/RG
1	1	1	1	1		YKYKSIAPKYANGLDIGKSPAA
1		1				GAISPCLTFVMSARRGGHRGQS
		1		1		ASGCRA
25547	55915	A	25688	931	1213	NLHPAPAKRRAPARPQSRLAHR
		1				QRGRMRGAPRPFRQRQIKLCY
1		1	1	1		ARCTPTICPTKVKSRSNTVTSG*
1			1	I		TWSPRQRAKWWKSAKPPSAGL
			1			TSSARHP
25548	55916	A	25689	999	1243	VDPVPWLPMALDITSTAPARQF
1	1	1	1	1		RKRIIASLMPT/WGTSLRRYSVP
1		1	1	1		PRRSGWKRWRFPPTGSTTCRPP
		1	1	1		FPAVCSSVCRLPATW
					L	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25549	55917	A	25690	1225	2341	ARTERLSNEGGSTRARGVYWD
						PNSDLCPTLDFSYKMPLLKNPL
		l				EQYYLVQGGFKRTDLNDTESD
1		1			ŀ	STTLVASRYWDLSSGWQRAIN
		1				LRWSLDHFTQGEITNTTMLFYP
						GVMISRTRSRGGLMPTWGDSO
						RYSIDYSNTAWGSDVDFSVFQA
		1				ONVWIRTLYDRHRFVTRGTLG
1						WIETGDFDKVPPDLRFFAGGDR
		1				SIRGYQY\KSIGPKLPNGD\LKG
						ASKLITGSLEYQYNVTGKCTK
						WOFGEWLAPGEVRLAPGATLA
		l				TPELVASCSTEGLNGLAANFHA
		l			1	ELRARLPWHGGAMKPRPVHLN
1		l				TWEGFYFDLQPDKVKALATAA
					1	AALGVERFVLDDGWFNARHH
						DRAGLGDWWPDATKFPQGLG
						ELVAHVNPFYA
25550	55918	Α	25691	45	233	SSYPRWWAAWWASTTARPSTR
						WRSSPR*SATTWASSPSPTSP*I
1		1				HDRPGIGATHSSRFIPLK
25551	55919	В	25692	1	558	
25552	55920	Α	25693	324	657	
25553	55921	Α	25694	831	1244	WQPGGR*WSRQRSADGTGPDD
		1				LAAAYFPGDRFYRN*PSERC*H
		Ļ				RRG
25554	55922	A	25695	1	1215 840	
25555		A	25696	1	1365	MPQNRGGFLDKKNPGAPLEGA
25556	55924	Α	23097	'	1303	VYVNCFTRFPGIGYEGRTAVFC
						GAAKVPPGLNYRGIGAFPGGNF
	l					ASKRSRGRNLAGARCLRFCPK\
						WO\NYSETASVOOON*SVLARA
						IERGINAPLA\SSCGRFFDAVPA
1						ALGCAPATLSYKGEAACALEA
1		İ				LAASCHGVTHPVTMPRVDNQL
1	l					DLATFWQQWLNWQAPVNQRA
1						WAFHDALAQGFAALMREQAT
						MRGITTLHPEGLERMSAGHES
						WLERRNGELGEGKGSKAYPTG
		1				DHKGADLYDDSNFLIQNIFVED
		1				TRGLLRQGREDLIERYKDPLNE
	1	1		1		NPKRCVEQLANWHKELEEYKK
				1	1	ASRIDIKPSREYASTIMNAIWTG
				1	1	EPSVIYGNVRNDGLIDNLPQGC
		1				CVEVACLVDANGIOPTKVGTLP
		1				SHLAAMMQTNINVQTLLTEAIL
						TENRORVYHAAMMOPHTAAV
					1	LGIDEIYALVDDLIAAHGDWLP
L	1	1			l	LOUDE LIVE ADDRESS HIS MAN

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amine acid	*=Stop codon, /=possible nucleotide
ĺ	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25557	55925	Α	25698	1	950	MPDEENRFNALKAVFSQLMTD
		1				ATLTPLFNYHYRISAPPGVNGL
		l				SMKRAVVVFSGGQDSTTCLVQ
					1	ALQQYDEVHCVTFDYGQRHRA
	1	1	İ			EIDVARELALKLGARAHKVLD
						VTLLNELAVSSLTRDSIPVPDYE
		l				PEADGIPNTFVPGRNILFLTLAA
						IYAYOVKAEAVITGVCETDFSG
					1	YPDCRDEFVKALNHAHKEKLD
1		1				EDCKRRMYTNPLRVLDSKNPE
		l				VQALLNDAPALGDYLDEESRE
						HFAGLCKLLESAGIAYTVNORL
	1	1				AVNPEFKADPVVDIYLVASGA
	ì					DTQSAAMALAERLRDELPGVK
			İ			LMTNHGGGNFKKQFARADKW
	Į.	l				GARVAVVLGESEVANGTAVVK
1		ı				DLRSGEQTAVAQDSVAAHLRT
İ		1				KEKDSVEIYENENDQVEAVKRI
		1			1	FAENGKALAVGVILGVGALIG
	1					WRYWNSHOVDSARSASLAYO
						NAVTAVSEGKPDSIPAAEKFAA
İ		1				ENKNTYGALASLELAQOFVDK
		1		1		NELEKAAAQLQQGLADTSDEN
		1	ļ			LKAVINLRLARVQVQLKQADA
		1				ALKTL*IPD*RPDAGLRCKRSPR
	1	1				SPAVCTDRONAHEIPRPDSHLM
1		1				PERR*EAPALPDFLNPARAAG
25558	55926	A	25699	1	3314	MKISRLGEAPDYRFSLANERTF
1		1				LAWIRTALGFLAAGVGLDQLA
						PDFATPVIRELLALLLCLFSGGL
						AMYGYLRWLRNEKAMRLKED
		i				LPYTNSLLIISLILMVVAVIVMG
		i				LRAMLMAMEPIWESDFHTLSY
						GFRPERSVHHAIRTVKLOLTDC
					ŀ	GETRGRWVIEGDLSSYFDTVHH
1						RLLMKAVRRRISDARFMTLLW
						KTIKAGHIDVEDKRAASEGVPQ
1						NKIISPLLSNIMLNEFDOYLHER
		1				YLSGKARKDRWYWNN
25559	55927	A	25700	997	1716	PYLTASSSAFQQLHLSGENHRD
		1			1	DGCAGYSRRTLAAQLQCHCEC
		1				DHNLPPDTPRLPRSGVVLPARF
		1				PRPLHTLISALHRRVLTRHARH
						ESSTLNPQRLPPAHRFFACQSRY
		1	1			VPGPAEYSYAVRSTDESG*A*W
			1			LRVPPNLIALTVQRSLPDLALPA
		1	1			ONCPPCRSMLEPAPYILLGMLA
				1		TWPACPG\HEVG*SHSAHPDEP
		1	1	1		ETLOTVSR*YRRFGRPVH*SVH
		1	1	1	1 .	VVGRYPHQACQCYLSSTAE
25560	55928	A	25701	1	769	
	1	1			.t	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25561	55929	A	25702	1	3707	I MVRSAVVAGIAQAALPQSVVA
23301	33929	<u>۱</u> ^	23702	1'	3707	WEYLVEDYDRIRNDIEAVLPEF
				l	i	ADYNORIRHPGGFHLINAAAER
				l		RWMTPSGKANFITSKGLLEDPS
						SAFNSKLVMATVRSHDQYNTTI
				l		YGMDDRYRGVFGQRDGYRDN
			l	l		CEEIAOLAEDCGNLFAVTVFRC
				l		PAGANLQGNRNVHCIDDLGKD
		l				RFNDIRNVOAAELLAEMAISSA
				l	ļ	QRRMRAAKKVVRKKLTSGPAL
				l		PGKLADCTAQDLNRTELFLWK
			1			GEQNALLRGFPAVRLHSLL
25562	55930	A	25703	1	369	LPSHGAGLGTCSLPCLSLPPTP
25502	33930	<u> </u> ^	23703	l'	309	WAPVOPEPPRRAPPPAPWRPVP
			İ			LTTQGLRN/DEHRVQDWQAAP
1						PAAPLKVCKYTNQHPVFSTRFV
			İ			NAPIDTLYLAALVRTWRTFMSS
					ŀ	SRIVNTPIGTLYLAQ
25563	55931	Ā	25704	1	444	MRLHSSALGRSMGLGAVEOGA
25505	33931	<u>۱</u> ^	23704	l'		ALVGEAPAAQEPTEAGEGSGM
	i					AGCSPKACPAGRQLRPGPA\AA
				ŀ		PSAGPPSPRPPGTPAGPOAPRAA
	İ					PVPARASPSTPPCKLRERAAAF
						A/EPRKGLPQCSGGLKGSSSAA
						KVGAQAEEAPRASESCEDC
25564	55932	A	25705	1767	2130	YTGQRLRRVYWVPQQCQPTCA
		1.		1,,,,		ALDFSPSLSCLPA/AAGLRTYSQ
						PCLSLPPTPWAPVOPEPPO*APP
						PAPRRP\AHRPPKG*GVQAHGA
						G\RQAAPPAAPVRDPLG\KPAGL
						LSLVGTWRTFMS
25565	55933	Α	25706	654	832	RRCARFLAGP*LPSHGAGLGTC
						SPPCLSLPPTPWAPVRPEPPRRA
				l		PPPAPRRPVLCVFS
25566	55934	В	25707	1	537	
25567	55935	Α	25708	1	455	HCGSVIGGFLVSLTLRTKLRTL
			İ			AVSVTALTVVCLEFIPSDVRMR
			İ			SVSSFWWVRSLAGSRVKLQTF
						AVTVTALKAASLELFVPPGGLV
1						VSLASGVKLQTAAAGK/RCLPV
			1			LRHAPALLSPWVVDGTGHRGA
1						GGGAHRGGSGRPGAHGGGGRL
25568	55936	Α	25709	1	314	SACREVWRERHEREPGLRGAL
		l		1		AGQLEFRVGVGLVRPALGGAG
		l				QPGAALDFSPGLSCLPA/AAGL
		İ				GTCSPPCLSLPPPPWAPVQPEPP
						RRAPPPVHGAQSHRPPKG
				<u> </u>		

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25569	55937	A	25710	144	519	HPGQRLRRVYWVPQQCQPIGA ELDFSPSLSCLPA/AAGLGTCSP PCLSLPPPPWAPVQPEPPQRAPP PAPW/WLSPIDHPRAEECECTA QDWQAALPAAPVWDPLEMSG LFDRAEKRYIRSFARKDSM
25570	55938	A	25711	271	743	ARTWNVPKVCVRIKANSHSIFT GLSCLPAGQGSGPAARIIA*ASD PLRGLLCGPSLLDE/PPPAPWR PVPSTTYGLRSAGEQRGTGRQL HLSAAPVRDPRGEAIWAPESGR SAASILKPARPPAHREERTTPDA PP*EL*HSPRRSAASLREDPWLH S
25571	55939	A	25712	1043	1348	GPARNRAQRRRAGTAGGPITPS AAAGPGAKPLIARRRQGWPAA PSAGPAKPTPTRISSWPAS\QPA AAVPARASPSTTLFKLREWAPA LASPERGSHSATVG
25572	55940	A	25713	22	226	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKAVDTQ RH
25573	55941	A	25714	166	714	
25574	55942	Α	25715	1	462	

Sociation of peptide sequence   Sociation of first sequence   Sociation of first sequence   Sociation of first sequence   Sociation of the s	SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
25575 55943 A 25716 I 924 MFAIISYSLAAVLLTATLTA IIISFPVALCLVIGANLGSGLL LINSAANAARRVALGSIL LINSAANAARRVALGSIL LIVGSLIILPFVHILAETMGKI PKAELVIYPHVFNLVRCLV PPVDPMARFCKTIRDEPELI LRPKHLDVSALDTPTLALAN RETCALATPWTDDGRKYAY ASGGRRSATKVMVVVTDG DGSMLKAVIDGCHNDNIR, AVLGYLNRNALDTKNLIKEI IASIPTERYFTNVSDEAALLE GTLGEQIFSIEDMDLGDEVY GRPHIPMIDPTLRNOLIADLG PQVRVLLLDVVIGGFATADD SLVSAWQKACAARLDNOP, IATVTGTERDPQCRSQQIATI AGIAVYSSLPEATLLAAALII SPAAQQHTPSLLENVAVINIG SFALELQSASRVVVHYQWSI AQQGK WLANPELLEADADA AAVIDILABIKEPILCAPND DARPLSAVQGEKIDEVFIGSG TNIGHFRAAGKLLDAHKGQ RLWAPPTRANDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPFRIR GANVFLASAELAAVAALIGI TPEEYQTTYVAQVDKTAVDT YLNFNQLSGYPTYAQVDKTAVDT YLNFNQLSGYPTYAQVDKTAVDT YLNFNQLSGYPTYAGVTFG YWQSFEDDHLPLAFFLARN PMKNCWKILDIEETTDVDIII YLALLPSFHPETDPOFFGKGL AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEF PSAWQRFIGQLYYCSMEEDI RWSLCTIAMNTAHLSFECV AERIRWLQEGRIGVPCSGRCGYQII DKRGHQHGGITALVQCGN DKRGHQHGGGITALVQCGN DKRGHQHGGGITALVQCGN							
25575 55943 A 25716 I 924 MFAIISYSSLAAVLLTATLTA IIISFPVALCLVIGANLGSGLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSALDTETLALAAN RETCALATPWTDDGRKYAY ASGGRRSATKWVVVTOG DGSMLKAVIDOCHDNILRI AVLGYLNRNALDTKNLIKEI IASIFIERYFFNNSDEAALLE GTLGEGIFSIEDMDLGDEVY GRPHPMIDPTLROLIADLG PQVRVLLLDVVIGFGATADF SLVSAWGRACAARLDNQFL IATVTGTERDPCCRSQQIATI AGIAVVSLIPEATLLAAALH SPAAQQHTPSLLENVAVINI SFALELQSASKPVVHYQWSI AGQGKWLANFELLEADAD/ AAVIDIDLADIKEPILCAPND DARPLSAVQGEKIDEVFIGS TNIGHFRAAGKLDAHKGQ RLWVAPPTRMDAAQLTEGG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPFRIRI GANVFLASAELAAVAALIGF TPEEFYGTYVAQVDKTAVDT YLNFNQLSQYTEKADGLLK RPWGRKILDTLATYHEOHRI GPGRERLRRMALPMEDEAL 25576 55944 A 25717 I 417 MGVLNINWLSEEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLRFLARX PMKNCWKILDIEETIDVDIII YLALLISFHIPETDPOGFRGL AYEALRIAGSPAKSWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGELDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV AERLRWLQSGRITGHDERLI RYSLCTIANNTAHLSFECV RYSLCTIANNTAHLSFECV RYSLCTIANNTAHLSFECV RYSLCTIANNTAHLSFECV RYSLCTIANNTAHLSFECV RYSLCTIANNTAHLSFECV RYSLCTIANNTAHLSFELV RYSLCTIANNTAHLSFELDIA RYSLCTIANTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
IIISPPVALCL/IIGANLGSGLL LINNSAANAAARRVALGSLL LINSSALIP.PVILLAETIMGKI PKAEL/IYPHYPYNLVRCLV PPVPPMARRCKTIRDEPELL LRPKHLDVSALDTPTLALAN RETCALATPWTDDGRKYAY ASGGRRSATK/MVVVTDGE DGSMLKAVIDQCHIDNILRI AVLGYLIRNALDTKNLIKEI IASIPTERYFINVSDEAALLE GTLGEGIFSIEDMLDGBVY GRPHPMIDTTLRNQLIADLG PQVRVLLLDVVIGGGATAD SLVSAWQKACAARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVVSSLPEATLLAAALI SPAAQQHTPSLLEWAVININ SFALELGASKPVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCARND DARPLSAVQGEKIDEVFIGS TINIGHRAAGKILDAHKGQ RLWVAPPTRNDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEYOTYVAQVDKTAVDT VLNFNQLSQYTEKADGLIK RPWRKLDTLATYHEQHRI GPGRELRRMALPHEDEAL 25576 55944 A 25717 I 417 MGVLNNIWLSEEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLRFLARY PMKNCWKILDIEETIDVDIII YLALLPSFHETETPOPOFRGL AYEEALRIAGSPAKSWWQPE EVAEHEILLAFRALLASDSE PSAWQRTIQQLNYGSMEEID RWSLCTIAMNTAHLSFECV AERLRWLQSPRIGGITALYQCGN DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN					sequence		
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EVAEHEILLAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIAMTAHLSFECV AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPV RRPDICTQHNDQSRCEGYQII DKRCHQHGGGTALYQCSN			1				YLALLPSFHPETDPQDFKQLRQ
PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV\ AERLRWLQEENTGEIDEEL FLYAIAKGNVFNFQTILHLP\ RRPDICTQHNDQSRCEGYQII DKRGHQHGGITALYQCS\			l				AYEEALRIAQSPAKSVWQPEEY
RWSLCTIAMNTAHLSFECVV AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPV RRPDICTQHNDQSRCEGVQII DKRGHQHGGGITALYQCGN							EVAEHEILLAFRALLASDSERFL
AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLP/ RRPDICTQHNDQSRCEGYQII DKRCHQHGGITALYQCS							PSAWQRFIQQLNYCSMEEIDEL
FLYAIAKGNVFNFOTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGTALYQCSN							RWSLCTIAMNTAHLSFECVVLL
RRPDICTQHNDQSRCEGYQII DKRGHQHGGGITALYQCGN							AERLRWLQEENTGEIDEEELGS
DKRGHQHGGGITALYQCGN							FLYAIAKGNVFNFQTILHLPVA
							RRPDICTQHNDQSRCEGYQILS
PRAKGERLFFDAPA*CASSAI							DKRGHQHGGGITALYQCGNAD
							PRAKGERLFFDAPA*CASSARV
CVLSLAGASKKSRSPFARGS.							CVLSLAGASKKSRSPFARGSAL
PHWYRAVMPPPCW							PHWYRAVMPPPCW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop endnn, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25577	55945	Α	25718	1680	2058	YRAYAPAFLPLSPSCPPLWRHC
						GSGRGENRRRDSSAHGPYAPRR
						QPDMPAHRQS*SFV/PASCSAC
						MDEPHKRLTVTAGTECGTSASS
		l				AALRAILKPCSSVCSSFFLLLLL
						PPPPPSSSSSSFFFLF
25578	55946	Α	25719	1115	3549	NPDRLLQLNLILETSK*QQMGD
						TRKKRS/NLTVAPIISPLKRYEQ
						HTELSRHINVVNLGDRNRRQQL
						ILDQGKSSQRNIYLSHVAQKIPG
						RATYALSHSVDMITIQLGTLLR
						CAPPHRRRYAGRFFCRSAGNFL
		l				NVQGFDAVLVAVKIIDLLLCLT
İ				ļ		IAPSLIVCTRLRSPWCGALRRCS
		1			-	TDGRSDLASSGVMFSIDTESAL
						TRWCLSLPHGALGKIIAEGLLS
1						VIASKASAIVTTVAVVPVTRRSS
		1				LVNWHSGGSGLWRCNRTDERD
						QQASQGTTRMGRTQRNYSPTR
						QAIHKTGSPTMATTSNTEQPPH
						EKPNTLTQHPRNPDRTIHPKAT
						HNELTQDTPQRDAKQNGEKTQ
						RKKNCLSELNDAEDQAERFQD
						RLMLKLQVTTKPCSMTRLRDC
						AGIWSAANRWSGIGIDRMIMLF
		l				TNSHTIATLFSSRRCAHRNKFH
						LMNEAVRRLLRSSFRKSVLRRD
						ASFHDNQRVHSLQLLKERKKSL
						IHGRICAAKASLFQTRRYRWQK
1						APLFSAQFRGRNRAVTHNRWV
						TTTTAIERTRARGLRPNSGRGF
						HSSPAWQLRHRKCRRCARRYH
		1				TVYWIKRRRSVARASTVVSGRI
		1				TSRRGENRRRDSSAIAHMLHAA
						KQTCLRIAVMIIRAASCSACMD
						EPPSDLTVTAGTDAGLAPAGYA
1						LNERROLLHALTKSTALRTAHR
						GPNRTGWLNRRIVRFVMTALF
25579	55947	A	25720	606	1562	
25580	55948	A	25721	688	762	OV DOCUMENT BERNALLY AGAINSTAN
25581	55949	Α	25722	492	737	SLPSGATLPPPALLLASAPDTA*
	l			I	1	WRCRER*YHLPAYAALSPAVA
	l					HRASLYSTLPSSVPWRRQCAGF
L	L				l	RARRSPEQAWAYPAR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25582	55950	A	25723	335	903	WVHDLPARKGSSARNIMLKSA PLRGHTRTRRKKMNIEANVAT PDARVAITIARFNNFINDSLLEG AIDALKRIGGVKDENITVVWVP GAYELPLAAGALAKTGKYDAG IALGTGIRGGTAHFEYVAGGAS NGLAHVGODSEIPVAFGVLTT ESI/EQAIERAGTKVGNKGAEA ALTALEMINVLKAIKA
25583	55951	A	25724	3644	4545	SEAWPWRTAGTCLLCLNTT/AH VDKAIESRTVVADVLAKENAL TGKLLTVSFQAHEAVIHGHIPA PEENLQVLAALRLQVLQGDYT LHAAIPPLEEVYSLQRLKARISQ KIKTFTPCERLEKRRISFLEGTL RRSFRTGSVVRQKVEEEQMLD MWIKEEVSSARASIIDK WRKFQ GMNQEQAMAKYMALIKEWPG YGSTLFDVECKEGGPPQELWL GVSADAVSVKRGEGRPLEVF QYEHILSFGAPLANTYKIVVDE RELLFETSEVVDVAKLMKAYIS MIVKRKPSTRSASSOGSSIR
25584	55952	A	25725	1	735	
25585	55953	A	25726	147	504	STCPASAPPRPSAGPRILSGSSAS GSPLGSSSASSPAVHKG*RFWL TG*CGP*VSAGNKULFERWDGS VQSIIPLQILESQGSKNLEVFFRG WMVAMDNRFVGLKGDSQQLS GQRIFKLG
25586	55954	Α	25727	1	639	
25587	55955	Α	25728	I	1247	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25588	55956	Α	25729	1	2376	MAEVEEKKQRIFRKFTYRGVD
ļ						LGQLLDMSFEQLRQLYGARQL
						RRLNHGLWRNAEAQAAFAAE
				l		APMLGQEGGADHREAGSGEDA
Ì						PAGYDHPSQDGGQQGGRLQRQ
						DLQPGGDQAGDDRPRPGRVLH
						HLQAQRGKKPM/ISTVTFGQ*P
						DPPLRAGQRL*RC/RLLIYGRGK
						CWALSGNP/RSGKTTLLKSISAR
						LTPQQGEIHYENRSLYAMSEAD
						RRRLLRTEWGVVHQHPLDGLR
l		l				RQVSAGGNIGERLMATGARHY
				1		GDIRATAQKWLEEVEIPANRID
					ŀ	DLPTTFLRATHTVKMFSIPGYSS
						PGQLLDPETNINIGTSYLQYVY
						QQFGNNRIFSSAAYNAGPGRVA
						TAIVLTLYIIYMVGFFATSGELT
			İ			YEVWIGFFASAFTKVFTLLALF
						SILIHAWIGMWQVLTDYVKPLA
	ļ	l				LRLMLQLVIVVALVVYVIYGFV
		l				VVWGMRAALQISQSGQTCALL
1		1				SKVFPTRSHTVSAQGGITVALG
						NTHEDNWEWHMYDTVKGSDY
						IDAGRKRQEEGDWNSGVGDPS
		1				DAGDRKHQLKAAQLRPEAIKQ
		l				RRIANRLKRRTQFPRHLKGFVN
		l				TLKPIHGGCSVGTKCPQMASLP
	1	l				EGLHHPVKLVFLGKPGCLLTDR
Į.	}	l				PLKGPNTAKPVAVDLNASATAI
		l		l		TSYSLYGGSMILLFLASTLYHAI
1	į	l		1		PHQRAKMWLKKFDHCAIYLLI
		l				AGTYTPFLLVGLDSPLARGLMI
25589	55957	Α	25730	219	652	SASWREAICLSRCRLPRSATAR
		l				GAGRGGCGLADRRASRQGKNL
		1				EAESAQEONGHOHRIHESOHPC
		l				QGGAPVSHHQAAVRLRESQIQ
		1				GAAEKR*PTGDVIHPGQPVSGG
		1				/LK*YPSIPTCLLTTRTASLLKPP
						GVRTSVCWQQLPR
25590	55958	A	25731	1902	2100	RKFFSSSSGRS*PVRCSKL*SSID
						A*PLERIKRSRSYOVGSVGLCL
						RKSFHSTSAISAMPIGAPG
25591	55959	A	25732	3223	3669	
20071	33737	1,,	20102		5007	L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
25592	55960	Α	25733	1	4325	MPEPPTHSMGSCAAGASLTSTA
		1				PCSTAPSPIDHLRAKECERTAQ
		l			1	DWQAAPPAALVRDPLAALVRT
		1				WRTFMSSSRIVNTPIGTLCLAQ
	ľ	1				GFQWFSVLSQVHASTDQEIQE
						MHDEQANPQNAVGTLDVGLID
					1	SVCASDSPDRPNSFVIITANRVL
						HCNADTPEEMHHWITLLQRSK
						GDTRVEGQEFIVRGWLHKEVK
						NSPKMSSLKLKKRWFVLTHIPG
						LLQEFREDALNWGPDEKIFKET
						ELVNDMDKINGRIERAE
25593	55961	A	25734	501	2871	TGCCCLRKTDCRRRESARGVH
				į.		AVYRRICARSMLLYRESVRPKA
		1				VTARVAVEAGIADYWYKYVG
						LNGAIVGMTTFGESAPAELLFE
				ì		EFGFTVDNPLASRAVRLRLPFN
1						NDQVEAAVGWKLAVERHNGP
		1				TALILSRQNLAQVERTPDQVKE
						IARGGYVLKDSGGKPDIILIATG
						SEMEITLQAAEKLAGEGRNVR
						VVSLPSTDIFDAQDEEYRESVLF
						SNVAARVAVEAGIADYWYKY
						VGLKGAIVGMTGYGESAPADK
						LFPFFGFTAENIVAKAHKVLGV
						KAGSHIPRKKYDVPGKKSFSPV
						KYSTIGSPSPERPVSITTIPNSFVI
l		1				ITANRVLHCNADTPEEMHHWIT
1		i				LLQRSKGDTRVEGQEFIVVEKL
		1				IRGLAMEDSRNMFALFEYNGH
						VDKAIESRTVVADVLAKFEKEP
l	1	1				VGKHLPTYDGQIAMGLESTAS
ŀ		1				VTRKHSSPSSLQNALSCETATSL
ĺ		ı				IERRVRMALGTGDRRGLNTWL
						ARLPMEAKEKDEWRYWQADL
						LLERGREAEAKEILHQLMQQR
						GFYPMVAAQRIGEEYELKIDKA
						PQNVDSALTQGPEMARVRELM
		1				YWNLDNTARSEWAN\LLKNKS
	1	1		1		KPDRAHLPGYASTTQWWILSV
l		1	1	1		QATT\AGNLGDHLKERFPLANN
		1		1		DLSKRYTSGKKIPQSYAMAIAR
		1				QKSAWNPKVKSPVGASGLMQI
ĺ		1		1	1	MPGTATHTVKMFSIPGYSSPGQ
25594	55962	A	25735	1	1195	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
25595	55963	A	25736	1931	2676	FCGNTHQTYLGWVGGVANSEA *GEKWGTPDLVG/AERTETIQR
l		1				LLGVCPEQGEGKIYIDGKQVDI
		1				RNCQQAIAQGIAMVPEDRKRD
						GIVPVMAVGKNITLAALNKFTG
	l	1				GISQLDDAAEQKCILESIQQLKV
						KTSSPDLAIGRLSGGNQQKAIL
						ARCLLLNPRILILDEPTRGIDIGA
	1					KYEIYKLINQLVQQGIAVIVISS
	1					ELPEVLGLSDRVLVMHEGKLK
						ANLINHNLTQEQVMEAALRSE
	L	_				HHVEKQSV
25596	55964	A	25737	1491	1667	TNGQWRAFYC*MRSGRNIRRR
						GEDISGGAGVSPRESPE*REVPE
		_				MGPGGAANRGTKRV
25597	55965	Α	25738	419	823	VTLVAITRPIHVNRLRQYLVAIS
						LNETFGPSCKPSRSPCSSLSTCC
ŀ	l					WNAGVMHKK*VQGGRLCSYR
	l	ļ		1		N*SICLVVISPVVMGKRCIS*RC
		1				TAVLAALTVTVPSGVVAAHSV
		_				MLPRLPMKRSSIVPLPSNWRTS
25598	55966	A	25739	591	968	VKQCKQADEH*EQSLIPLERRR
				İ		TTPLSVPQL/GKALTTVSFCASG
ļ		1				GTSVNSLSHTS*ECMASAVAVK
		1				FTFPNLAVNFCTAAMAGPKVA
	1					LTSTLARIQAGSLARTGGRAYR
		١	0.00.10		1000	WSRSTMLAKSFWCLMAL
25599	55967	A	25740	764	1005	QARPRAPRRAPYPILIRSSIITLIY
	1					/DGQRLGHLDDGTDSWNHVPT
		ł				LNGQCTLVLIHEYVDTRGPEIK TILVISWWNILVFH
25500	55968	١.	25741	463	786	TILVISW WNILVFH
25600 25601	55969	A	25741	3	646	
25602	55970	A	25743	1	3008	MTMLOIVGALILLIAGFAILRLL
25002	1559/0	A	23743	1	3008	FRALISTASALAGLILLCLFGPA
ĺ		1				LLAGYITERITRLFHIRWLAGVF
		1			İ	LTIAGMIISFMWGLDGKHIALE
		ļ.				AHTFDSVKFILTTALAGGLLAV
		1				PLQIKNIQQNGITPEDISKEINGY
	1					
						YCCFYTAFFLMACSDQRRLRG AMDKRYKFILVGFGEVFVFNLE
1				1		
l		1				SLDSGKKIHLLRRSHEEVMGSV
1	1			1		MRTGTIDKGILPFIHHTRGNEIL
1		1		1		FIPALFILFSLGGAVFGMGEEAV
		$\perp$	L	L	l	AFAIIIA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		_				
25603	55971	A	25744	2	3494	TITNLRPAAPGICEMAQGLSAG
						GEYTGASIFVAEYSPDRRRGFM
						GSWLDLRSIAEIELGAGGVGLIS
						TIVGEANFLDWGWRIPFFIALPL
			ŀ			GIIGLYLRHALEDTPAFQQHVD
			İ			KLEQGDREGLQDGPKVSLKEIA
						TKYWRSLLTCIGLVIATNVTYY
						MLLTYMPSYLSHNLHYSEDHG
i						ALIIIAIMIGMLFVQPVMGLLSD
					İ	RFGRRPFVLLGSVALFVLAIPAF
		l				ILINSNVIGLNLLPAMFPTHIRYS
		l				ALLLEMKN
25604	55972	Α	25745	1	277	
25605	55973	Α	25746	902	1006	
25606	55974	A	25747	2	1265	
25607	55975	Α	25748	409	525	
25608	55976	Α	25749	91	431	NHKPGNIDVARRIQRGFAGDQI
						GHLRPVERQCSPDKRRFIAADG
						REIRGKQRAGHIFQLLSRCLLQI
		1				LNHCQRRAAHFRFQLSNQRHQ
						QLLPV/HYHAAEREYPAGACLV
						RWLL
25609	55977	Α	25750	3	71	
25610	55978	Α	25751	1	1212	
25611	55979	Α	25752	Ĭ	2786	MAAVIEQIRRAVLALVTGVVHP
			ŀ			GDIPVVWDIVWNATAAFIAVIII
1		İ		ł		SLLLDESGFFEWAALHVLRWG
			1			YGPGRLPFNRIGLIRRITRRIRQR
		1				LLFGLVTFILLLNRSQNPAQDIQ
						LLAFRARTGKQTAQFIHHLPRM
1						VFTDKTGSSNGLAPQGQCSAQ
		1				GELILNEKLAKQLVTAANWVK
1						MOSDEGEINPVDILRWPGVMA
						AQEQDLDAIAAEILAALDGTLD
						DFIVARETEGOSGLKRVYHSPG
						APDIREFTRDAIP
25612	55980	A	25753	5	402	EIFSVVWIIMTRGDVVTISRWR
		1		[		VSSSPLETWNKRWAKISPAPFS
						LLPISRLEKSEGDWLPETVISAF
	l		1			NMPSSLSLIISSL*FKVRDV*HFF
			ĺ			/RI*TLRGHYRVINWPNFNIVVS
						QGIGKRLANSWLVFTLFHRI
25613	55981	A	25754	48	219	PETCGHLWAYVWPSCAAV\GL
23013	22901	^	20104	70	-17	YFKVHVLG*RSVTPVTDIVKLL
						EFTRLRLPGYTKSIE
25614	55982	A	25755	1	912	El React Of I Rolls
23014	22702	<u>_</u>	23133	l	/12	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last aminu acid	*=Stop endnn, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25615	55983	Α	25756	1	1857	MRVCARACVRTRTRMCVYAH
		1				TCVCVRTYAYVRVRVRVRVHVRA
		1				RVRVCAYARTRVRNSLSILPFIC
		1				LTLATPIHHIHOEEFNIRGIVPVI
	1	1				RRVKPDLAIGIDITPSCDTPDLH
		1				DYSEVRINGGVGITCLNYHGRO
	1	1				TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
		1				GWEIGFSPLALLLAFLCSTSPGF
- 1		1				GDPDGLGVIAYQDTVRPNAAT
		ŀ				AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
		ŀ				KAVTELNQHAPLAMVGDGIND
						APAMKAAAIGIAMGSGTDVAL
		1				ETADAALTHNHLRGLVQMIEL
						ARATHANIRONITIALGLKGIFL
		1				VTTLDDRVVAGSAGRYGGDGA
		1	l			GDSECVKIVAQEIRQTDRNIER
		1				DRSPRPSGERVRVRGKGGIEAN
		1				QPLSTAFTNQITIRQSIRLFSNQF
		l	l			VFHKGISRVVAGSSAIISNVSPG
		ı	l	ł		CILRTPNCRRGFPISCTGEGKAA
		1			1	YGWQRDGGHAEYLLAEEKDLI
						LLPDALSYEDGAFISCGVGTAY
						EGILRGEVSGSDNVLVVGLGPV
						GMMAMMLAKGRGAKRIIGVD
			1			MLPERLAMAKQLGVMDHGY*I
			İ			LPDVY/V*IGVARVSWMNGRID
						SELRTRVRAYAHTRTRARTCTR
						TRTRTYAYVRTHTHVCAYTHM
	1	1				RVRVRTHARAHTR
25616	55984	Α	25757	3	1180	SKLGTRRSVVWA*SPSTSPTLW
		1				CSTFSAAGHSSMKRMNEFVDL
				1		LPAQQRMKGENWYRGTADAV
						TQNLDIIRRYKAEYVVILAGDHI
						YKQDYSRMLIDHVEKGARCTV
		1				ACMPVPIEEASAFGVMAVDEN
		1				DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
						RDENSSHDFGKDLIPKITEAGLA
						YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
		1				PAGPPLPLPAARSEAPKAAGTV
						ASVPSIAPARLRPVPDPVELVLV
						AAEFITPGDPTPRLHGSGFIDIR
						QIHHQTRSHLEGVKTGIRFLNH
						FSGNPQGGIAHVNGVARFQVK
		1		1		QCHQAWGQQYAARLRFQARGI
		1				SLQIAIHRVDIIHRFDVRQL
25617	55985	A	25758	16	543	
25618	55986		25759	1	3387	
		1' 1				

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25619	55987	A	25760	1688	2234	LSVGKTFPVLVPAAFRKVSATG
		1				AAVPGTPSILALPSYSTTPFGVC
		1		l		TSASMNVPVLTLRIRTRVTGEV
						AAIKPFSMANAPTPDSILPQLGV
		l		l		VSTRCS*TITCANR*STSARGSL
		1				ERLIMATLL/WVAGTFD*SVWF
		1				GHDTDVVTLYRFHEALCYSVT
						LRTPHRRVLRFKSQHPGELACF SPVA
25620	55988	A	25761	905	4762	PPHNWMPSNATPGIAFVWCAY
						GAI/LPGDAPVPVVDDYRKVVR
		i				KDTKGLIARWKYFWMSVIALG
	1	l				VAFALYLAGKDTPATOLVVPFF
	ł	l		}	1	KDVMPOLGLFYILLAYFVIVGT
	}	1	į			GNAVNLTDGLDGLAIMPTVFV
	1	l				AGGFALVAWATGNMNFASYL
	ļ	l				HIPYLRHAGELVIVCTAIVGAG
	1	l				LGFLWFNTYPAQVFMGDVGSL
	1	l				ALGGALGIIAVLLRQEFLLVIM
		1				GGVFVVETLSVILQVGSFKLRG
		l				QRIFRMAPIHHHYELKGWP
25621	55989	Α	25762	1	1448	MCHVLLAGRQRRTAGPEHALT
	1	l				PPECGSAAIGPAVYKWAHATG
	İ	1				VMIPDRPRSPHAGAEERHWHH
		l				PQPELISQRLGSFSSGPTKYIHEF
					1	QYLTLSYNLTWSDLNVILTFILP
						LDEWERVFSLAQSHTDNCRLH
		l				KPDLQEGIREVPQEDPQWNYQ
						ENSPGIARRDYMISCLVEGLKK
		1	1			AAYKAINYDKLKETTQGTDKN
		1				PAQSMACLAATMRHFAALDPE
	l l	1				ALAPHRDVNHGIKLTCKTIRSSI
		l				DISREIRAPRECRSTEMASWHPP
	1	l				ADLTECPVESGYSVLSGRTDCQ
	ł	l				YSHTVRRACLTTIDSRPAVRQL
		l				LKIREVQLLSLLRGCVRSRRSGS
	1	1				INAQYCRCLERVVTLPFFDSGPS
	1		l			LMNHAPHLYFAWQQLVEKSQL
	1	1	l			MLRLATEEQWDELIASEMAYV
	1	1	l			NAVQEIAHLTEEVDPSTTMQEQ
	1	1	1			LRPMLRLILDNESKVKQVLQIR
	1	1	l			Q\DGLAKLVEQLRHLSKKHHLD
	1	ĺ		l		TDSTSSSLPGVRTPYSPIRGGEE

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25622	55990	A	25763	1029	1665	RPESISSVASKTRLGRSFHGAAR
-		l				RTREYHSSTCNASIAAAATV\A
ł		l				AQGHPDTTSTPPASVDTTATNT
		1		l	1	QTPAVTAPAPAVDPOONAVVS
		l			i	PSOANVDTAATPAPTAATTPDG
		l		l		AAPLPTDQAGVTTPVADPNAL
		1				VMNFTADCWLEVTDATGKKLF
		l				SGMORKDGNLNLTGOAPYKLK
		l				IGAPAAVQIQYQGKPVDLSRFIR
	1	l		1		TNOVARLTLNAEQSPAQ
25623	5599I	Α	25764	658	1307	SNRLYTDVESINEIEGIYMKLRF
		l				ISSALAAALFAATGSYAAVVDG
		l			ŀ	GTIHFEGELVNAACSVNTDSAD
	ł	l				QVVTLGQYRTDIFNAVGNTSAL
1	1	1				IPFTIQLNDCDPVVAANAAVAF
	1	l				SGQADAINDNLLAIASSTNTTT
		l				ATGVGIEILDNTSAILKPDGNSF
	ŀ	1				STN\QNLIPGT\NVLHGLAFRAR
	Į.	l				CVSTANLRVPRPICFDPGSSYQA
						NTIGSGRCADCQPDA
25624	55992	Α	25765	167	232	
25625	55993	Α	25766	441	686	
25626	55994	A	25767	206	331	
25627	55995	A	25768	674	900	VVPICTMLEEALERQNLTASLC
		l	l			G*LKKACGRSWQTSPIKRSLNG
						AKFSRTSIIMGFITAEKWSGWEI
25628	55996	A	25769	41	222	WSARNVTS
25629	55997	A	25770	17	525	ESLECSGPSWNASGTQSGFYCH
23029	33337	^	23770	1''	323	RIAPILPEKRLARMVEKTWGLG
		l		l		LRRRTGFRRQNLGGGTGTLVE
		l				CTSENS\KPSKSSFRKORRGORR
	1	l				EGH*SLRR*IRRERTERMOASR
		l				VTWNSFPQVPAAKKPSSLSESG
1		1				*P*ATNYTREODSMWNCVHHY
						WOPPTSVSRLVHLNSG
25630	55998	A	25771	698	1051	PYLRIRLTALISRSSTVMRILFAI
		1	l	1		SKRPIT*PKRPKPTTMTWGLSSL
l	1		l	l		THGFSSSSSGPLNWRDSHLSTSF
						ISNGVVIMESVTVTSNNAIWSPS
l				l		SSVAAVNTSRTPEAAIKRNTGR
	1		l	1		SK
25631	55999	Α	25772	1	2204	
		_				

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	Incation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25632	56000	IA.	25773	3	891	RYRNQDDHELQIHTGTRFYVEL
23032	30000	^	23113	3	1051	CGFRVNPPWLATDVTHAAMAL
		l				
		l				LTLVTTGLHIVGEWGKHATPPV
					i .	PYSICSNPPRRAAYITVWRNRPC
		1				TLGDHLFSIAYPRGLRYDMGG
		1		1		GGEGTA WANVRQALARTTGR
		1				AQHWTKDNAKSSREARHPRQN
	1	1		1		KTKTHLGKPVLRWV/DPSFDQS
						KYDSIVWNPI/TYYPVPKPSTQV
						GQKV/LDKILNYTNTEMKEAIA
						H/DTSKEGLQFYEVVPVALVVA
						GTQMATGLRTMDTRLYFEGELI
						DAAPNKPVIKVVRQGEEPDWP
		_				SKGDAGDGEKVPSSLSESG
25633	56001	Α	25774	1	285	
25634	56002	Α	25775	1	302	SFSSFTQRTASVIISSTSTQSRLA
		l				TSPILAIARARTSRRCPEKPQLG
	1				1	YPDSAAHVFQQDRATKYVINR
	1	1				NSKKP*ICSACRSTVSTRQHRR
						WRGSLQPLSQ
25635	56003	Α	25776	307	473	
25636	56004	В	25777	67	809	
25637	56005	A	25778	44	1519	MAIN OUT WATER TO SEE THE
25638	56006	Α	25779	1	1519	MINRLQHTVYTHKWNSYRTEP DRRHTALRNSFCLVRLNDSSHS
1		1				
1		ı				RSLDSKQGHTEITFAATEHPPSP
}		1				VSLRIHDVAFDDGRQTSRAPCF
l		1				NLEQPGKLDCTKRLISDCWVM
l		1				HPGESWHGFKDIPDNWSMLDPI
ĺ	1	1	l			KISILAPGMGEDGELEETGVPA
		1				ALVTAWLGRHGIVPTRTTDFQI
ŀ		1				MFLFSMGVTRGKWGTLVNTLC
	İ	1	l			SFKRHYDANTPLAQVMPELVE
	1	1			i	QYPDTYANMGIHDLGDTMFA
	1		1			WLKENYSGARLNEAYS/GLPSII
						ERHVVDAQGYRGGGMLCSCES
		<u> </u>				NFCVSLLRIQAS
25639	56007	Α	25780	461	789	HHVLSELQQLYTAYRSVDHIID
		ļ				HSLAIARAPQRRRCPEKPQLGY
1		1				PDSLQHVFQQDRATKYVINGTS
l						KKP*ICSACRSTVTHGHTDAGE
						EVWNPFAVLVPSGKDARVWG
25640	56008	В	25781	1	990	
25641	56009	A	25782	1	3066	
25642	56010	Α	25783	583	904	WGIRTTDFQIMFLFSMGVTRGK
l		1		1	1	WGTLVNTLCSFKRHYDANTPL
[		1		1	i	AQVMPELVEQYPGR*FTGVRK
l				1	1	KSNN*FRQFGGVDTAGNNL\SEI
l	I	1				FSASASAEIFPANSFCNRLA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25643	56011	A	25784	331	660	TGIQLPGAP*SQPWSTRRRAVV RPLYRVN*AVP*NR*VIRSKRA MPKRTDIKSILILGAGPIVIGQRL GWRDSDGVRLCGVLGSQENVC ELDEKGEERWSISGTSSEFTR
25644	56012	A	25785		798	MSDAEDGARTTLGSGNAVERL ADALSQQNVTVIKSTSLDDGFA ILSSNEAIDCLMFSYQMEHPDE HQNVRQLIGKLHERQLNVPVFL EGAWILEDTADFIAGÏRAVAAM TTYRQQLIPHFSALMKYSDIQ SEYSWAAPGHQGGVGFTKTPA GREYIDYYRLLRVAWVLHKTE CRLINFPETIPFONSFRVDIEVSN ESPDEEVKLRRHHLARCMKNF KTDIYFVSTFEPSTKSVDLLTVE TPAGT
25645	56013	A	25786	211	414	RVCECIQLRRIEIFRFMISSQPNL PEDLHPQIIAKPSQKRLIEQ*SSK LTVTKARRQGSRYKSSRFFS
25646	56014	A	25787	1694	4974	ISLISAKPVYMVPSRNRYGIIG PIVPQEMQPETLQKKISSPLT KDKAGQKPSYCVVTNCTYDG VCYNAKEAQD/LLEKTSDR.HF DEAWYGY/ARNPIYADHYAM RG/EEGDHNGPTASYIHVREGV GRLNFFRR/OAYMMHATTSPL YAICASNDVAV/SMMDGNSGLS LTQEDCWYMHPGESW/HGFKD DGELEE/TGVPAALYSNLCLSSG TTGLSTFALLYSNLCLSSG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25647	56015	A	25788		1709	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSADP ELRIKVVKAVIEOHMSLNQAA AHFMLAGSGSVARWLKVVEE GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK LASALSTMRTLKSVFSEIYHENG GRYGYRRVTLSLHEGKQINH KAVQRLMGTLSLKAAIKVKRY RSYRGEVGQTAPNVLGRFKA TRPNEKWYTDVTEFAVNGRKL VLSPVIDLFNNEVISYSLSERPV MNMYENMLDQAFKKLNPHEH PVLHSDQGWQYRMRYQNILK EHGIKQSMSRKGNCLDNAVVE CFFGTLKSECPYLDEFSNISELK DAVTEVIEYYSRRISLKLKGL TPIEYRNGTYMPRVNCPLFDTL RIPDIGGVVRARIAKLKNDTD MAIIDKRRPRANVSQWHIIIGD
						VAGRDCVLVDDMIDTGGTLCK AAEALKERGAKRVFAYATHPIF SGNAANNLRNSVIDEVV/DLRY HSAER*NQITAERAYSDPVRKI
25648	56016	A	25789	2902	3271	SSAARHCAGCGDVRSVCRSGR ADAPRMHPGESWHGFKDIPDN WSMLDPIKISILAPGMGEDGE/P TRTTDFQIMFLFSMGVTRGKW GTLVNTLCSFKRHYDANTPLA IOVMPELVEQYPAFVINQ
25649	56017	А	25790	185	663	SPVPSSRPSTRHRLPDGSSSSQFS SAIAARKVVNSCILCSKICQN*F NRRAASPLKRLP*SGA SGMITIP NQPAPAQIPAK*LYTRLDEVKP* *KITHGNGVSFCPTG*A*RTGIS ASSRDLEVQSKKRSFPALNWPA VYCCSALGSAPKCKPIPFLRAT V

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25650	56018	A	25791	684	4208	NGLFWLFQPWLFADETRRRLE
23030	30018	^	23791	084	4208	ERFRDRYQIIHHSSQVCHSDQA
		1				VYVLTQERVNERDDIVDIDLFV
ŀ		i			i	IDEFYKLAFRQLKSGDIDHQDE
l		ı			i	RVIELNIALSKLLKVSROFYLTG
		1				PFVNSIRGLEKLGYPHTFVSTDF
		į.				NTVALDVKTSASKRMTTKPSS
		1				KRWGKSRTCVDADHIKNGIGI.
		1				HFGALPRALQQYTADQFNAGK
	ì	l				LRFLLCTSTIIEGVNTIAKNVVIY
1	ŀ	l				DNRAGSTRTISADIINSVICGLN
		l				TLKSFDTRWALL
	24010	١.	25792	1	896	ILKSFDIRWALL
25651	56019	A	25792	231	721	IITAEKGRSREQQLAIL\PLNLAD
25652	36020	IA.	25 /93	231	1/21	MROLOOOHSOTRLADTAADGL
		l				RHFTAQQRLMPLQLQAIFVTGQ
	1					ROLMLORVGY/R/LHGSPWRKA
į.						OTHLPVPGSTPEYRRSDPHGPA
		1				LTGCSSHHNPVRARRGMTIAOL
		l				
						AANPDKEYRARSFAIARSRPLA SRSGYETVTPGC
25652	56021	A	25794		933	MLEAAVCLCVFVSCSLAEGRA
25653	36021	l <sup>A</sup>	23/94	11	933	CCRVAVSIPVSVRARIHLLESDH
1	i					LGRFREPKSIPRKDAQMDTFRT
		1				MVREPATFLDQVDGLQQSDDIL
		l				RLLPPELATLGITELEYEFYRRL
		l				VEKQLLTYRLHGESWREKVIER
						PVVHKDYDEOPRGPFIVCVDTS
						GSMGGFNEQCAKAFCLALMLI
						AIANKWRCY\IMLSS\TEIVRYE
1						LSGPQGIEQAIRFLSQQFRGGTD
1					1	LASCFRAIMERLQSREWFDADA
		1				VVISDFIAQRLPDDVTSKVKEL
		1				QRVHQHRFHAVAMSAHGKPGI
27674	7.6022	_	25505	02	1100	MRIFDHIWRFDTGMRSRLLRR
25654	56022	C	25795	83	1108	
25655	56023	Α	25796	1	747	L

					In a second second	
SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	hod	in USSN 09/540,217	codon for peptide	of pentide sequence	deletion, \=possible nucleotide insertion)
	sequence		02/340,217	sequence	or peparati sequence	accented to possible state conducting critically
		_				
25656	56024	Α	25797	25	1741	IMERLKRMSVFAKVVEFGSFTA
		1				AARQLQMSVSSISQTVSKLEDE
	l	1	Į.			LQVKLLNRSTRSIGLTEAGRIYY
		1				QGCRRMLHEVQDV\HEHLYAL
	l	1		I		NNTPIGTLRIGCSSTMAQNVLA
	ŀ	1				GLTAKMLKEYPGLSVNLVTGIP
	i	l				APDLIADGLDVVIRVGALQDSS
		1				LFSRRLGAMPMVVCAAKSYLT
ļ		l				QYGIPEKPADLSSHSWLEYSVR
	l					TDNEFEL\IAPEGISTRLIPQGRF
		1		i		VTNDPMTLVRWLTAGAGIAYV
						PLMWVINEINRGELEILLPRYQS
		l	}	ł		DPRPVYALYTEKDKLPLKVQV
			Ì			VINSLTDYFVETPTPLSSLTSLPT
						IEICCMVSIPGTNQRLRPFTGFA
						THRLQSDLLLQVMTISRGRFSR
	1	1		i		SARFNGPTPSGRRLIRVIISTESG
		1		i		SRSSNPRTTGCFEEHCDHYRAII
		ı				DSADGLPMVVYNIPALSGVKLT
				1		LDQINTLVTLPGVGALKQTSGD
		1				LYQMEQIRREHPDLVLYNGYD
	1	1				EIFASGLLAGADGGIGSTYNIM
		l				GWRYQGIVKALKEGDIQTAQK
	1	I				LQTECNKVIDLLIKTGVFRGLK
	1	1			1	TVLHYMDVVSVPLCRKPFGPV
						DEKYLPELKALAQQLMQERG
25657	56025	A	25798	1	1005	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25658	56026	Α	25799	1	2392	MEMVAASKMRKSQDRMAASR
						PYAETMRKVIGHLAHGNLEYK
		ŀ				HPYLEDRDVKRVGYLVVSTDR
İ		l				GLCGGLNINLFKKLLAEMKTW
						TDKGVQCDLAMIGSKGVSFFNS
						VGGNVVAQVTGMGDNPSLSEL
				i		IGPVKVMLQAYDEGRLDKLYI
1		ĺ				VSNKFINTMSQVPTISQLLPLPA
		1				SDDDDLKHKSWDYLYEPDPKA
		1				LLEOCSCMLRSPAWGITSTDTT
				1		RARTDLACPIWLLLDPYPKLMG
		1		1		NAPKALASVDKRGVPVNTILVS
		l				ALVTALCVLINYLAPESAFGLL
		l				MALVVSALVINWAMISLAHMK
		1				FRRAKOEOGVVTRFPALLYPLG
		1			l .	NWICLLFMAAVLVIMLMTPGM
						AISVYLIPPLQTNTFNSTTIAMA
i					l	DYQMESLSAEINFAAAKLARA
		l				CADEWTARTPEKPRYVAGVLG
		l				PTNRTASISPDVNDPAFRNITFD
		l				GLVAAYRESTKALVEGGADLIL
I		l				IETVFDTLNAKAAVFAVKTEFE
		l				ALGVELPIMISGTITDASGRTLS
		1				GOTTEAFYNSLRHAEALTFGLN
						CALGPDELRQYVQELSRIAECY
İ		l				VTAHPNAGLPNAFGEYDLDAD
		l				TMAKQIREWAQAGFLNIVRGC
					i .	CGTTPOHIAEMSPGRKRLTRAE
						SSSVPSTLPGKAWLEHALPLIAE
		l			I	QL/QGRRSAVFIPF\AGVTQTWD
					i .	DYTAKTAAVLAPLGVSVTGIHS
						VVDPVAAIENAEIVIVGGGNTF
25659	56027	A	25800	412	1115	LAGEVMDLLLLSNSTLPGKAW
25055	2002/	ľ.	2000			LEHALPLIAEQLOGRRSAVFIPF
						AGVTOTWDDYTAKTVAVLAPL
	1	ľ				GISVTGIHSVVDPVAAIENAEIVI
						VGGGNTFQLLKQCRERGLLAPI
						TDVVKRGALYIGWSAGANLAC
	1					PTIRTINDMPIVDPOGFDALNLF
		l				PLQINPHFTNALPEGHKGDPRL
		1				FR\IRELLVVAPELTIIGLPEGNW
		1	1		1	ITVSKGHATLGGPNTTYVFKAG
		1			1	EEAVPLEAGHRF
25660	56028	A	25801	1	360	MDHAIAGIAVQFRGGNLLRFK
23000	30028	l^	23001	I.	1	AFQQRVKYRMCQAERAINRLF
	1	1			1	NIAVKRLTGNRLDDKSKOHIIDI
1		1	1		1	AVDIPKWSDHLHIIRRKHHDPT
		1			1	QDSGTHLPAVADDGFRTSVRN
		1	Ì			RSA*HIRYLTRC*KALNRNKLPP
		1	1		1	
				L	L	RN*TAIPAMA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25661	56029	A	25802	1032	1233	LVQFLRICFHILQRF/LPSH*RQF
				1		DESLRALPVSFLCWRTDSDFPA
		į.		1	l	DISYONYR*YNREPYLPRPDSG
25662	56030	Α	25803	I	1394	MTRDGLANKALAVARTLADSI
23002	50050	1	23003	Ι'	1.371	EIROGLOKKPOESGIOAIAEAV
					1	KRNDLLFIVVTDMQSLRYSHPE
	1				i	AQRIGQPFKGDDILKALNGEEN
				1		VAINRGFLAQALRVFTPIYDEN
				I	1	HKQIGVINDSRWSIIWSVLFGM
1				I		LVGLIGTCILVKVLKKILFGLEP
		1			1	YEISTLFEQRQAMLQSIKEGVV
		1				
					1	AVDDRGEVTLINDAAQELLNY
					i	RKSQDDEKLSTLSHSWSQVVD
		1		1		VSEVLRDGTPRRDEEITIKDRLI
						LINTVPVRSNGVIIGAISTFRDK
				1		EVRKLMQRLDGLVNYADALRI
				1		RSRLEHILHNQRVPFIMKLHHR
						MLRHFIAASVIVLTSSFLIFELV
		1				ASDRAMSAYLRYIVQKADSSFI
						YDKYQNQSIAAHVMRALAAEG
						SEVSPEQRRAICEAFESANNTH
1		1				GLNLTAHK\SRAYAAHYKPHPI
						TATQLWK\RSTITRF*SGSGRQP
	20001		25004		1010	PPG*LRFRSWDGRREISLLSRSL
25663 25664	56031 56032	A	25804 25805	14	219	
25665	56033	A	25805	744	1566	FASWLRVFSITNCAAPVTSESC
23003	30033	l^	23800	/***	1300	ALDLGSAEAKAWIGVENPHRA
						DVLTELRRSTVARVCTGRAGP
l					1	PRTQALLRFLADHSRSKDTVLK
				1		EVPEEWVKAQGLLEVRSEISDK
						NLYLTRPDMGRRLCAEAVEAL
l			l			KAQCVANPDVQVVISDGLSTD
l						
1						AITVNYEEILPPLMAGLKQAGL
l	į.					KVGTPFFVRYGRVKIEDQIGEIL
		1	i			GAKVVILLVGERPGLGQSESLS
		1				CYAVYSPRMATTVEADRTCIY
				1		NIHQGGTPPVEAAAVIVDLAKR
	45004	<del> </del> -		40.6		MLEQKAF\GINMTR
25666 25667	56034 56035	A	25807 25808	596 151	745 660	ETTERI CODEVRA ANIII UCEC
2300/	30033	l <sup>A</sup>	23808	1,21	000	STTERLGDDFVRAANIILHCEG
l		1	l			KVVVSGIGKSGHIGKKIAATLA
		1				STGTPAFFVHPAEALHGDLGMI
	1	1	1			ESRDVMLFISYSGGAKELDLIIP
1	1	1	1			RLEDKSIALAPNSRTVIT*CWFS
			1	1		AGDGGLPGPDYGQDFAAHPAG
		1		1		AGALYKCRDLINDNILRTVSCQ
	L	1_		L		SHDDGDIRGMAFARQ
25668	56036	A	25809	314	583	
25669	56037	A	25810	Į1	2982	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=passible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25670	56038	A	25811	120	1790	EGLKTKGEKASPPSCLSFCKNE
23070	30036	l^	23011	120	1790	FVISSTDYALSQSQSGGVMHRQ
		1			-	
		ı				SFFLVPLICLSSALWAAPATVN
		ı				VEVLQDKLDHPWALAFLPDNH
		l				GMLITLRGGELRHWQAGKGLS
		l				APLSGVPDVWAHGQGGLLDVV *APDFAQSRRIWLSYSEVGDDG
		l				KAGTAVGYGRLSDDLSKVTDF
		l				
		ı		l		RAVFROMPKLSTGNHFGGRLV
		l				FDGKGYLFIALGENNQRPTAQD
20071	56020	<del>  -</del>	25012	707	1141	HRVPSWYK
25671	56039	A	25812	707	1141	ASHTATSPRPVRLSSSIASITLAV
		1				NATCGMASSRRIR*CTLFSKRA
		l				PSAPAGWERAKSSSLNPRACM1
		l				AIASASPIIRVLTVLEVGAKCIG
l		l				QGSRSDSTELSPFIKMVPPNSLT
		l				TALAVIPPFSLSDTLPEVLISLSL
05600	55040	١.	0.0010	210	2162	YNTLF
25672	56040	A	25813	215	2160	EINSITSRLSIIPRSPCSASAGWT
		l				KKAGVPVLASVAAIFLPMWPD
		ı				LPIPETTTLPSQCKMILAARTKS
		1				SPR/RSNIMTHIRIEKGTGGWGG
		l				PLELKATPGKKIVYITAGTRPAI
		1				VDKLAQLTGWQAIDGFKEGEP
		l				AEAEIGVAVIDCGGTLRCGIYP
		l				KRRIPTINIHSTGKSGPLAQYIVE
ŀ		1				DIYVSGGKEENITVVGDATPQP
		1				SFVGPDYDTSEKLMIVRKKPIG
		İ				VQMLYQVGTVSMLLYTRTIIQT
						KMTPRTIVTISHSVRNAGDSFFS
						IASNOPMPPTAKKIEPLAISLLS
						AEAPTRLSELKARIGEPRWSIEA
						IKPMPISTHKPNMQAITPPARRA
						ILSPCACESRSRQEPCPPGCHCS
						CPNHSCRSRLKGVLSMEQYLL
						QQKHVGTPPGPFRPPDTNQPCW
						KTKPSQREEYTRRVGFTGHSNQ
		1				GAKIIRTHIICRRRTSFALERPGD
						GFQAVVGGTVLMGLPRTKNVG
			l			LPVTILGRVHRRSSERFPRTSES
			I			AINRKDAGPKDPVRQRLAYKK
						HPMERRHGPHVVARTFGRAIPT
	1					LGPHRTVLSTRFQVAKNPLGPI
	1					GPSPLAVLTWTVPRPKNGRRG
	1					GKQRARIICQSRREASCNNVCL
						ARSSGVFKGFSPVSSSGEHTGN
	L					KYSAYSFSLCPLFVFLPLSGRLL

SEO ID	SEO ID NO:	Met	SEO ID NO:	No. of the least	N 1	Amino acid sequence ( X=Unknown.
NO:	of peptide		in USSN	location of first		*=Stop codon. /=possible nucleotide
140.	sequence	liida	09/540.217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25673	56041	A	25814	11	613	RLSSVFVSKSLASWRSCNCSFS
						GPLVRLTIRP\LSPPDVRLLLSPS
						VVHAYNCPHQETQRHHTHHLT
						P/RLPNHGQIAISAMVYSSPATN
			ĺ			SMLRQLLIQHVEQIGSVPLVMD
						AISLVEAHD/RSAAG*SRPLY*R
						AN*SSRY*VSYARKRVRQAKSR
						/HGKPSKKVLAKRAVPNRVCRC
	1					CNRVKRRCICQPKRRKCMTLPV
						RATR
25674	56042	В	25815	1	1920	
25675	56043	A	25816	247	1182	EAVMRQTKTGILLANLGTPDAP
						TPEAVKRYLKQFLSDRRVVDTS
	1					RLLWWPLLRGVILPLRSPRVAK
						LYASVWMEG\GSPLMVYSRQQ
	İ					QQALAQRLPEMPVALGMSYGS
	1					PSLESAVDELLAEHVDHIVVLP
	1	1	İ			LYPQFSCSTVGAVWDELARILA
				i	1	RKRSIPGISFIRDYADNHDYINA
	1					LANSVRASFAKHGEPDLLLLSY
						HGIPQRYADEGDSLRELYAVA
						NPNPGPGMGVLLAYMFFGRGS
	1					AKQSAGGSGLDGLLRRTPPITP
	ł				ļ	GGYFSVFVWKSLGSWRSCNCS
	1		l	l	1	FSGPLVGLTIRPRFTAGRSPTSF
						AQRCTCL
25676	56044	В	25817	1	651	_
25677	56045	A	25818	1	1647	
25678	56046	A	25819	1	1506	

SEOID	SEO ID NO:	Met	SEO ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25679	56047	Α	25820	645	2161	LDRCALNVTAQPSIECQVANAC
						LSPKGEFEYLOIDAPTPOALLSE
						IEKCWHRHRNVWPDHTINLAL
		l	l			AIHGOVDPVTGVSQTMPQAPW
		1			ŀ	TTPVEVKYLLEEKLGIRVMVDN
			ŀ			DCQLHYCKTAILNWSRKMALS
			İ			ROKFTFERLRRFTLPEGKKOTF
			Ì			LWDADVTTLACRATSGAKAFV
						FOSVYAGKTLRMTIGNINDWKI
			Ì			DDARAEARRLQTLIDTGIDPRIA
					l	KAVKIAEAESLQAESRKTKVTF
						SVAWEDYLQELRTGISAKTKRP
					l	YSTRYIADHINLSSRGGESPGLG
		l				LLLAFTLFGKGMSKRSAPGAMI
						IHFLGGIHELYFPYVLMKPLTII
		l				AMIAGGMSGTWMFNLLDGGL
						VAGPSPGSIFAYLALTPKGSFLA
	l		i			TIAGVTVGTLVSFAITSLILKME
	İ					KTVETESEDEFAOSANAVKAM
						KOEGAFSLSRVKRIAFVCDAG
				i		MGSSAMGATT\FRKRLEKAGL
						AIEVKHYAIENVPADADIVVTH
			ĺ			ASLEGRVKRVTDKPLYGPAVV
25680	56048	A	25821	2	341	ASELORVIROVIDRIETGIAVV
25681	56049	A	25822	218	469	LICAQGRRSPSRESTRQPKVLTL
23001	50045	^	23622	12.10	100	ACHNGSVSVVVLSPNSLYIEVV
						VPS*CNAATGPVVTCLYKGKFC
			l			PILILLYTSTRVSSCI
25682	56050	A	25823	1	3966	112122 11311113331
25683	56051	A	25824	2	728	
25684	56052	Α	25825	528	1123	DAEEGPDHRYLSSAHGGGSAS
						OPPSCAVTACRWPWRGRGCRA
		1	ł			GVWNOPTA AOGRSWPVGKTSO
						*GOGSTCKSQTWGFRGQRLPQ
		ı				DAPAPPASLCASFHLVEAGASA
			ĺ			DSGDTRRMTIR/FASKTVARAK
	1	l	l	l	I	RIIRVLRFSPLWVATRSLASTAI
	1	l	l			KIACCASEPGSFLQLWKPRSMA
	1					PVHRCTWHEACPEGOROMSCV
			1			SSTGL
25685	56053	A	25826	ī	492	

NO.	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
25686   56054   A   25827   1740   3858   ADAAGTEKTATVSRYHFYLI							
25686   56054   A   25827   1740   3858   ADAAGTEKTATVSRYHFYLI		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
PRSCRSVIDVRSWWRFSIMD SRSIPRAISICARGKPVTAKI QGTMPEPSNKAIILPIRFPEPG LMIIKKSGGRWQLSLLASVV AFFLNTAYAWQEYUPTOJI LSTERYTWDSDHQPDYNDIL RIQSSQRALGLEVNLAETPY VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFOD TTLTPDF.WHASVSTLGWRV; RLGDLRPWAQISYNQQFGEN WKAQSGLSRNTATNONGNN DVTVGADMLLANQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITOPALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLGERGVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFA YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVYEKDYT ESMRKPQYWMLAVMFLTAG SGLVIGVAKDLAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLFAPLNAVTFSALACVAFF GGTTTVFPSLICGSIIASLFGG VTFYVFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 36055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMYLFRLCEHCLNPSC ATCPSGAIYKBEEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDRVQLMSALQSVLAUG SRCCDRVQHRSLQSVLIPSUTTCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDRVQLMSALQSVLAUG SRCCDRVQHRSLQSVLIPSUTTCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDRVQLMSALGSVARASS	İ				sequence		
PRSGRSVIDVRSWWRESIMD SRSIPRAISICARGKPVVTAKI QGTMPEPSNKAILPIRFPPG LMIIKKSGGRWQLSLLASVV AFFLNTAYAWQGEYIDTDÜ LSTERYTWDSDHQPDYNDIL RIQSSQRALGLEVNLAEETPI VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFGD TTLTDPLWHASVSTLGWRV RLGDLRPWAQISYNQQFGEN WKAQSLSRNTATNNONGNI DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIOPALGSVYTWSLIP ALSAKLDAPVSQVAFSFGLL GLAISSSVGKLQERFQVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWPFPERKGLISAFA VGLGSLGFKFIDTOLLETVG KTFVWGAIALLMIVFGATLM DAPRQEVKTSNGVVEKDYTI ESMRRPQYWMLAVMFLTAG SGLVVIGVAKDIAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLFAPLNAVTPFSLICGSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  WYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSSPYFGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SR°CDRVQLMSALQSVLANGS	25686	56054	Α	25827	1740	3858	ADAAGTEKTATVSRYHFYLRY
SRSIPRAISICARGKPVYTAKI QGTMPEPSNKAIIIPIRFFPOX LMIIKKSGGRWQLSLLASVY AFFLNTAYAWQQEYIVDTQI LSTERTYTWSDDIIQPDYNDII RIGQSQRALGLEVNLAEETP VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFQD TTI.TDPLWHASVSTLGWRVI RLGDLRPWAGISYNQOFGER WKAQSGLSRMTATNONGNI DVTVADMLLANQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIQFALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFQVKR MASGILLGLGFFTAHSDNL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLOFKFDITOTLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVYEKDYT ESMRRPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGML LLFAPLNAVTFFAALACVAFP GGTTTVFPSLICGSIIASLFGG VTFYVIFALLILSLALSTTIRQ GKMLHFTYLTTSALFPAGFK GKSCHCFVFYFFALACVAFF ELKARAEKALDDVKKRLLY WRRROICALRRISSSPYDGILG ECIASFDRNFEAMQKEMYG ENTFMMYLFRLCEHCLNPSC ATCPSGATYREEDGIVLIOQ CRGWBLISGCPYKKILY GKSKCHCFVFRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFFTLVLVLPAI SR*CDRVQLKREEGGVUTCU TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFTTLVVLPAI			ľ				PRSGRSVIDVRSWWRFSIMDAL
LMIIKKSGGRWOLSLLASVV AFFLNTAYAWQQEYIVDTQI LSTERYTWDSDIQPDYNDIL RIGSSQRALGLEVNLAEETP VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFOD TTLTDPLWHASVSTLGWRVI RLGDLRPWAQISYNQOFGEH WKAQSGLSRMTATNQNGNI DVTVGAMLLINQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFOVRR MASGILGLGFFLTAHSDNL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLGFRFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPRQEVKTSNGVYENDYT ESMRRPQYWMLAWHFLTAG SGLVIGVAKDLQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIKVITIGQVISLVGMI LLFAPLNAVTFFSALIGCSIIASLFGG VTFVFFFALICSSIIASLFGG VTFYVFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGFK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRRDICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIIFVHFFTLVVLPAI SR*CDRVQLMSALQSSLARIAS SR*CDRVQLMSALQSVLATRAG SR*CDRVQLMSALGSVLATRAG SR*CDRVQLMSALGSCPYKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIIFVHFFTLVVLPAI SR*CDRVQLMSALGSVLATRAG SR*CDRVQLMSCR*CDRVCLMSCR*CDRVCLMSCR*CDRVCL							SRSIPRAISICARGKPVVTAKFK
AFFLNTAYAWQGEYIVDTOI LSTERYTWDSDHQPDYNDIL RIQSSQRALGLEVNLAEETPY VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFGD TTLTDPLWHASVSTLGWRVI RLGDLRPWAGJSYNQQFGEN WKAQSGLSRMTATNONGNU DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIQFALGSVYTWSLFP ALSAKLDAPVSQVAFSGELL GLAISSSVAGKLQERFGVKR MASGILGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATL DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAK SGLYVIGVAKDIAQSAGYI LSMCKYSNGVVEKDYT ESMRKPQYWMLAVMFLTAK GGTIVFPSLICGSIIASLFGG VTFYVFALLILSLALSTTIRQ QKMLHFTYLTTSALFFAGRK GGTITVFPSLICGSIIASLFGG VTFYVFALLILSLALSTTIRQ QKMLHFTYLTTSALFFAGRK ELAPLANATTSALFFAGRC ENTSMMYLFRLCEHCLNPSC ATCPSGATYREEDGIVLIOG CRGWELCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFFTLVVLPAI SR*CDKVQLMSALGSVLSTAGS							QGTMPEPSNKAIILPIRFFPGVV
LSTERYTWOSDIGPDYNDIL RIQSSQRALGLEVNLAEETP VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFGD TTLTDPLWHASVSTLGWRV) RLGDLRPWAQISYNQQFGEN WKAQSGLSRMTATNNONGNV DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIOFALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFA VGLGSLGFKFIDTOLLETVG KTFTWGAIALLMIVFGATLM DAPRQEVKTSNGVVEKDYT ESMRRPQYWMLAVMFLTAG SGLVVIGVAKDIAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLTAPLNAVTFFSALIGCSIIASLFGG VTFYVFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGATYKEEDGIVLIOG CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SR*CDRVQLMSALGSVALGSS							LMIIKKSGGRWQLSLLASVVIS
RIQSSORALGLEYNLAEETPY VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFGD TTILTDPLWHASVSTLGWRVI RLGDLRPWAGISYNQOFGEN WKAQSGLSRMTATNONGON DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITICPALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLOFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLA DAPKQEVKTSNGVYEKDYT ESMRRPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAALACVAFP GGTITVFPSLICGSIIASLFGG VTFYVIFALLILSLALSTTIRQ GKMLHFTYLTTSALFPAGFK GKSCHFCVFYUFALLILSLALSTTIRQ QKMLHFTYLTTSALFPAGFK ELARAEKALDDVKKRLLY WRROJCALRRISSPYPGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGATYKEEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKCHFCVPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHFYHTTVLVLPAI SR*CDRVQLMSALQSVLARAS SR*CDRVQLMSALGSVSATAS							AFFLNTAYAWQQEYIVDTQPG
VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFGD TTILTDFLWHASVSTLGWRVI RLGDLRFWAQISYNQOFGEN WKAQSGLSRMTATNOQROM DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGITITGFAGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLOERFGVKK* MASGILLGLGFFLTAHSDNLI MLWLSAGVLVGLADGAGYI TLSNCVKFPFERKGLISAFAI YGLGSLGFKPIDTGLLETVG KTFVIWGAIALLMIVFGATLA DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDLAGSLAVLG SDKLARIEVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFF GGTITVFPSLIGGSIIASLFGG VTFYVIFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY WRRRICIGALRRISSPYPGHG ECIASPBRYFFAMGKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOG CRGWBLCISGCPYKKIYPNW GKSSKCIFCYPRIESGOPTVC TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHFFTLVLVEAI SR*CDRVQLMSALGSVARXAS							LSTERYTWDSDHQPDYNDILSQ
VAALHYDGTTTSMYNEFGO TTLTDPLWHASVSTLGWRVI RLGDLRPWAQISYNQQFGEH WKAQSGLSRMTATNQNGNN DVTVGAMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPEFKGLISAFAI YGLGSLGFKFIDTQLETVG KTFVIWGAIALLMIVFGATLI DAPRQEVKTSNGVYEKDYT ESMRKPQYWMLAWHFLTAG SGLVIGVAKDLQSSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIKVITIGQVISLVGM LLFAPLNAVTFFSALIGCSIIASLFGG VTFYVFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGFK  25687 56055 A 25828 2 356  WYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMYLFRLCEHCLNPSC ATCPSGAIYKEEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLYVLPAI							RIQSSQRALGLEVNLAEETPVD
TTLTDPLWHASVSTLGWRVI RLGDLRPWAQISYNQQFGEN WKAQSGLSRMTATNONGNU DVTVGADMLLNQNIAAYAA QAENTTNINSDYLYTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKQERFGVKR MASGILLGLGFFLTAHSDNLI MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLGSLGFKFUIDTQLLETVG KTFVIWGAIALHMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAC SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKLARIEVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFI GGTTTVFPSLICGSIIASLFGG VTFYVFFALLISLALSTTIRGQ QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSSPYPGIH ECIASPBRNFEAMQKERMYG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOQ CRGWBLCISGCPYKKIYPNW GKSSKGIFCYPRISSGPYTCC TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHFFT-TLVUFAI SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS							VTSSMSMGWNFPLYEQVTTGP
RLGDLRPWAQISYNQOFGEN WKAQSGLSRNTATNONGNU DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITOPALGSVYTWSLIP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKEPPERKGLISAFA YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMYFGATLM DAPRQEVKTSNOVVEKDYTL ESMRKPQYWMLAVMFLTAG SGLVIGVAKDLAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLFAPLNAVTFFSALIGCSHIASLFGG VTFYVIFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  WYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLMPSC ATCPSGAIYKREEDGIVLIDG CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLFAI SR*CDRVQLMSALGSVARAS				İ			VAALHYDGTTTSMYNEFGDST
WKAQSGLSRMTATNOMGNI DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TILGTITIOFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFOVER MASGILLGLGFFLTAHSDNL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLOFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVEKDYTI ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQGSLAHLD SAANAVTVISIANLSGRLVLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFALICASHAL GGTITVFPSLICGSIIASLFGG VTFYVIFALLILSLALSTTIRQ GKMLHFTYLTTSALFPAGFK GKSGTEVGENGAL Z5688 56056 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLLY WRROICALRRISSSPYDGHG ECIASFDRNFEAMMCEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFF*TLYVLPAI SR*CDRVQLMASLQSVARAS							TTLTDPLWHASVSTLGWRVDS
DVTVGADMLLNQNIAAYAA							RLGDLRPWAQISYNQQFGENI
QAENTTNNSDYL YTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFLTAISDNLL MLWLSAGVLVGLADGAGVI TLSNCVKWFPERKGLISAFAI YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFSALIGCSIIASLFGG VTFYVIFALILISLALSTTIEQ GTITYPFSLIGGSIIASLFGG VTFYVIFALILISLALSTTIRG QKMLHFTYLTTSALFPAGFK  25687 56055 A 25828 2 356  25687 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRROJCALRRISRSPYPGIG ECIASFDRNFEAMQKEMYGG ENTFMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLYVLPAI SR*CDRVQLMSALQSVARAS				ŀ			WKAQSGLSRMTATNQNGNWL
TILGTITTOPALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLOERFGVKR MASGILLGLGFFLTAHSDNLI ML.WLSAGVLVGLADGAGYI TILSNCVKWFPERKGLISAFAI YGLOSLGFFKTHDTOLLETYG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFP GGTITVFPSLICGSIIASLFGG VTFYVIFALLISLALSTTIRGO QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGHE ECIASPBRYFEAMQKEMYG ENTFMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOD CRGWRLCISGCPYKKIYFNW GKSSKCIFCYPRISSGPYTCC TCYGRIRYLGVULYELTAQQ PVWPPDIFVHFFT*LTVLVFAI SR*CDRVQLMASLQSVARAS							DVTVGADMLLNQNIAAYAALT
ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFA VGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLM DAPKQEV KTSNGVVEKDYTI ESMRRPQYWMLAVMFLTAG SGLVVIGVAKDIAGSLAHLD SAANAVTVISIANLSGRIJVLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFSAIGCSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK 25687 56055 A 25828 2 356  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKRRLJY WRRRQICALRRISRSPYPGHE ECIASFDRNFEAMOKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDG CRGWBLCISGCPYKKIYFNW GKSEKGIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFF*TLVVLPAI SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARASS							QAENTTNNSDYLYTMGRTRWL
GLAISSVAGKLÖERFÖVER MASGILLGLGFFLTAHSDNLI MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLGFKPIDTOLLETVG KTFVIWGAIALLMIVEGATLA DAPKGEVKTSNGVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANISGRIVLG LLFAPINAVTFFALICUSH LLFAPINAVTFFALICUSH GGTITVFPSLICGSIIASLFGG VTFYVIFALILISLAISTIRQ QKM.HFTYLTTSALFAGRK QKM.HFTYLTTSALFAGRK URRAGVAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA			i	ŀ			TLIGTIITQFALGSVYTWSLFNG
MASGILLGIGFFLTANSDALI MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGILSAFAI YGLGSLGFKFIDITQLLETVG KTFVIWGAIALIMIVGGATLA DAPKQEVKTSNGVVEKDYTI ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDLAGSLALIG SAANAVTVISIANLSGRIJVLG SDKLARRIVTITGQVISLVGM LLFAPLNAVTFFAAIACVAFI GGTITVFPSLIGGSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  25688 36056 A 25829 I I307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQIGALRRISSRYPGHE ECIASFDRNFEAMGKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEGGIVLIOG CRGWBLCISGCPYKKIYFNW GKSSKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFT-TLVUFAI SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS		ł					ALSAKLDAPVSQVAFSFGLLSL
MLWLSAGVILVGLADGAGYI TILSNCVKWFPERKGLISAFAI YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKISNGVEKDYTI ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFALICUSIASLFGG VTFYVIFALILISLALSTTIRQ QKMLHFTYLTTSALFPAGPK 25687 56055 A 25828 2 356  25687 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRROICALRRISRSPYPGIG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVVLPAI SR*CDRVQLMASLQSVARAS							GLAISSSVAGKLQERFGVKRVT
TLSNCVKWFPERKGLISAFAI YGLGSLGFKFUDTOLLETYG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIKVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFP GGTITVFPSLICGSIIASLFGG VTFYVIFALLISLALSTTIRQ QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGHE ECIASFDRNFEAMQKEMYGG ENTFMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKGIFCYPRFIESGGPYTCG TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFT-TLVUFAI SR*CDRVQLMASLQSVARAS							MASGILLGLGFFLTAHSDNLM
VGLGSLGFKFIDTOLLETVG   KTFVIWG AIALLMIVFGATLM DAPKQEV KTSNGVVEKDYTI   ESMRKPQYWMLAVMFLTAG   SGLVVIGVAKDIQASLAHLD   SAANAVTVISIANLSGRIJVLG   SDKIARIRVITIGQVISILVGM   LLTAPLNAVTIFFAAIACVAFF   GGTITVFPSLICGSIIASLFGG   VTFYVFFALLISLALSTTIRG   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   SF0555   A 25828   2 356		l	l				MLWLSAGVLVGLADGAGYLL
KTFVIWGAIALLMIVPGATLA   DAPKQEVKTSNGVVEKDYTI   ESMRKPQYWMLAVMFLTAK   SGLYVIGVAKDIAQSLAHLD   SAANAYTVISIANISGRIVLG   SGLYRIGANISGRIVCI   SDKIARRVITIGQVISLVGM   LLFAPLNAVTFFAAIACVAFP   GGTITVFPSLICGSIIASLFGG   VTFVVIFALLISLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   QKMLHFTYLTTSALFFAGFK   S6055   A 25828   2 356			1				TLSNCVKWFPERKGLISAFAIGS
DAPKQEVKTSNGVVEKDYTI ESMRKPQYWHLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANI.SGRLYLLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFI GGTITVFPSLICGSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK 25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGHE ECIASPBRNFEAMQKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEGGIVLIOQ CRGWBLCISGCPYKKIYPNW GKSSKCIFCYPRIESGGPYTCG TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHFFT-TLVUFAI SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS							YGLGSLGFKF\IDTQLLETVGLE
ESMRRPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFF GGTITVFPSLIGGSIIASLFGG VTFYVIFALILISLALSTTIRQ QKM.HFTYLTTSALFAGFK 25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLLY WRRROJCALREISRSPYDGILG ECIASFDRNFEAMQKEMYGG ENTFMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVVLPAI SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS			1				KTFVIWGAIALLMIVFGATLMK
SGLVVIGVAKDIAQSLAHLD   SAANAVTVISIANIASGRLVLC   SDKIARIRVITIGQVISLVGM,   LLFAPLNAVTFFAAIACVAFF   GGTTTVFFSLIGCSIIASLFGG   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   VTFYVIFALLISLALSTTIRQ   VTFYVI				١.			DAPKQEVKTSNGVVEKDYTLA
SAANAVTVISIANLSGRIJVLC   SDKIARIRVITIGQVISLVGM/   LLFAPLNAVTVFSAIAGCVAFF   GGTITVPFSLIGGSIIASLFGG   VTFYVFFALLISLALSTTIRG   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK			1	ŀ			ESMRKPQYWMLAVMFLTACM
SDKJARIRVITIGQVISLVGM/ LLFAPLNAVTFFAAIACVAF9 GGTITVFPSLICGSIIASLFGG VTFVVIFALLILSLALSTTIRQ QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY, WRRRQICALRRISRSPYPGHQ ECIASPDRNFEAMQKEMYGG ENTFMMYLPRLCEHCLPSC A TCPSGAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS				ľ			SGLYVIGVAKDIAQSLAHLDVV
LLFAPLNAVTFFAAIACVAFP							SAANAVTVISIANLSGRLVLGIL
GGTITYPPSLICGSIIASLFGG			1				SDKIARIRVITIGQVISLVGMAA
VTFVVIFALLILSLALSTTIRQ				i			LLFAPLNAVTFFAAIACVAFNF
QKMLHFTYLTTSALFPAGPK   25687   56055   A   25828   2   356     25688   56056   A   25829   1   1307   MYETLEEVLRSSGDPADQKY   ELKARAEKALDDVKKRLLY   WRRROJCALRRISSRYPGHE   ECIASFDRNFEAMQKEMYGG   ENTFMMYLFRLCEHCLMPSC   ATCPSGATYKEEDGIVLIOP   GKSEKCIFCYPKIYFNW   GKSEKCIFCYPKIFSOGPTYCC   TCVGRIRYLGVLLYELTAQQ   PVWPPDIFVHFF*TLYULPAI   SR**CDRVQLMASLQSVARAS    SR**CDRVQLMASLQSVARAS    SR**CDRVQLMASLQSVARAS							GGTITVFPSL\ICGSIIASLFGGFY
25687   56055   A   25828   2   356							VTFYVIFALLILSLALSTTIRQPE
25688 56056 A 25829 I I307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGIE ECIASPBRYEFAMQKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRISSGQPYCC TCYCRIRYLGVLLYELTAQQ PVWPPDIEVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS							QKMLHFTYLTTSALFPAGPKRN
ELKARAEKALDDVKKRKLY WRRROICALRRISRSPYPGHO ECIASFDRNFEAM MOKEMYGO ENTFMMYLPRLCEHCLNPSC ATCPSCAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHEVHPF*TLYVLPAI SR*CDRVQLMASLOSVARAS					2		
WRROJCALRRISRSPYGHG ECIASFDRNFEAMOKEMYGG ENITFMMYLPRLEGHCLIPSC ATCPSGAIYKREEGGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHEVHPF*TLYVLPAI SR*CDRVQLMASLOSVARAS	25688	56056	Α	25829	1	1307	
ECIASFDRNFEAMOKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDO CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRISGOPTVC: TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFF*TLYULPAI SR*CDRVQLMASLQSVARAS							
ENTFMMYLPRLCEHCLNPSC A TCPSCAIYKREEGGIVLIDQ CRGWALCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC: TCVGRIRYLGVLLYELTAQQ PVWPPDHEVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS							WRRRQICALRRISRSPYPGHQL
ATCPSGAIYKREEDGIVLIDQ CRGWRLGISGCPYKKIYFNW GKSKKCIFCYPRIESGGPYCC TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS							
CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC: TCVGRIRYLGVLLYELTAQQ PVWPPDHYHPF*TLYVLBARA SR*CDRVQLMASLQSVARAS		l					ENTFMMYLPRLCEHCLNPSCV
GKSEKCIFCYPRIESGQPTVC: TCVGRIRYLGVLLYELTAQQ PVWPPDHFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS		1					ATCPSGAIYKREEDGIVLIDQDK
TCVGRIRYLGVLL/SELTAQQ PVWPPDIFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS		1	1		l		CRGWRLCISGCPYKKIYFNWKS
PVWPPDHFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS		1					GKSEKCIFCYPRIESGQPTVCSE
SR*CDRVQLMASLQSVARAS			٠.				TCVGRIRYLGVLLYELTAQQFF
		1					PVWPPDHFVHPF*TLYVLPAPP
I I I I I I I I I I I I I I I I I I I							SR*CDRVQLMASLQSVARASRE
				1			YRWYGFSR*TPRKALALAQLRP
AESSPTAPDCN			L				AESSPTAPDCN

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	-	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
		<u> </u>	1		14460	
25689	56057	A	25830	583	1369	RHQLNSIASPAGGRWKDIGWF
						NFPQSNLCLKREKQDESCSLTQ
						ALPSELKVSADNVSLTGAVSLA
						SMLTEIFLLQQAQGMPEPGWG
						RITDSHQWNTLLSLHNAQFYLL
l						QRTPEVARSRATPLLDLIKTALT
						PHPPQKQAYGGT\LPLPVRFMA
	1					GPDTNLANLGGALKFNWTLPG
ļ						QPDNTPPGGELVFERWRRLSDN
	1	İ				SQWIQVSLVFQTLQQMRDKTP
						LSLNTPPGEVKLTLAGCEERNA
1						QGMCSLAGFTQIVNEARIPACS
25690	56058	Α	25831	199	543	
25691	56059	Α	25832	1	642	EASIFRRLSVYDNLMAVLQIRD
		1				DLSAEQREDRANELMEEFHIEH
						LRDSMGQ*SARPGRCRAGAQ*
			1			CV*CR*PRSGQPRQTVRRAE*IS
		1				DSQPVRGQFLHG/VRSPPESDCP
		1				MLSRRCSM*NSSISSFARSSRCS
		1				ADKSSRICSTAIRLS
25692	56060	A	25833	3	329	
25693	56061	A	25834	1974	2195	
25694	56062	A	25835	1	615	
25695	56063	A	25836	2	166	
25696	56064	Α	25837	2	189	STPGNWRFTTTYPLNCATRWK
						M*FLIVATMAPSVYWSLPRNIA
		l				AAKPTTPPTPSRRSGARGK
25697	56065	Α	25838	64	354	
25698	56066	A	25839	1123	1845	
25699	56067	Α	25840	1120	2097	
25700	56068	A	25841	124	548	CROMVGTRRGGEQGKEVIDGY
		1				GKPATFYQMQDNGKPVEGHAS
l		1				OMHYELAKDFVVLTGNAYLQ
1		1				OVDSNIKGDKITYLVKEOKMO
		1				AFSDKGKRVTTVLVPSQLAKA
1		1				YKG\VAW*KTSA*PSTPGKLSV
		1				CWGQTVPVRPPLSTWL
25701	56069	A	25842	77	514	CWGQTTT TRITEST WE
25701	56070	A	25843	2487	5738	RRAAGLPGRNDAGLARSHOWA
23,02	155075	1	23043		I	GSADTGSEKQHELQLRIQGEPV
		1				SGOLNLAGSFDRKEERWKG\TL
		1				SNTRFQTPVGPWSLTRDIALDY
		1				
1	1	1			l	RNKEQKISIGPHCWLNPNAELC
		1				VPQTIDAGAEGRAVVNLNRFD
		1	1			LAMLKPFMPETTQASGIFTGKA
1		1	1		I	DVAWDTTKEGLPQGSITLSGRN
		1	1		<b>f</b>	VQVTQTVN\DAALPVAFQTLNL
1		1				TAELRNNRAELGWTIRLTNNG
		1				QFDGQVQVTDPQGRRNLGGNV
	L	L			L	NIRNFNLAMINPIFTRG
25703	56071	Α	25844	538	777	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
25704	56072	IA	25845	489	2797	TRRRRTMIALIQRVTRASVTV
	l			ĺ		EGEVTGEIGAGLLVLLGVEKDD
						DEQKANRLCERVLGYRIFSDAE
						GKMNLNVHQAAGSVLVVSQFT
		ı				LAADTERGMRPSFSKGMSQLP
		l				GLSRETRESIAMYHLRVPQTEE
						ELERYYQFRWEMLRKPLHQPK
	l					GSERDA WDAMAHHQMVVDEQ
		ľ		İ		GNLVAVGRLYINADNEASIRFM
						AVHPDVQDKGLGTLMAMTLES
						VAPYFSGSETGMMTLNRYRLR
						HMAKQGNRSAKRVEKLLRKPD
						RLISLVLIGNNLVNILASALGTI
						VGMRLYGDAGVAIATGVLTFV
						VLVFAEVLPKTIAALYPEKVAY
						PSSFLLAPLQILMMPLVWLLNA
						ITRMLMRMMGIKTDIVDMLLS
		1				VLDLEKM/TVDDIMLPRSEIIGI
		1				DINDDWKSIL/R/QLSHSPHGAIV
	1	ı				LYRDSLDDAISMLRVREAWRL
						MSEKKEFTKETMLRAADEIYFV
						PEGTPLSTQLVKFQRNKKKVGL
	ŀ					VVNEYGDIQGLVTVEDILEEIV
						GDFTTSMSPTLAEEVTPQNDGS
		1			·	VIIDGTANVREINKAFNWHLPE
		1				DDARTVNGVILEALEEIPVAGT
	I	1				RVRIGEYDIDILDKLSFCFRYSN
		1				HRRTNRTTIQRITFLHNAQYVT
l						WRNVIRFHHCDGLMHIRVQWD
l		1				VSFGDHFNAKLTHNIQHRLQRQ
l		1				LNAFNHRRHIRVSFISHFQRTIQ
						AINHRQQFVDEFLQREFVGFFNI
25705	56073	A	25846	87	199	QPASVQTAGAGCRL*LHQRQW
	1	l			l	RECLVLDSKRRGDGVL

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25706	56074	Α	25847	1167	3306	GKSMDKELPWLADNAO\LELK
						YKKGKTPLSHRRWPGEPVSVIT
						GSLIQTLGDELLQKAEKKKNIV
				l		WRYENFSLEWQSAITQAINLIG
						EHKPSIPARTMAALACIAQNDS
		l				QQLLDEIVQQEGLEYATEVVIA
						RQFIARCYESDPLVVTLQYQDE
		l		l		DYGYGYRSETYNEFDLRLRKH
						LSLAEESCWQRCADKLIAALPG
		1				INKVRRPFIALILPEKPEIANELA
1		1				VPALREFLAATKMPATCTLKGL
		1			1	GAVEADYPYYLGMLGMHGTK
						AANFAVQECDLLIAVGARFDD
					1	RVTGKLNTFAPHASVIHMDIDP
						AEMNKLRQAHLRDEHSWRYD
	ŀ					HPGDAIYAPLLLKQLSDRKPAD
1						CVVTTDVGQHQMWAAQHIAH
						TRPENFITSSGLGTMGFGLPAA
						VGAQVARPNDTVVCISGDGSF
		1				MMNVQELGTVKRKQLPLKIVL
		1			1	LDNQRLGMVRQWQQLFFQER
		l			l	YSETTLTDNPDFLMLASAFGIH
		l			1	GQHITRKDQVEAALDTMLNSD
		1				GPYLLHVSIDELENVWPLVPPG
		1				ASNYKKHHKLKQTFGVKIIPDV
		1				HDPSQAQPVADVVNVIQLPAFL
		1				ARQTDLVETHGENRPGQMGNI
	1	1				VDKFKEGGNEKVILCDRGANF
ļ	1	1	1			GYDNLVVDMLGFSIMKKVSGN
		1				SPVIFDVTHALQCRDPFGAASG
1						GRRAQVAELARAGMAVGLAG
		<u> </u>			60.5	LFIEAHPDPEHAKCDGPSALPL
25707	56075	Α	25848	I	695	MATRASVTPMSLFSAGTCLLST
						SCVLSPVGDTAEESCWQRCAD
					I	KLIAALPGINKVRRPFIALILPEK
	l	l				PEIANELVGLECPRTHFHSKEW
		1				LKVVANDPTAVRKLEHYWSQD
	i	1				IFSDREASYMSHENHFGYAACA ALLREOGLAAIPRLAMYAHKE
		1				
						DCGSLLVQINHPQVIRTLLLVA
					1	DKNKPSLQRVAKYHKNFPHAT LAALAELLALTEPPA/RPWLSN
1		1	1			HRRQKAACTAKSTR
25708	56076	A	25849	823	1091	CVRFARINCSDRRSRCFAGFNH
25/08	30076	A	23849	023	1071	VLNKALGVHINHFG/YSACAP*
						CRYPPHAAGEFYPDPCRHKGTT
						GYRHROGYPPPGEPPPRASWLD
1					1	LR
25709	56077	A	25850	714	875	EFSSARISRTSRLKYTNGCCRL
23709	55077	<u> </u> ^	23030	l	10,5	WSAFCRLRTATTVPPARP*QLR
				1	1	PDRSRAQCQ
			<u> </u>			

SEQ 1D	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25710	56078	Α	25851	2730	2893	WPVGERLAPGDYPVI*TGQLCT
	ĺ					AAGD/EWRR*KVRRHQPLWRG
						FPNRRYMAWRSA
25711	56079	Α	25852	750	929	SFHPAGRRYLYRHSSRSGNITN
						GCCRLWSAFCRLRTATTVPPAR
						P*QLRPDRSRAQCPV
25712	56080	A	25853	2	2427	CRQHHRWHSGSTAVYRRVLITS
		1				KCWNVFIRTKTWTVSILTTSVV
		İ				CASARRVCVPAPRAVSSRCLSV
		i				TTLIPSASTPW*LAHRISLAAR*
		ł				AFWFNCRIPAGIDNVKVLERIH
		Į.				PDKDVDGFHPYNVGRLCQRAP
		ŀ		1		RLRPCTPRGIVTLLERYNIDTFG
				1		LNAVVIGASNIVGRPMSMELLL
		1		1		AGCTTTVTHRFTKNLRHHVEN
			ļ	ŀ		ADLLIVAVGKPGFIPGDWIKEG
	1	1				AIVIDVGINRLENGKVVGDVVF
		1			i .	EDAAKRASYITPVPGGVGPMT
						VATLIETRYROGKMFDGSSIGG
		1	l			WKGINESDMVLMPDASTAVID
		1				PFFADSTLIIRCDILEPGTLQGYD
		1				RDPRSIAKRAEDYLRSTGIADT
		1		l	Į.	VLFGPEPEFFLFDDIRFGSSISGS
		1		ŀ		HVAIDDIEGAWNSSTQYEGGN
ŀ				1		KGHRPAVKGGYFPVPPVDSAQ
l		1				DIRSEMCLVMEOMGLVVEAHH
			i			HEVATAGONEVATRENTMTKK
						ADEIQIYKYVVHNVAHRFGKT
i		1				ATFMPKPMFGDNGSGSPPSOPO
i			1			SQPTPPEILLQALLSAGCFYAVY
i	1					YVTYKTRLRKRVADVPRRPLFT
		1		1		MNRVETNLTWVILMGIALVSV
						GIFFMHNGFLLFRLNSYSQIFSS
						EVSGVALKRFFYFFIPAMLVVY
		1				FLRQDSKAWLFFLVSTVAFGLL
						TYMIVGGTRANIIIAFAIFLFIGII
l						RGWISLWMLAAAGVLGIVGMF
		1				WLALKRYGMNVSGDEAFYTFL
25713	56081	A	25854	502	885	
25714	56082	A	25855	233	738	SNSCKRTKIISDVTSVFHAIFPAI
1		1	1	1		KITAPNSPRLRVNDSATPLTSAG
l		1	1		1	ESSGSTTLQKLCQRVAPSVSAA
		1	1			SSYSGPNLFOHRLHGTHPKRNA
ĺ		1	1			GKGHSHRNPQPCIGDFDIKLRQ
l			1			PFTVKTLYVKEKGQR*GGDRV
l		1	1		1	LPAORVNPSAHOAACGLGSDS
		1	1	1		GLGSTPSADRKRR
L	L	_	L		I	OLOGIFOADKKKK

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25715 56083	56083	Α	25856	1	2363	MRRQDTGRRGRKRRDAGRWQ WRYWGKGSFTPMNATWDVAC KGEWHDSTITLTDLSTGFDQLQ YGTMTVEKPRLILDKPIVWVRL AQHPSFSGALSLDAGQTLFTGG
						SVLPPSTLKFSVDGRDPTYFLFK GDLHAGEIGPVRVNGRWDGIR LRGNAWWPKQSLTVFQPLVPP DWKMNLRDGELYAQVAFSAA
						PEQGFRAGGHGVLKGGSAWM PDNQVNGVDFVLPFRFADGAW HLGTRGPVTLRIAKQRKEMRN NNLRQFKLLGPDVGFDSINDRP MAEELSKLLSKONEENLLPKTI
						LYCLNPRDNEVLGTMIENGASF AANPLYFDPKNIVELAIEAGCN CVASTYGVLASVSRRYAHRIPF LVKLNHNETLSYPNTYDQTLY
						ASVEQAFNMGAVAVGATIYFG SEESRRQIEEISAAFERAHELGM DGGWIGLMIKPLGRWSLIMEID EGFAVGMSPAELSAEQLLSKL
						WLWEGKAERYGWGRKSMDKI LPRLADNAQLELKYKKGKTPLS HRRWPGEPVSVITGSLIQTLGD ELLQKAEKKKNIVWRYENFSLI
						WQSAITQAINLIGEHKPSIPART MAALACIAQNDSQQLLDEIVQ QEGLEYATEVVIARQFIARCYE SDPLVVTLQYQDEDYGYGYRS
		L				ETYNEFDLRLRKHLSLAEESCW QRCADKLIAALPGINKVRRPFIA
25716	56084	A	25857	1	4440	MNRFDGAKQNVVGADAHHLA DTAVKRNQSLFQLRASGHPRLF AGGGKAVFHGRFAAKKIEAVA FYFRHLIALLVVOMHFKLVKG
						NVDVVFTAQLIDSTVQLIDSTTT VTQFTHIQTQLMRSVEWLTDN GSCYRANETRQFARMLGLEPK NTAVRSPESNGIAESFVKTIKRD
						YISIMPKPDGLTAAKNLAEAFE HYNEWHPHKAGTLTNEQWQQ VTAELHDRMMETVFFALDDAE
						QLFAHHQPTPVTSVDLLGQG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25717	56085	A	25858	1	3705	MEEYGGVDVRLYRIPDPMAFL
		1		ŀ		ROOKNLHRIVVOPOYLGDGLN
		1				NTLTWLWDNWYGKSRRVMOR
		1	ł			TFSSOSRONVTOALPELOLGNA
1		l				IIKPSRYVONNOFSPLKKYPLVK
						QFRYPLWQAKPFEPQQGSRGL
		1				YLVEAMVGGYRATTGGVVSDI
		1				VALSKVSSKELLVWTAGKKOV
		l				NEPGSEIFGLTALRITAENODCA
						SLTPETFLPRIHVIKGVNISTATV
		l				CROCEDAPCANVCPNGAISRDK
						GFVHCEARTLHLFAKT
25718	56086	Α	25859	123	923	TDSPYERGHLMSNLLGPRDAN
						GIPVPMTVDESIASMKASLLKKI
						KRSAYVYRVDCGGCNGCEIEIF
		İ				ATLSPLFDAERFGIKVVPSPRHA
						DILLFTGAVTRAMRSPALRAW
		l				QSAPDPKICIS\YGACGNSGGIF
			1			HDLYCVWGGTDKIVPVDVYIP
		1				GCPPTP\AATLYGFAMALGLLE
		ĺ				QKIHARGPGELDEQPAEILHGD
			1		İ	MVQPLRVKVDREARRLAGYRY
						GRQ\VADDSFTQLGQGEEQVAR
		-	İ			WLEAENDPRLNEIVSHLNHVVE
25719	56087	A	25860	1337	1516	KLKSKSAKRHKFITPILAWRILI
		1				HYLQRVAV*WGSRLL*LFLITIP
						SRWRLLPHNTGKG
25720	56088	A	25861	1	545	MARLAALKACETVYSMGVRSH
		l				RRSPLEHLWQLKDQLVNEGEL
		l				VLETLVIDGDENTVLVPGDRYA
		l				QMRNVYFIPSALALKNWLKKC
		l				GFVDIRIADVSR/ITTTEEQRRTE
						WMVTESLADFLDPHDPGKTVE
						GYPAPKRARNRNRAEDHRQRL
		1				RHRTRKKQTHGQRRRHRPEPA
		_				QRQPQTGTTD
25721	56089	Α	25862	620	1117	
25722	56090	A	25863	1	1188	
25723	56091	Α	25864	231	407	
25724	56092	Α	25865	1	501	
25725	56093	В	25866	1	2373	
25726	56094	A	25867	1	2211	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25727	56095	A	25868	2093	3589	GGINGKNFWFFLSPFTPCVGRC
						HSRVQLANSHLVDVDETPPSSA
1						AVHLYATDADSIGNCGTDREFO
		l				PCNPIRRHAFCCERLQNGYHRS
						GYAFHLGHYGDRKVITNFYSLI
						AKNHLSHWLETLPAQIANWQR
						EQQHGLFKQWSNAVEFLPEIKP
						YRLDLLHSVTAESEEPLSAGQI
		l				KRIETLMRNLMPWRKGPFSLY
		l				GVNIDTEWRSDWKWDRVLPHL
		l				SDLTGRTILDVGCGSGYHMWR
		l				MIGAGAHLAVGIDPTQLFLCQF
						EAVRKLLGNDQRAHLLPL/GIE
						QLPALKAFDTVFSMGVLYHRR
İ						SPLEHLWQLKDQLVNEGELVL
						ETLVIDGDENTVLVPGDRYAQ
						MRNVYFIPSALALKNWLKKCG
						FVDIRIADVSVTTTEEQRRTEW
						MVTESLADFLDPHDPAIFQIWP
	•					CTFMHAYHAFFDPVSHHRACQ
						NLTTFVPDTHQIAIRNTKACSIF
						VSFALRTTHSCAISHSSLEDPPA
				_		LFKIADRMEQNLELLATAGNLG
25728	56096	Α	25869	231	1785	DDEVHRYSELRTRTVPSYPPER
						SGEAKTAAQRAGTAFRRGRGA
			l		l	GVPFNLQQRSDRWCS*RSQQN
			1		l	A*RLIGLHGQNSRSVPQLPMES
				1	l	ASVA*RCGSIIEKTTLSSRPFYW
						CPGCQHYADRFGA

SEQ ID	SEO ID NO:	Mer	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
				<u></u>		
25729	56097	Α	25870	1818	3311	RMAIQFRTLSLRWCWKISLVSS
		1				FTVVKAMTIRIVAMRQLLRQQ
		l				KQRTFVC*SS/TVDGVLSDGLIY
ļ		1				MGNNGEELKAFNVRDGYGIRC
		l				ALTSDIEVAIITGRKAKLVEDR\
		l				LPHWGSLTCIRGSQTN*SPLAIC
	l	l				WKNWRLP/QENVAYVGDDLID
		l				WPVMEKVGLSVAVDDAHPLL
		l		•		GTEIDAYIENADYQYNKKRLRE
						IDRRVRYLTKCLENLKIVDYSP
		1				QQEGKVFFGAWVEIENDDGVT
		1			1	HRFRIVGYDEIFGRKDYISIDSP
		1				MARALLKKEVGDLAVVNTPAG
1		1			į.	
	ĺ	1				EASWYVNAIEYVKPRLNQTVR
						LLLEHEMGQVWISGEISNFTQP
	i					ASGHWYFTLKDDTAQVRCAM
				l		FRNSNRRVTFRPQHGQQVLVR
				}		ANITLYEPRGDYQIIVESMQPA
						GEGLLQQKYEQLKAKLQAEGL
						FDQQYKKPLPSPAHCVGVITSK
1		1				TGAALHDILHVLKRRDPSLPVII
						YPAAVQGDDAPGQIVRAIELAN
		1				QRNECDVLRPCVWCRRVRCRR
25730	56098	Α	25871	1	3465	
25731	56099	Α	25872	I	3126	
25732	56100	Α	25873	1	1722	MSSLSQAASSVEKRTNARYWI
		l			Į.	VVMLFIVTSFNYGDRATLSIAG
		l			F	SEMAKHIGLDPVGMGYVFSAF
						SWAYVIGQIPGFVDIFSGFGIIV
			l		8	ALFTLRFLVGLAEAPSFPGQSRI
					l	VGDWFPAQDRGTGVSIFTPFIL
						RKGDLRPIWVVILMAGOLHAL
					l	MSTLEDTPFSNKAGMRLRRWI
	ı	1			i	NAAVMRLNPLACLATRSNOVN
	i		1			WLLLTGNISVYPVGSSEPTRRR
				1		STPINSTPHENKTILPINARYSPT
			1			LPSSDGTRWTTRIDDKPTVGHK
					I	FARYWDVELREIP\MRPG\QLFR
	1				1	DPKRMIEGCAENPL\GV\VPTFG
		1			I	
	l		1		İ	VTYAGNYEFPQPLPDALNKFQ
		l	l		1	ADPGIDIDMHIDAASGGFLAPF
					l	VAPDIVWDFRLPRVKSISASGH
1		1				KFGLAPLGCGWVIWRDEEALP
1		1				QELVFNVDYLGGQIGTFAINFS
1		1				RPAGQVIAQYYEFLRLGREGYT
		1				KSTQPARGSPPANNCQAQPETP
		1				DRAVIHPTDGYESAATIIVLSPP
1		1		I	I	TASDSDPAHRDQRVVKTDAWS
	1					VVPGSTSEYPRRYKAEWFCQPF
		1			İ	AVLPAILAWSAALWRYQPRAR
		1			1	RRKADYGCRALNSLKNELTTP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25733	56101	Α	25874	1	2385	
25734	56102	Α	25875	1	1767	
25735	56103	Α	25876	1	2079	
25736	56104	A	25877	368	1261	TSPRARPAQGSRGAEL/HLTE KGVNRRAFVGJFESSGKRWAT EREYAFRQLVAEEKYRQVVYQ GLETAPENWQHAQNRLADWL QTLPPQTGIIAVTDARARHLQV CEHLHIPVPEKLCVIGIDNEELT RYLSRVALSSVAGGARQMGYQ AAKLLHRLLDKEEMPLQRILVP PVRVIERRSTDYRSLTDPAVIQA MINYIRNHACKGIKVDQVLDAV
25737	56105	A	25878		868	GISRSNLEKRFKEEVGETHAMI HAEKLEKARSLLISTTLSINEISQ MCGYPSLQYFYSVFKKAYDTT PKEVFAIVNSEVML MTSLKNSMKWDEERFGLEYDL
						DIYMIVAVDFFNMGAMENKGI. NIFNSKYVLARTDATADKOYLD IERVIGHEYFHNWTONRYVTCRD WFQLSLKEGLTVFRDQEFSSDL GSRAVNRINNYRTMGLGPAE DASPMAHPIRPDMVIEMNNFYT LITVYEKGAEVIGMITPPLFQGE HCPONVILTCALEDPTRKYVLKP LCRPPLSLCNRKRYMCRIFTSS ASTILLISRGAVCWNSRITIVSM RSSRRVTSVWLSAPTPIILSPAIF IVRWVLLDSNPLIYYKAWSCW CSRK
25738	56106	A	25879	2097	2512	NTPVRPDVGT**TEEHGGAESGE *RNSRELRENDKA*LHQYHAGP DGKNLAEAFEHYNEWHHAGAL GYWRTVD/DMRGR*PQEPSLMI RAGRSSSPVQWQRIPLLIPGRKG DRMQKTVIPGSLFAGMPYAQPS IKTELAG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25739	56107	A	25880	71	2613	QRKPTSSRKGLSARMMSGLTG TITTVSTGWCTTRGHMMSSRW SKVAJFTTRSGGRVAKRVWRR ERDLTGWMSLSRKPQVTWYG GSFTPLIRVETATAVRRRRWQ WGIPAGTVQMLDGHLESEILADR WGIPAGTVQMLDGHLESEILADR WSEESRRWLASCGLTVEQMKK TSIHASIVRHKLLTAEQALKLL KEFAQLAFKNOPMMYGNWAQ SILHGGVIASALDVAAGLVCVG STLTRHETTISEDELRQRLSRMGT IDLRVDYLRPGRGERFTATSSL TAGGNKVAXAVELINEEGLIY ASATATYMSKSMFLAVATILIS KSSLSRLTYAEGFVHYHRQNRH LERRDSVRPYDASFVVVLLNRR SYHITRYPDTVATHRQDLVTAIF TLYGGFQCGGVLGTQLEDVTND DTTFDQQFTLAIRAWIASHHVT DICNFRGSDLAIPVDAEVFTID CYSTSSETIFRRYDDLTVALEDVTN SYSTSTAFTRRYDDLTVALEDVTN STYSTERYBOLTVALEDVTN STSSETIFRRYDDLTVALEDVTN STYSTERYBOLTVALEDVTN STSSETIFRRYDDLTVALEDVTN STSSETIFRRYDDLTVALEDVTN STSSETIFRRYDDLTVALEDVTN STSSETIFRRYDDLTVALEDVTN STSSETIFRRYDDLTVALEDVTN STSSETIFRRYDDLTVALEDVTN SQTGTAYERLSTALTVAQVCG SCRLCHYAYGTYARLASSSII DNRSRQHLNDVGLTAWDCVIIS GNIGGFGQARTIATTQAYLCHP
25740	56108	A	25881	71	3478	VRWLPGLEIQNYADASLFADES LRWRSSYEVEKLPEEHTKSSTA CCLSSHPSTTATALRSLSPVRK
						WPKISALIPWEWAMCSLLSHGL MLSGRSLVAWCWTVI.VQNAS TSGRSISGRCHPCCKASSISLVD SALSFILFTLRFLVGLAEAPSP GNSRIVAAWFPARKGTGINEUS PLANTALEGLGGSGDALCTQC EAEGRHITTYLDRPDVLARTT TKILADKIKYPPLLSNGNR VG ELENGRHWVQWQDFPKPCYL FALVAGDFDVLRDTFTTRSGRE VALELYVDRGN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25741	56109	Α	25882	90	629	PGDWGRRQLIGS*KTPGSVFKK
	1	i .				GKSSTPN\DPFLKDKTQDRSGL
	1			i		ATFTMDGQI\RLFYQ\DISGNHS
						GK\QSLPPAQVIVSNSVDHLKIT GVEDHKPIFAGAGKPYQNLRQF
						IDEGNYTSGDNHTLRDPHYVED
						KAHKYLV/FEANTGTENGYOG
İ		l				EESLFNKAYYGGGTNFFRGSSR
		1				VDLOAC
25742	56110	A	25883	I	3066	TELQUE
25743	56111	A	25884	104	547	LFPRLLSCLTTPPHCSFSICFVIC
20110		1		1		SRTLILKGSSLMYVFCLPNTAIV
		ļ.				MALSPRGWRSKFGMPVDSKGP
		l				PWLFKFLKNGLNFLLHSVGTRD
l				ĺ		LSRLSTILSPLYNTVAPGAN*CR
		l l				ELKLVLDADDVLSTEVKRVITS
		1				SASNITPAFFCS
25744	56112	Α	25885	3	4288	
25745	56113	Α	25886	2	2222	DFADFGTTIKQDFRLLGQTSVD
	1	1				RLLQLSQGQAVKGNQLLPVSLP
		ı				QHTIPDVFIWMLSNNRRVAYA
		ı	1	i		RIASKDLLYSPVAGQMGKHCG
		ı				KIKTHFLKIPKQQQNEKYQVPQ
		1				FDQSTIKNIESAKGLDVWNSWP
		1				LQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYOKDFRLL
		1				GOTSVDRLLQLSQGQAVKGNQ
						LLPVSLVKRKTTLAPNTOTASP
	1	1				RALADSLM/SWHDRFPDWKAG
1		1				RILPISEPPSNRIFACWGKPAWT
		1				ACCNSLRARR*RAISCCPSHW*
		1				KEKPPWRPIRKPPLPARWPIH*C
						SWHDRFPDWKAGRKGSDAHRF
		1				GSWKFQLQRVSG\SATFTWGG
	1					KIR\LYSADYSGNHYGKQSLPS
	1	1				GQVNGSNSDDTLKINGVEDHK
	1	1				TILDGDGKTYQNVQQFIDEGNY
	İ					TSGDNHTLRDPHYVEDKGHKY
						LVFEANTGTENGYQGEESLFNK
	1	1	1			AYYGGGTNFFRKESQKLQQSA
		1	1			KKRDAELANGALGIIELNNDYT
	1	1	1			LKKVMKPLITSNTIRKSDGTLQ
		1		1		EHDGICEIHVAKYAEIFGLTSAE
1	1		1			ASKDIRQALKSFAGKEVVFYRP
1	1		1			EEDAGDEKGYESFPWFIKRAHS
						PSRGLYSVHINPYLIPFFIGLQNR
	1		1			FTQFRLSETKEITNPYAMRLYES
	1	1	1			LCQYRKPDGSGIVSLKIDWIIER
						YQLPQSYQRMPDFRRRFLQVC
	1	L		ļ	0.00	VNEINSRTPMRLSYRMGVRGK
25746	56114	В	25887	1	2640	ſ

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
0.57.47	56115	<u> </u>	25000	Linos	1629	
25747 25748	56115	A	25888	1291	2925	NSLORSHPNAANS/WHNKLWR
25748	20110	Α	25889	1187	2923	SHSDSDLSDHHEPICKPGLELN
						KKDITTSADQIAEVKTMESHPPI
						PPVFVEHMVPQDANQKGLCTK
						ERMICLEFTSREFHAGQIEDELN
						LNDINGCSSGSTLEDPQFNDDSP
						EARKITRRWRIGEAADLVGVSS
	i					QAIRDAEKAGRLPHPDMEIRGR
						VEQRVGYTIEQINHMRDVFGTR
	1			1		LRRAEDVFPPVIGVAAHKGGV
	l					YKTSVSVHLAQDLALKGLRVL
	l					LVEGNDPQGTASMYHGWVPD
	1					LHIHAEDTLLPFYLGEKDDVTY
						AIKPTCWPGLDIIPSCLALHRIET
	ì		ŀ			ELMGKFDEGKLPTDPHLMLRL
	ļ.					AIETVAHDYDVIVIDSAPNLEDP
	ŀ					RVGVMARGNAITLPVCGRDVK
	ŀ					FTLEVLRGDSVEKTSRVWSGNE
						RDQELLTEDALDDLIPSFLLTGQ
	İ					QTPAFGRRVSGVIEIADGSRRR
ĺ				l		KAAALTESDYRVLVGELDDEQ
		1				MAALSRLGNDYRPTSAYERGO
		l		l		RYASRLONEFAGNISALADAEN
		l	ŀ			ISRKIITRCINTAKLPKSVVALFS
						HPGELSARSGDALQKAFTDKEE
	l	ı		l		LLKOOASNLHEOKKAGVIFEAE
	1	1		i		EVITLLTSVL
25749	56117	В	25890	1	1954	
25750	56118	Α	25891	1	454	MERRNRRTGRTEKARIWEVTD
1					l	RTVRTWIGEAVAAAAAADGVTF
		l			l	SVPVTPHTFRHSYAMHMLYAG
		l			l	IPLKVLOSLMGHKSISSTEVYTK
		l			1	VFALDVAARHRAIR\VPRQQGD
		1				YRTRIWKFEDGLSNVLVIOLNK
	1	1	l	1		LIICVMCLVRDCDVLKTYFHL
25751	56119	A	25892	10	144	FLFIGKGFLKGIT*PGOIVORG*E
23,31	130117	l^	12072	1."	l	KKSNT*FRQFGGVDTAGNNLT
I	1	1	f		ı	KKSINI TRQEGOVDINGINILI

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25752	56120	Α	25893	888	892	TVDLDACTKGVLTFTTALLAG
				1		GANQAFAKENTKKAYKETYGV
						SHITRHDMLQIFKQQQNEKYQV
		l				PQFDQSTIKNIESAKGLDVWDS
ĺ						WPLQNADGTVAEYNGYHVVF
						ALAGSPKDADDTSIYMFYQKV
1						GDNSIDSWKNAGRVFKDSDKF
						DANDPILKDQTQEWSGSATFTS
		l		l		DGKIRLFYTDYSGKHYGKQSLT
						TAQVNVSKSDDTLKINGVEDH
		l l				KTIFDGDGKTYQNVQQFIDEGN
						YTSGDNHTLRDPHYV/EDKGH
						KYLVFEANTGTENGYQGEESLF
						NKAYYGGGTNFFRKESQKLQQ
İ						SAKKRDAELANGALGIIELNND
		1		l		YTLKKVMKPLITSNTVTDEIER
				l		ANVFKMNGKWYLFTDSRGSK
						MTIDDLWKFELENDDLEYLVE
				l		ENSKQKTIQDVIWLFLTAYTHI
				!		RGATQAFAKENNQKAYKETYG
						VSHITRHDMLQIPKQQQNEKYQ
1						VPQFDQSTIKNIESAKGLDVWD
				1		SWPLQNADGTVAEYNGYHVVF
				ŀ		ALAGSPKDADDTSIYMFYQKV
l						GDNSIDSWKNAGRVFKDSDKF
l						DANDPILKDQTQEWSGSATFTS
						DGKIRLFYTDYSGKHYGKQSLT
	1	l				TAQVNVSKSDDTLKINGVEDH
					1	KTIFDGDGKTYQNVQQFIDEGN
1					i	YTPGDNHTLRDPHYVKTKAMR

SEO IP	SEO ID NO.	Dito:	SEO ID NO.	Nucleotida	Nucleatide location of last	Amino acid sequence (X=Unknown,
SEQ ID NO:	of peptide	hod	SEQ ID NO: in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence	1	
25753	56121	A	25894	1424	3807	HPLWKWLEGDMNMNIKKIVK
						QATVLTFTTA/LLAGGATQAFA
		1				KENNQKAYKETYGVSHITRHD
				l	1	MLQIPKQQQNEKYQVPQFDQS
		1				TIKNIESAKGLDVWDSWPLON
		ı				ADGTVAEYNGYHVVFALAGSP
		l				KDADDTSIYMFYQKVGDNSIDS
						WKNAGRVFKDSDKFDANDPIL
1		1				KDQTQEWSGSATFTSDGKIRLF
		1				YTDYSGKHYGKQSLTTAQVNV
		1		1		SKSDDTLKINGVEDHKTIFDGD
		1		1		GKTYQNVQQFIDEGNYTGDPL
		1				EAETAVINHKKRKNSPRIVQSN
		1		1		DLTEAAYSLSRDQKRMLYLFV
		1				DQIRKSDGTLQEHDGICEIHVA
		1				KYAEIFGLTSAEASKDIROALKS
						FAGKEVVFYRPEEDAGDEKGY
		1		l		ESFPWFIKRAHSPSRGLYSVHIN
		1				PYLIPFFIGLQNRFTQFRLSETKE
		1				ITNPYAMRLYESLCOYRKPDGS
						GIVSLKIDWIIERYQLPQSYQRT
		1				PDFRRRFLQVCVNEINGAVIGIP
		1				CVSIRKPDGSGIVSIKIAWIIERY
						QPPQSYQRMPDFRRRFLQSRPA
		1				CMHDWLCAEALAWSIQTASYL
		1				VTMQVNLTSLSSDTDRDLSVVS
				1		NSGWVSSGSLVRFNTIKTSSGEI
		1		•		KRTVPRILPDPDDPRSAIAEAPS
		l				EMPGHEVPVEEHFPEAGTNSGS
		1				PQGARKGDESMTKASDSSSPSC
						SSGPRVPKGAAPGSQTGKKQQS
		1				TALOASTLAPANLLPKAVHLA
25754	56122	١.	2000	3	2356	TAEQASTEAT ANEET KA VIIEA
25755	56123	A	25895 25896	1	2610	
25756	56124	A	25897	1	2496	
25757	56125	В	25898	1	3198	
25758	56126	A	25899		5274	
25759			25900	1		
25760	56127	A_			585	
	56128	A	25901	1	2469	
25761	56129	Α	25902	1	1914	
25762 25763	56130	A	25903 25904	1367	2259 1959	VI Ved ID ADI OND VICOVOCO
25/63	120131	A	25904	1367	1959	KLVTLHMDLSWR\NSGYQSQE
	1	1				T*K*PANRPVKRPH*GGI*\FSRD
	l	1	l	1		QKRMLYLFVDQIRKSDGTLQE
	l	1	l	1		HDGICEIHVAKYAEIFGLTSAEA
	l	1	1	1		SKDIRQALKSF/DGEGSIYSR*A
	1	l		1		HGAA*PSHRKDRESADLGSDG
1		1	1	1		QNDKGH\QYLVFEANTGTENG
			l	1		YQGEESLFNKAYYGGGTNFFR
				1		KESHKLQQSAKKLDAELSNGA
L	1	1	l	I		LGFIE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25764	56132	Α	25905	1	2418	
25765	56133	Α	25906	3	1918	
25766	56134	Α	25907	1242	1463	
25767	56135	Α	25908	1907	5097	TSKKIVKQAPVLTFTTA/LLAGO
		1				AIQAFAKENNHKAYKETYGVS
						HITRHDMLOIPKOOONEKYOVE
		l				OFDOSTIKNIESAKGLDVWDSW
						PLONADGTVAEYNGYHVVFAL
		l				AGSPKDADDTSIYMFYOKVGD
						NSIDSWKNAGRVFKDSDKFDA
						NDPILKDOTQEWSGSATFTSDG
						KIRLFYTDYSGKHYGKOSLTTA
						OVNVSKSDDTLKINGVEDHKTI
						FDGDGKTYONVOOFIDEGNEGI
						LPISEPPIKODFRLLG
25768	56136	A	25909	610	2303	SLPNLDNAAICSSSSSPTRTR*SI.
23700	20120	ľ	20,00	010	2505	SEGATQ\AFAKEKYPHKHTKKR
						SGVFHITRHDMLQIPKQQQNEK
						YOVPOFDOSTIKNIESAKALDV
						WDSWPLONADGTVAEYNGYH
						VVFALAGSPKDADDTSIYMFY
						OKVGDNSIDSWKNAGRVFKDS
	i	l				DKFDANDPILKDOTOEWSGSA
						TFTSDGKIRLFYTDYSGKHYGK
	1					OSLTTAOVNVSKSDDTLKINGV
	1					EDHKTIFDGDGKTYONVOOFID
	l					EGNYTSGDNHTLRDPHYVEDK
					i .	GHKYRGPLESPSTHQAEFNPTS
						CVSSLGTLQGFPAPAWLALAHP
						VHPLKHKSGGSNRLSAAIWGIK
		l				RKPARVCPGTGIHASSQIQGEW
	ŀ			1		RTECAVGPKAKAKATAGWRR
						GNNQHISSTYDINRADTQVRRA
						VNNYDIIVMSNSFNGQSEHQTY
		l				ESIVIDSAPNLGIGTINVVCAAD
						VLIVPTPAELFDYTSALQFFDM
				1		LRDLLKNVDLKGFEPDVRILLT
ĺ			İ			KYSNSNGSQSPWMEEQIRDAW
		1				GSMVLKNVVRETDEVGKGQIR
	l	ĺ				MRTVFEQAIDQRSSTGAWRNA
						LSIWEPVCNEIFDRLIKPRWEIR
25769	56137	Α	25910	1	2103	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
25770	56138	A	25911	i	2124	MNMNIKKIVKOATVLTFTTALL
					i	AGGATQAFAKENNQKANKETY
		l			·	GVSHITRHDMLQIPKQQQNEKY
			ŀ			QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFFKR
						GAIFRVHKHAVNPMSPKCRRPC
ŀ						GRQAYPLVNWEDRNGRSQKTV
				i		HTEGDMNMNIKKIVKQATVLT
ŀ						FTTALLAGGATQAFAKENNQK
						AYKET/YPKQQQNEKYQVPQF
İ						DQSTIKNIESAKG\LDVWDSWP
						LQNADGTVAEYNGYHVVSALA
ŀ						GSPKDADDTSIYMFYQKVGDN
						SIDSWKNAGRVFKDSDKFDAN
						DPILKDQTQEWSGSATFTSDGR
1	1					RSLESTTTAARPIWRKDVGGDQ
						TQEWSGSAPFTSDGKIRLFYTD
					1	YSGKHYGKQSLTTAQVNVSKS
				l		DDTLKINGVEDHKTIFDGDGKT
į.				1		YQNVQQFIDEGNYTSGDNHTL
						RDPHYVEDKGHKYLVFEANTG
					1	TENGYQGEESLFNKAYYGGGT
ŀ		1	i			NFFRKESQKLQQSAKKRDAEL
1						ANGALGIIELNNDYTLKKVMKP
						LITSNTVTDEIERANVFKMNGK
			i	i		WYLFTDSRGSKMTIDGINSNDI
İ						YMLGYVSNSLTGPYKPLNTTG
ł		l	i			LVLQMGLDPNDVTWASLEPHE
1			l	l		SFQWVRGLASSGVKLQTSVVL
1			l	l		QLIKAMWTQRVSSSKVYCKEQ
						MNNASTMSKRTSAGCHCWQG
25771	56139	Α	25912	1	3987	
25772	56140	Α	25913	1	2235	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
		<u> </u>				
25773	56141	A	25914	1	1950	MNMNIKKIVKQATVLTFTTALL
	ŀ					AGGATQAFAKENNQKAYKETY
	l .	1			i	GVSHITRHDMLQIPKQQQNEKY
				l		QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
				l		VFALAGSPKDADDTSIYMFYQ
1	1					KVGDNSIDSWKNAGRVFKDSD
1				l		KFDANDPILKDQTQEWSGSATF
	i i	1			i	TSDGKIRLFYTGSLNSSKTEKY
1	1	1				QVPHIDQSTIKNIESAKGLDVW
		1		l		DSWPLONADGTVAEYNGYHV
1				1		VFALAGSPKDADDTSIYMFYO
						KVGDNSIDSWKNAGRVFKDSD
1	1	1	į .			KFDANDPILKDQTQEWSGSATF
						TSDGKIRLFYTDYSGKHYGKQS
1					i .	LTTAQVNVSKSDDTLKINGVED
				i		HKTIFDGDGKTYQNVQQFIDEG
	i					NYTSGDNHTLRDPHYVEDKGH
	İ					KYL/VFEANTGTEEHPQPQ\ERP
	1					RTOSFTSAFAERRECIPNVPADT
	1				l .	KLSKIKTLRLATSYIAYLMDLL
	1	l			l	AKDDQNGEAEAFKAEIKKTDV
						KEEKRKKELASKCLDLEQLGAS
						VEPTGNLRTKITKEKPRHTGPPE
					i	VVVPGCCPHRSRAYKSDKYAH
	1	1				TLTVTASQHAPPPPTHMEGFEL
					i .	FHLPDLCSPSQDAQTTGRTQMK
	1					PDHSPRPSHRVPQAKGNNVVIT
					1	SYMTNRGFFEDKKATFAPSFLM
		L				NIKGNKTSVVKNSILEQGQLTV
25774	56142	Α	25915	1	2448	
25775	56143	A	25916	1312	1974	
25776	56144	Α	25917	2	1778	
25777	56145	A	25918	1366	2673	
25778	56146	В	25919	1	1938	
25779	56147	В	25920	1	2262	
25780	56148	A	25921	1	2100	
25781	56149	В	25922	7145	7154	
25782	56150	A	25923	2085	11232	VNSEGSEPADRKKPVHTEEAM
	1	1	ł			NMTIKKIVKQATVLTLTTALLA
	1			l		EGATQAFAKENNQKAYKETYG
	1	1	į	l		VSHITRHDMLQIPKQQQNEKYQ
	l .	1				VPQFDQSTIKNIESAKGLDVWD
1	1	1	l	1	1	SWPLQNADGTVAEYNGYHVVF
1	1	1		1	ŀ	ALAGSPKDADDTSIYMFYQKV
	1	1	l			GDNSIDSWKNAGRVFKDSDKF
			l			DANDPILKDQTQEWSGSATFTS
						DGKIRLFYTDYSGKHYGKQSLT
1	1	1	l	I		TAQVNVSKSDDTLK\INGVEDH
	1	1	l			KPILDGGGKTYQNVQQFI
25783	56151	A	25924	153	293	
23.03	1-2.2.	11	1	1	E	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25784	56152	Α	25925	420	687	
25785	56153	A	25926	242	491	WLHVQPLHDEHHCWI*YPADT DGVRPAFQRSPALSPEHGCVPY TPARQGSVRSKGPCTSALLYVE CSIAAPDRKHSCHKSDQS
25786	56154	Α	25927	2	113	
25787	56155	A	25928	779	862	NSTLPRCASTTFARY*AIPIKVFS ILP
25788	56156	A	25929	282	443	FSAGFLNLRYAQKFPSSYPPV** CYRPIYYPASDPCRNRLLYPAD VPYQALLD
25789	56157	Α	25930	3	89	
25790	56158	Α	25931	614	823	
25791	56159	Α	25932	1229	1427	
25792	56160	A	25933	1965	2682	FAVPCRTSFGSIETVSIPGRDT* SA*AYRVQVDSHRPRLAHNVQ HRT*RGEVLLAGVPRHVAEREI ATLAGSFSLHEQNIHNLPRDQG PGNTVSLEVESENITERFEVVGE KRVSAEVVAAQLVKEVKRYLA STAAVGEVLADQLVLPMALAG AGEFTVAHPSCHLLTNIAVVER FLPVRFSLIETDGVTRQLLGVSY RILAMGHAEFLQIADMRNDGG WRDFQFSGNLVMDEPNRSAQT YIKLVKSRLGTTKR
25793	56161	A	25934	261	563	RHSRGRSALRQISPEC*IHVCSPP PVQQLHPGYGNAIPLSYGHRNQ PDESDDAPVPPGWCQRYNLHQ KSTAHCGGYTIHADLVKTRCW LAPHRLPPGPGR
25794	56162	В	25935	1	1329	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hed	in USSN	lucation of first		*=Stop codon, /=possible nucleotide
l	sequence		09/540,217	codon for peptide		deletion, :-possible nucleotide insertion)
			1	sequence		
25795	56163	A	25936	761	3224	RGGAVTAKAPPDISAISALTAV
25.55	50105	ľ.	20,50	" "		KHGNCSSLTPLLNPPGSDVIVC
1		1			1	AEMDEOWGYVGAKSRORWLF
	1	1				YAYDSLRKTVVAHVFGERTMA
	1					TLGRLMSLLSPFDVVIWMTDG
		l				WPLYESRLKGKLHSNEGDAVL
		ĺ				LEIEQEVSSVDSSFNSTLGPTFN
				l		TRTIQNAVLVKTGETVVLGGLL
				l		DDFSKEQVSKVPLLGDIPLVGQ
						LFRYTSTERAKRNLMVFIRPTII
	ł			l		RDDDVYRSLSKEKYTRYROEO
		1				QQRIDGKSKALVGSEDLPVLDE
		1		l		NTFNSHAPAPSSRWALAQRIGV
1		1				SRVDMQQHVRRPPVNLSPKRE
						NVIAGYLSNSVARKORHIOTGT
						VFHQLMNLLRDGINIIFMNFKY
						OFIVYLHFLLSPKWVMYNRKC
		l				VNGMLLIASVPATWMLSRYRS
						SHRWIAKEIPMGKTOPLPILLLG
						/GGRRIGLALA\WHFIIQKQPVIV
		1	i			SYRTHYPAIDGLINAGAQCIQA
		1				DFSTTDGVMAFADELLKSTHG
		ı				LRAILHHASAWMAEKPGAPLA
		l				DVLACMMQIHVNTPYLLNHAL
		l				ERLLRGHGHAASDIIHFTDYVV
		l				ERGSDKHIAYAASKAALDNMT
		1				RSFARKLAPEVKRQTATRAGH
		1				RGINQLSRYYRRALARQNQRR
		1				MVELRSLRFMYRHRPRSFVLW
		1				QATRLHRLNIAVRHRKPDARPL
		1				PAIQRNTDIAIKQPKRAVITGNH
				1		HRSTFVPTRLAQTGSEIRRHAM
25796	56164	Α	25937	3	543	
25797	56165	Α	25938	209	343	LSPPMSSFLATVFRSIAWLLTAK
						SIRYRTT*RWIRCAAVWLTMD
25798	56166	A	25939	547	640	
25799	56167	A	25940	174	583	
25800	56168	A	25941	2001	2610	DVLV\RKHNGHWTVELYSDSIP
1						RLQINQHYASMCNNARNDGDS
	1	1		1		QFIRSNLQDAKWLIKSLESRND
	1			1		TLLRVSRCIVEQQQAFFEQGEE
				I		YMKPMVLADIAQAVEMHESTI
	1	1		I		SRVTTQKYLHSPRGIFELKYFFS
		l				SHVNTEGGGEASSTAIRALVKK
		1		I	1	LIAAENPAKPLSDSKLTSLLSEQ
	1				1	GIMVARRTVAKYRESLSIPPSN
				1	1	ORKOLV
25801	56169	A	25942	329	484	TROLSLLVRMTL*AFVRKRRSS
		ľ				LA*KPLWSWLSSVKSQPGWKL
		1			1	MLARWKSF
		-				

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25802	56170	A	25943	1	1785	
25803	56171	Α	25944	2493	2696	
25804	56172	Α	25945	1	1861	
25805	56173	Α	25946	456	700	
25806	56174	Α	25947	1	2413	MPVIKVRENEPFDVALRRFKRS
						CEKAGVLAEVRRREFYEKPTTE
1		l				RSRYDLVDRNNNIVLEYRKKEL
1						VRLTLTDPVTGKSGEVKSLVSS
l						LQTKYALKGYNVEATALEAAG
ł						GKVVTTGKDILVRKPTLDLPLE
			İ			VRRKMWFKPFMQSYLVVFIGY
	ļ					LTMYLIRKNFNIAQNDMISTYG
						LSMTQLGMIGLGFSITYGVGKT
						LVSYYADGKNTKQFLPFMLILS
						AICMLGFSASMGSGSVSLFLMI
1						AFYALSGFFQ\ST\GGSCSYST\IT
1		İ				\KWTPRKKRGTFLGFWNISHNL
l						GGAGAAGVALFGANYLFDGH
	ļ				1	VIGMFIFPSHALIVGFIGLRYGS
1						DSPESYGLGKAEELFGEEISEED
			1			KETESTDMTKWQIFVEYVLKN
1						KVIWLLCFANIFL\YVVRIGIDQ
						WSTVYAFQELKLSKAVAIQGFT
		1				LFEAGALVGNGCSYAQGMWG
						KTAETSDLQDLLIAALQGLSAW
		1				AVKAREYGIINHDVDSFAPRAF
						FSTLTNVNFDSPRIVGYAREAIA
1						LREALKAQCLAVDANARVDNP
						MADLQLVSDDLGELQRQAAEF
						TPNKDKAAIGENILGLRLLCLY
						GLKVFNGREDQLDSCYHGNRQ
		1				LRGSLRLLFLAFIRQRLRDLIITA
ì		1				HRVIRVNRQHAALGVKHCRLP GITGNRIQRQATQYRDRRGTGQ
		1				NOCMRGDMOOLFADIANVAN
		1				TFAOIIAGRGRKFGANLLHIAD
0.000	26186	-	0.5040		2720	TFAQIIAGRGRAFGANLLHIAD
25807 25808	56175	B A	25948 25949	1518	3738 2124	DCFCGSRHDKLPSAHQCSAKPG
25808	301/6	A	23949	1318	2124	SDRFWRSHADAAYAHDGGIQP
						VLCASRSNGCLQKPKCHTIVSG
		1				RCPLQQIGS\SVFPSGDAANVAS
			1	1		FSCACDNAGSAQHRTLLLGKQ
		1		1		FFNCRNAFHFNRNSRQTALKSG
		1		1		ISWVTFQLILKQQPRPVIMTKM
		1		1		AIGFRKV*SQRNIIRHLLVYIFKF
		1		1		ADGGCFVVIFLCLQRFIETGINN
				1		KMG
25809	56177	С	25950	1	747	
25810	56178	Ā	25951	168	332	CAWRAVCAAW/PTGASC/CNN
		1	1	1		DRFVFQILRSFEHDNSEDKPGP
		ı		1		GMPPHGWRTQFWGG

SEO ID	ICEO ID NO	IMa:	SEQ ID NO:	Nucleotide	Nucleatide Inesting of last	Amino acid sequence ( X=Unknown,
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
NO:	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			,	sequence		
25811	56179	A	25952	l l	2706	
25812	56180	A	25953	1	1062	
25813	56181	A	25954	i	855	
25814	56182	c	25955	1	2412	
25815	56183	Ā	25956	279	713	RCDAAAGAVLHSAGLLRHCGY
23013	30183	^	23930	219	1/13	WORGKPDRWSRRPGNYADRIC
l		1				RRWFCAGGVGDROYELCOLLA
Į.	1					YTVSATRRGTGYCLYRDSRGR
ŀ	1	1				TGLPVV*HLSGAGLYGRCRFAG
						VRWCVRHYRRTATSGIPAGDY
						GGRVRGRNAFCHPAVAP
0.001.6	27104	<del>  -</del>	25957	,	769	MDFAETELEFIKFWGDIITNKLN
25816	56184	Α	25957	1	/69	
						EALAAQGDNVVINLASDEYFKS VKPKKLNAEIIKPVFLDEKNGK
1				1		FKIISFYAKKARGLMSRFIIENR
İ						
						LTKPEQLTGFNSEGYFFDEDSSS
		i				NGELVFKRYEQRAECRIVTRHL SFSGDVCLDHDRRDDHEELSY
1						GGAAVAAVLVIEPNKLAFDGS
		1				
		1				GYLAWEGLICMQEIGKC/YRRT
						SGDCA*VAGRAQTG*VSGWAL
		İ				SRGKNQPGVGCEAGARRHARE
2 - 2 - 2	44104	-	05050	Į. —	2472	ARIGDERHRLAPRDML
25817	56185	В	25958 25959	11200	4492	DCGGVRSORPDOR*DWNR*GA
25818	56186	Α	25959	4300	4492	
1		1	1			GGESDS*SLATGGQAAEGVAV WRYSARWR*PLFAGRCARAGG
1		1	1			
24010	46107	-	25050	40	2000	D
25819	56187	B	25960 25961	49 266	3000 812	LLRWRPGALALGHKLVAGEIR
25820	20198	I <sup>A</sup>	25961	200	812	OORMDAWRAACLONPOGILCC
	1	1				ARGGQRSHIVQSWLHAAGIDY
1		1				PLVEGGYKALRQTAIQATIELA
1		1				OKPIVLIGGCTGSGKTLLVQQQ
1	1	1				ANG/VDLEGLARHRGSAFGRTE
		ı				DELGKLAQTSTSSPAHWRETSK
		ı				CGGFLCPIFLTNMRTPLPVCAT
1	i .	ı				VLPYLAIATV
25821	56189	1	25962	761	874	VLFILAIAIV
25821	56190	A	25962	2	304	MAAYGSGIFAQTYIEAFGISTIQ
23822	30190	I^	23963	1	304	PASCSPVNQYITAAFVLFGNVA
	1	ı				HALLIALORRNRRHLORRKGA
		ı				VIVIAFNTSOGA/VPAFCCOP*S
	1	1	1			RYASPPCCSFSTA
26022	56191	<del> </del> -	25964	109	777	KIASIFCCSFSIA
25823 25824	56191	A	25964	5	187	ITHKKPPPSWRSALLPAAGVFS
25824	30192	Ι^	23903	l <sup>3</sup>	107	RRYMPALCE*HWAS*RMRAEA
		1				
25026	56102	١.	25066	,	711	TETFSDCTMPIIGMMMS
25825	56193	A	25966	1	711	
25826	56194	A	25967	757	1026 750	
25827	56195	A	25968	1	/30	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25828	56196	A	25969	l 1	1065	MKVLEKRNNASSEPEEKNEIRA
		1				AREHAGFTLOELVCLGASGRK
		ı			i	VQGEAANAEEEVAAGELDNIA
		l				KITNEGSYTEOOIFNEGYMWLS
	]	l				TLMKIKENKISCSWATOSHFOG
						SIDAGELEHLTPERVWKETESA
						LTTRNPQVFFQVLRDCGALRVL
		İ				FPEIDALFGVPAPAKWHPEIDT
					1	GIHTLMTLSMAAMLSPOVDVR
		1		i		FATLCHDLGKGLTPPELWPRH
		ł				GHGPAGVKLVEOLCORLRVPN
		ŀ				EIRDLARLVAEFHDLIHTFPML
		1				NPKTIVKLFDSIDAWRKPORVE
	1					OLALTSEADVRGRTGFESADYF
						OGRWLREAWEVAOSVPTKAV
		1		l		VEAGFKGVEIREELTRRIAAG
		ı		1		LRG*VSRSHPHLPNAEPKNH/AS
		1				NYLIPSMPGVNRSVSSNWR*PA
						RLTCAAE/HGFESADYPQGRWL
İ						REAWEVAQSVPTKAVVEAGFK
		1				GVEIREELTRRRIAAGLRGMPT
25829	56197	Α	25970	2373	2597	SADDKADSVA*YLRLASA*TNS
		1				CRPYRRPSAPVCRRAPAI*G*TP
						QNYGPPSSCPAGGFWRYPVDPF
1			İ			RFSGFVH
25830	56198	Α	25971	2616	2777	TSVRKRFSTLSGKPVAKAGRKR
					1	PPPCR*TPTANGHPKPCRPPVW
						CHPAPVARP
25831	56199	В	25972	1	1449	
25832	56200	Α	25973	1076	1477	CAVRRSITWCKLSSKTPVRPLR
						PSTYRDCLTVSIALTPPASEKVK
		1				RRPVPAVKSAMKVPPGAAQSR
ŀ		1				KRVWLVSPFPTCEFLASNSRGK
		1				KISVSLSALSPRWTS*PKARWA
		1				ARRLTTNLVVRH*TATSVLMK
						KK
25833	56201	Α	25974	1	3552	
25834	56202	Α	25975	196	493	KRCRFADRPGDPGRQGTPAATT
		1				FGGMSFVTILPAPIPELSPMVTP
		1	1			GLITT*LPIQTLLPIVIGKEYISPF
		l				FLNSWCTGCPVTERVTLGAIST
1	1	1		1		LSPIVTV

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
				sequence		
25835	56203	A	25976	1	3917	MTDKHQQHRYVAAPGPFVGD
					\	KCOVAGDPLMLRRALSNLLSN
						ALRYTPTGETIVVRCQTVDHLV
		1				QVIVENPGTPIAPEHLPRLFDRF
		l				YRVDPSRQRKGEGSGIGLAIVK
						SIVVAHKGTVAVTSDARGTSGL
						DDFFIDVVYWVRRIKRKLSVYR
		l	i			RIPRMSYRELYKPDEQPLAIMV
						PAWNERASSAIWRAGGTTLDT
						KFLFVGLPGPILGSCKVPFEFLE
						VACPPSGGPVGPPWRRPCRGA
						AAAICASPAAIILAPT
25836	56204	A	25977	3	292	GDMQRLNSLFC/SVAYSVLEQP
						DEDEGRDSINIVNPSGRPHVSSG
						ATPAVREYAAHGFHLYGLRQR
	İ					VGEVRVDLQREQIYASKPCGST
					-	IGISLVVR
25837	56205	Α	25978	2	181	SARRLR/RSKHRFRILNRRYSHA
						HS\MLGDMQRLNSLFC/SVAYS
						VLEQPDEDEGRDSINIVN
25838	56206	A	25979	I	2781	
25839 25840	56207 56208	A	25980 25981	I 635	2554 741	
25840	56208	A	25981	91	501	LWIRLAKRSGKAIKERRDFIFRL
23641	36209	^	23982	191	301	CTHRVRQGTALLRLFQHSGGN
				l		RLMKLDNQHLRLRISNHRAFHF
			ł	i		RHRTTVKQSQQTFRYPWLYRV
						RHWGQKPKTDNFHGLLARIFG
		1				NSRSKTWGENR*EHSVLEOPDE
						DEGRDEY
25842	56210	A	25983	2153	3062	APVMPPERLPVIAVROYPTANC
		1				CSDCLAAASRFFLASVAAPEOT
				l		DADTRRSRVAVGRRKTRSNSA
		l				NOPRPRRDWRELOLMDRLARV
			l			AQARASFAARETLRIGDAMEQ
		1				MMEGLNKVMHGEPRQEKELR
						KLADDINVLYTAIKLYLARMPK
		1				EELAEEESRRWAEIIEMSLNLEQ
						ASDIVERMG\GELVDKSWAAR
						RAFSLDGLKELDALYEQLLSNL
			1	İ		KLAMSVFFSGDVTSARRLRRSK
						HRFRILNRRYSHAHVDRLHQQ
				1		NVQSIETSSLHLGLLGDMQRLN
L		L				SLFCSVAYSVLEQPDEDEGRDE
25843	56211	Α	25984	135	308	KLSLRLGIFPRPSLFPRPTPSPST
						PAPAS*PAPS*VSPSPRTATPSCP
		L	L			TSYSSFPCH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25844	56212	Α	25985	3	663	ARGKKPPRRGKEDFWDLSIATR
			Ì			VSVNPIKFPVEA*PFLKP\LQQV
					1	S\GPLGGRLPLPIPGNLLLQVAD
			l			GTLSLTGTDLEMEMVARVALV
			l			QPHEPGATTVPARKFFDICRGL
			l			PEGAEIAVQLEGERMLVRSGRS
		1				RFSLSTLPAADFPNLDDWQSEV
			l			<b>EFTLPOATMKRLIEATOFSMAH</b>
	l					QDVRYYLNGMLFETEGEELRT
				1		VATDGHRLAVCSMPIGQSLPSH
25845	56213	Α	25986	1	1077	,
25846	56214	Α	25987	I	1323	MHSGTFNPQDFGWQGLTLTPA
		1				AAIHIRELEILDEYGIPNAWQGE
		l				TNFWGSTAVSIDRLAAYKDVD
						VLCFDHDNSKDMDALMATPL
	1					WQAMPFVRAGRFQRVPAVWF
						YGATLSAMHFVRVLDNAIGVIV
			Ì			ATALTWMNFSQALPRSOWAQ
		1	l	1		AAWSPDIDVIEOMIFHYSLLPRL
						AISLLVGAGLGLDVRYYLNGM
						LFETEGEELRTVATDGHRLAVC
			ŀ			SMPIGQSLPSHSVIVPRKGVIEL
						MRMLDGGDNPLRVQIGSNNIR
			ŀ			AHVGDFIF\TSKLVDGRFPDYRR
			l			VLPKNPDKHLEAGCDLLKOAF
						ARAAILSNEKFRGVRLYVSENO
						LKITANNPEQEEAEEILDVTYSG
			l			AEMEIGFNVSY\VLDVLNALKC
			l		ł	ENVRMMLTDSVSSVQIEDAAS
				1		OS\AAYVVMPMRLEGSPPLGNP
						EFOKISSPCALYIALCSKARHHT
			ŀ			GRYLGLCGL
25847	56215	Α	25988	211	475	GAIGVFTAGKLTRASVYHQAR
						RFMQRETVWLVEDEQGIADTL
			ŀ			VYMLQQEGFAVEVFERGLPVL
			ŀ			DKARKQVPDVMILDVGLPDISG
			1	1		FELCROLLALHPALPVLFLTAR
				1	1	SEEVDRLLGLEIGADDYVAKPF
				1		SPREVCARVRTLLRRVKKFSTP
				1		SPVIRIGHFELNEPAAQISWFDT
			l			PLALTRYEFIVLKT\LLKSPGRV
			1	1		WSRQQLMDSVWEDAQDTTSH
	1			1	1	VVAFATILQGISRDLRRRILPYCI
	l	l	l	1	ł	RCRRERCTGTALWQ

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide scquence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25848	56216	A	25989	1661	2499	OMAHDEOWLTPRILUTAATLC NQNAPROGSPLWLGVUDLGTCD VYSMYVDRDGQPVAVCLDWA DVVRDGIVWDFFGAVTIVRRHE DTLEQQFGRERSHAATSFDG DPRISINVLESAGLEVSHVLDEP TAVADLLQLDNAGVVDIGGGT TGGAIVKKGKYTYSADEATGGH HIFLTFAGNRISI.EEAEQYKRG HGEEIWPAVRVYEKMADIVA RHIEGQGITDLWLAGGSCMQP GVAELFRKQPFALVHLPQHSL HTPLAIASSGREKAEGLYAK
25849	56217	А	25990	915	1518	ISGHAPDLNGAPATAHIQPGGR YPAPRSVRRATDNGYPAGDPLE WRSTAQVFVSSRRRVSLENDRK TVLTRCWSAAH*FALPAPLCAG RTGERKNRRFHTPTRCGGEQF APAASRCAGRRGDASGRSTTS RRPAPSHCPVQ*GGHRSTTSTS TSRRPGQSARPYSGPEYRE*Y CSAQRFFINDGSRPPVVRQAGR AQFP
25850	56218	A	25991	1	1254	
25851	56219	A	25992	675	835	VRWCWIFPSQ*TLFQKRAGHA APSADVLHESCQHFLNLLNRLG RHYDFGEGEP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25852	56220	Α	25993	1	2255	MRESPTRDDSKNTVNTTIRIRIH
						NSYTEOLOIVTNSYCTKOWHV
						HHTAKPYAHIQRPATPDAQLTK
l		1		l		MOEEEEVEPEPEMEAEVEPEPN
				I		PEEAETESESMNORDVRGTVRI
		1				VLKTFNNCRDTVFVAFEVNNT
ĺ		l		1		VSLLVATTDMTSGDTAIVVTTT
		i i				GFAVFFQQRSKSAANEVQILAF
		ı				FQGDVSFFPVATTTDTLSVTFN
		1				FPFNYQGVNDFDFDFKQFLHSS
		1				FDFCFGRVFSNFEYLHGARAHA
		1				CIPPSACIGEVLETSSFDIRVSVY
		l				RSSCVCVRLRESSTGDRYFGGL
		l				SLQMMRKATGLTDITSDTPGNT
		l				DDQRWHPEHGLTQRMQKEQE
		l				LVKEPEGAARDGDGEAEAWGE
1		1				VKAKSSGCVGTRASSHLFRCNV
		1				CELHFKESSELLQHPCTPSGERP
		l		1		FRCGECQKAFKRPSG\LRQHER
		1		l		THSAERPFKCDLCPMGFKQQY
	1					ALMRHRRTHKTEEPFKCGLCE
	ĺ	1		l		KGFGQPSHLLYHQHVHTLETLF
						KCPVCQKGFDQSAELLRHKCLF
		1				GAAERPFKCPVCNKAYKRASA
		1				LQKHQLAHCAAAEKPLRCTLC
						ERRFFSSSEFVQHRCDPAREKPL
		1				KCPDCEKRFKYASDLQRHRRV
		1				HTGEKPYKCPNCDKAFKQREH
1		1			l	LNKHQGVHAREQQFKCVWCG
		ł				ERFLDVALLQEHSAQHSAAAA
		1				AAEGAYQQTLHHPRRQQQQY
						WQLLCARNNVKLCMHILFSPH
25853	56221	Α	25994	98	596	YSGIIMAQSKLYPVVMAGGSGS
		l			1	RLWPLSRVLYPKQFLCLKGDLT
		1				MLQTTICRLNGVECESPVVICN
						EQPRFIVAHQMRQLNELSENIIL
						EPAGRTTAPTIAPAALAANRHS
						PESAPLMLVLATDHVIANEDAV
		1			1	RAPVK\NAIPYPKKGKLVTFGIG
				1		LDGRVPRYNM
25854	56222	A	25995	3	554	
25855	56223	Α	25996	1	222	

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
		$\vdash$				
25856	56224	Α	25997	I	1043	MKVKVLSLLVPALLVAGAANA
		1				AEVYNKDGNKLDLYGKVDGL
		l				HYFSDNKDVDGDQTYMRLGFK
						GETQVTDQLTGYGQWEYQIQG
	1	l				NSAENENNSWTRVAFASLKFQ
		l				DVGSFDYGRNYGVVYDVTSW
	İ	l				TDVLPEFGGDTYGSDNFMQQR
						GNGFATYRDTDVFGLVPTRLHF
		l				ARVCCALRELKDAGADRIWYI
						ADAFRAGLSVDGVFNLTNIDR
		l				WFLHINRAKDKNHMIISIDAEK
1		l				AFDKIQQPFMLKTLNKLGIDGT
		l				YFRIIRAIYDKPTANIILNGOKLE
		l				AFPLKTGTRQGCPLSPLLFNIVL
						EVLARAIRQEKEIKGIQLGKEEV
		1				KLSLFADDMIVYLENPIVSAON
		l				LLKLISDFSKVSGYKINVQKSQT
						FLYTNNRQTESQIMSELPFTIAS
		ı				RRIKYLGIQ*IRY*WDVFQNNK
						SYL*QTHSQYHTEWAKTGSIPF
						ENWHKTGMPSLTAPIOHSVGSS
						GOGNOAGEGNKGYSIRKRGSOI
						VPVCRRHDCLSRKPHRLSPKSP
25857	56225	A	25998	1	3339	VEVERHDELSKREHKLSEKSE
25858	56226	A	25999	1440	1880	AAQHASVYLYQNRIRGAVPPV
23838	30220	l^	23999	1440	1880	RFFHADQRTRRDGADGKORHA
1						TETLCRIAEKISSSREQDWLHCD
						ERQSLYEWTW*PYSPHSGRSQK
						EKROT*TAILDAYCADCFRCGR
						GVFARRERRTKRDRPGNAGTG
25859	56227	ļ	26000	ļ. ——	2277	GDCPCWLRRQYECVRL
25860	56228	A A	26000	1	1845	
25861	56229	A	26002	56	113	OOOPNPTRDQLQLAILHNIRGIR
23801	30229	Ι^	20002	36	113	
25862	56230	c	26003	1	2317	KIYG*IQSATREAG*GHSPQY
25862	56231	A	26003	3	2168	
25864	56232	A	26005	670	2541	
25865	56233	A	26005	98	944	YSGIIMAOSKLYPVVMAGGSGS
23803	30233	I <sup>A</sup>	20000	98 '	944	
						RLWPLSRVLYPKQFLCLKGDLT
						MLQTTICRLNGVECESPVVICN
ļ						EQHRFIVAEQLRQLNKLTENIIL
						EPAGRNTAPAIALA ALAAKRHS
		1		1		PESDPLMLVLAADHVIADEDAF
		1		I		RAAVRNAMPYAEAGKLVTFGI
	1	i		1		VPDLPETGYGYIRRGEVSAGEQ
		1		1		DMVAFEVAQFVEKPNLETAQA
		1				YVASGEYYWNSGMFLFRAGRY
		1				LEELKKYRPDILDACEKAMSAV
1			1			DPDLNFIRVDEEA/FLACPEESG
		1				DYAAMGRTGDAVVPLSLGAH
					1	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown. *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25866	56234	A	26007	3	417	
25867	56235	А	26008	507	717	WPEAEYLDNADAVLAMYHD/Q GLPVLKYQGFGRGVNIT/LGLPF IRTSVDHGTALEWRTCKPMVP DSIVSCIL
25868	56236	А	26009	5	378	MAVCSSLSPRRSPAFL/HDFTDV WTHHLVFGVNP*RGLHIGTALT DHVG/ENGNYSSD*HGTALTD HVGKTETILPTKYANIYSINTSK DRFLTKPAFAEVVLFLHPRELQ TCSFFLSQNMLVKVGHQRHWF TEVDVTLTEITOLA
25869	56237	A	26010	I	469	MQKEYAYWMÖGLKTCKPDNR KNALSNFGWYPSQPLLGRSRY ATTESWVEDIATAKSNPNRLPL KFTATCALPLRLAGFQ\PRWMD NPQQLNTLAPPASYRSI*TA*CL K*KNPRPRQQSCRR*RDGNQYE TLANARQKGIEKTCGTINKAG MPITT

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25870	56238	Α	26011	2	1854	CGGTLARACDGCLNGEFAA/LI
		1				TGPVHKGVINDAGI/PFTGHTEF
						FEERSQAKK/VVMMLATEELRV
		1				ALATT/HLPLRDIADAITPALL/H
						QPKYLDNADAVLAMY/HDQGL
		1				PVLKYQGFGRGV/NITLGLPFIR
		l		ŀ		TSVGHG/TALELAGRGQ/ADVG
		1				SFIRPYSAIK*L*NAGASVRWLS
						ERRICRAITGPVHKGVINDAGIP
						LPVIPSFSKSVRRRKRCDDAGD
		1				RRTSRGAGNDALPLRDIADAIT
						PALLHNRNILITPTPCWRCTRSG
						SSRAKIPGLRARCDITLGLPFIRT
				ł		SVGHGQPLNWRDVANRCWQF
				l		YTPLFCHQMIVKPMHNRIPRAT
						YRGAVKSAIGLGCCCLKASATF
						CAYRWRRSGRRDQSRFRYFEIA
		1	Ì			GIRSRGINFIACPTCSRRNLMLS
	İ	i		i		VRLTRWSNAWRYHHSDGRFD
						YRLRGECPGEALVSTLGVTGG
						NKKAASMKMGAQRPSGQQDM
		l				IDQLEARIRAKASQRTKRVELT
		ł				FSRLKNNNVEKQDTALFALYQ
		1				RRLRCVRKVRRYVMAAVSAGO
		1				GGGVCAVSAYMPLNRLPNAQE
		l				ANNEYTSFENCIKCTVCTTACR
		I				VTLRNNDPKLPYLVKAGLKMK
		1				RVTRSPRRYCAAASATHRFNDE
i	1	Į.				RAGKVQGMPDINKLPADRETC
	ł	1				STLTCARSRQNQTNPYPANRAA
1		1				NAYQVVLATKALEKVSMKSP
	1	1	1		1	WQHKVSSPAAVRHLPSITQRRT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25871	56239	A	26012	1	1504	MGIVASASVQAAEIYNKDGNK
2.5071	30237	ľ.,	20012	ľ	1	LDVYGKVKAMHYMSDNASKD
		1				GDOSYIRFGFKGETOINDOLTG
					1	YGRWEAEFAAWTDMFPEFGG
					İ	DSSAQTDNFMTKRASGLATYR
						KTTSSAYRWPELNLQYHRCTS
						AARAMLLSGRPVMQINERTAV
						RRQMTVYLRVERIHEIDPLVSL
				ļ		SHSMSVIPIDVERPIAAAPCTPG
						LWRTKTPLRVPSTYPLRLPGRA
						RVVCHRTFRLHLCKDWVFMFS
				ŀ		GLLIILVPLIVGYLIPLROQAAL
		1				KVINQLLSWMVYLILFFMGISL
		1				AFLDNPRPYLADSVPDROLLAP
		ı		1	ŀ	VNSISRYKTIEWLNYIATELHK
		l		1		GFTPLFRPDTPEEYKPTVRAHSE
		l		l		KKLOYVNEALKDEHWICGORF
		l				TIADAYLFTVLRWAYAVKLNL
1		1	1			EGLEHIAAFMORMAERPEVOD
	ļ	1				ALSAEGLKGSRHLSAGARRLIL
		1				GIIVTFSLILALICVTQPFNPLAQ
						FIFLMLLWGVALIVRRMPGRFS
		1				ALMLIVLSLTVSCRYIWWRYTS
						TLNWDDPVSLVCGLILLFAETY
		1				AWIVLVLGYFOVVWPLNROPV
		1		l		PLPKDMSLWPSVDIFVPTYNED
		1				LNVTPDELKQVLDVAAALKAL
1		1				RAENISTKVFNSGLGISVFRDNS
		1		l		TRTRFSYASALNLLGLAQQDLD
		i				EGKSQIAHGETVRETANMISFC
İ		1				ADAIGIRDDMYLGAGNAYMRE
						VGAALDDGYKQASGFSEPAMR
25872	56240	A	26013	2903	3024	
25873	56241	Α	26014	123	335	
25874	56242	Α	26015	2634	2787	
25875	56243	Α	26016	1477	2485	NPEQLMVKTQRVVITPGEPAGI
						GPDLVVQLAQREWPVELVVCA
1						DATLLTNRAAMLGLPLTLRPYS
						PNSPAQPQTAGTLTLLPVALRA
						PVTAGQLAVENGHYVVETLAR
						ACDGCLNGEFAALITGPG\HKG
						VINDAGIPFTGHTEFFEERSQAK
						KVVMMLATEELRVGLATTHLP
		1	1	1	1	VRDIADAITPALLHEGIAILHHD
						LRTKFGIGEPRILV\GGLNPHAG
		1		1		EG\GPMGTEEIDTIIPVLNELRA
						QGMKLNGPLPADTLFQPKYLD
		1				NADAVRPMYHDQGLPVLKYQ
		1	1	1	1	GFGRGVNITLGLPFIRTSVDRGT
		1		1		ALELAGRGK\ADVGSFITALNL
	1	l	l			AIKMIVNTQ

SEQ ID	lero in vo	Tar.	SEQ ID NO:	No. of a state	Numberside togetion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	· .			sequence		
0.0000		15	26017		3432	
25876	56244	В	26017	1385	2536	KSSQSHLITGMLEHVFVKSGDT
258//	36243	A	26018	1383	2550	
						PSR/LPELMNGAQALANQINT/F
					į.	VLNDADGAQAIQLGAN/HVWK
						LNGKPDDRMIED/YAGVMADTI
						RQHGADGL/VLLPNTRRGKLLA
						AKL\PDASRTGETH/TVEWQAP
						AVAITRTATQARQSNSVDLDK
	i					ARLVVSVGRGITDSQTLRLYYI
						RLPPSLMGMRLTVFLLPICGFH
						RVGPPTLLSVLATNRNRNAKVF
1						AHKNAPKFRSHTASEQWKSSIA
1						HNKGVHPRVTSHTHARHSLME
		1				TDIPHNIHSGHASPADITRHRAQ
					l	VFNSVPKMASPIGDRVPTLHTQ
		l				HNSPANTGKAQSLLTCGPAAES
				1	l .	CCRLIPRQMVSLVFRLKARLLLI
				i		TTELPKGLVPVATISGTGNFGN
		<u> </u>			1000	TQSANPYRPSENTDLSLS
25878	56246	A	26019	926	1293	LSPNPKEPSCRTRLKKSGFFTRI
	l					SAGAEPLMAIPARLSNSLACGA
		1				RDSAAKE/GFVVVPVCVAVEA
		1				DIAELDDEERDEFMADVGFT\V
				ŀ		GVKEVRAWTIPVGATAPQAAG
25879	56247	A	26020	,	1278	KIHTDFEKGFIRAQT
25880	56248	A	26020	678	1526	ERNTNTCEVVPNRKRAYASHD
23000	30248	^	20021	070	1320	MELSISPVGKGASKGEVNPADD
						IEVINTELALADLDTCERAIHRV
						OKKAKGGDKDAKAELAVLEK
						CL\PQLENAGMLRALDLSAEEK
	1	1				AAIRYLSFLTLKPTMYIANVNE
						DGFENNPYLDQVREIAAKEGSV
						VVPVCAAVEADIAELDDEERDE
						FMOELGLEEPGLNRVIRAGYKL
1	1	1				LNLQTYFTAGVKEVRAWTIPV
	1					GATAPQAAGKIHTDFEKGFIRA
						QTISFEDFITYKGEQGAKEAGK
						MRAEGKDYIVKDGDVMNFLFN
25001	66240	<u> </u>	26022	1177	1605	MRAEGRDTIVKDGDVMNFLFN
25881 25882	56249 56250	A	26022	1177	644	MDNHIALDFLLASECGSVYVY
23882	30230	^	20023	1	044	ATTHGRNMAGARALWRATGM
1	]	1			1	
	1	1			1	TDADFGKPIIAVVNSFTQFVPG HVHLRDLGKLVAEQIEAAGGV
1	1	1			1	AKEFNTIAVDDGIAMGHGGML
1	1	1			I	YSLPSRELIADSVEYMVNAHCA
1	1	1			1	
	1				1	DAMVCISNCDKITPGMLMASL
					1	RLNIPVIFVSGGPMEAGKTKLS
	1				I	DQIIKLDLVDAMIQGADPKIN/D
25883	66261	В	26024	1	1944	YQSRGRRCPNRCFRCKNQAGS
23883	56251	B	20024	J <u>.</u>	1394	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25884	56252	A	26025	1 ,	1488	
25885	56253	Α	26026	1	1919	MNKAHFVSNLGATKCCPLSFLF
						YRWRRVIAFVVAFYFRHLIDLL
1				1	i	VVQMHFKLVKGNVDVVFTAQ
		l				LIDSTVQLIDSTTTVTQFTHIQT
1		ŀ		1		QLMIQRAGTKCRKEDFRHCVGI
1		l				LEPEWYPIIVVRVVVDVSQFEV
		ŀ				RSQSLIFAVGEGITCIYTQFITHA
					i	VVRLTVNFHVVAQLSSPDWNR
		ŀ				PETLPVRSHVTSITQFEVVTGFQ
						TEAPSVGVGATVNVSTVAHGC
		ŀ				RQVVVEVRVAQATINKDVVRE
						VSRRVDVGSLAVLIHLTRTVIH
						VTFSEACSRTDDPLSVVTVNFG
						NTDHDAVNILIIVDGAVVAVEV
						TTEVAYPCAAVISQAMTRVGQ
						TSTNGVWTISSVNAFQIRTGAA
		i				RSLAPPWSLTEKVFCGTTMER
		ĺ				MRAALEAIMPFTESSSATQAPY
						LPCGRECGLAVRQFFGRGEGIE
				l		TVAYLFRIIRVVRTRVLSIGGFS
			ļ.			RTRISSTPVKIATLRQNRSDCHA
		l l		l		AMIADTYRQVTPTDPFSRHPFS
		ŀ				RVLRGLFFIIFKDTKAHNGIGMI
		l				GGVNRRADYLNLLEKVFGDRV
		l			}	SSPQWQATLKAIVPSYGRKLNG
		l				DVAATERELQYTSEVVGLNYD
		l				KPQAADNNRQHKVRAARSRRQ
1						NRPDRGSQIADSTAGARCRFQT
		l	ļ.	l		PTAGDGA*SAASTAAPI/MLNLL
		l				EKVFGDRVSSPQWQATLKAIVF
1		l		I	1	SYGRKLNGDVAATERELQYTS
						EVVGLNYDKPQAADNNRQHK
25886	56254	Α	26027	I	2130	
25887	56255	Α	26028	1144	1309	PGGSTPMAVEDPDFRSSERVLR
1		l		l		FQPAVSVYGPEQPAV*DYAQTS
		_				YLRTRPRRSDP
25888	56256	Α	26029	1	3546	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
25889	56257	Α	26030	1097	3332	TRVLVLDHRLLRCLYATVCAG
				l		ASWGMNPVVCSQQIDPQFHTM
		1				LMICASEEAQRMQQASEDEFN
						RALNIAFDNRLGLCKVESARQV
				1		FPLTGRYARQFASHRLALVGD
		l				AAHTIHPLAGQGVNLGFMDAA
				ļ.		ELIAELKRLHRQGKDIGQYIYL
						RRYERSRKHSAALMLADSFVR
			1	l		TTHALRRSHGGFPRLDDAAAL
				ŀ		RFANRRTSCERNDDNTWSRSL
						YADLKNGTAQNIRAKFVFIGAG
}						GAALKLLQESGIPEAKDYAGFP
İ			1			VGGQFLVSENPDVVNHHLAKV
		l				YGKASVGAPPMSVPHIDTRV\L
						DGKRVVLFGPFATFSTKFLKNG
1		l				SLWDLMSSTTTSNVMPMMHV
		1				GLDNFDLVKYLVSQVMLSEED
		1				RFEALKEYYPQAKKEDWRLW
		1				QAGQRVQIIKRDAEKGGVLRL
			ŀ			GTEVVSDQQGTIAALLGASPGA
					1	STAAPIMLNLLEKVFGDRVSSP
		l	İ	1		QWQATLKAIVPSYGRKLNGDV
		1				AATERERKTLHVIFNDLRPEOC
		1	ŀ			EAGKSPSRVQLQTWTNGGMLN
		1	Į.	ļ		APLSLRLTLVEKLASMLDPGHL
		ŀ				ALTQIAQHLALLQKMDHRQHS
		Į				AFPELPQQIAALYEWFSARCRW
						KEKALTQRGLLVQAGDQSEQIF
		1				TRWRAGAYNAWSLPGRCFIVL
			ŀ			EELRWGAFGDACRLGSPQAVA
		1		1		LLLGDLLEKATQHLAESINAAP
		1				TTRHYYHQWFASSTVPTGGEH
25890	56258	Α	26031	115	654	HATQTMTPWFLYLIRTADNKL
23890	30236	l^	20031	1113	054	YTGITTDVERRYQQHQSGKGA
						KALTGGSARSPLIKKALAEOLP
						GIPIAGGDDFGSVTAGLAR*RF
		1				HORHGPCWSMKAESLOLCRAD
		l				CORREQPMSFGGHFRHYRLSVC
		ļ				
		1		l		WRYRFIRPEHKTAFTARFPVDN
		1	1	l		RLGQMVAKPFHLLNATTGNIC
25001	56250	-	26022		240	GCFNTKRP
25891	56259	A	26032	1	348 906	
25892	56260	A .	26033			
25893	56261	В	26034	59	910	
25894	56262	A	26035	1	3684	
25895	56263	A_	26036	l	2634	

SEQ ID NO:   SEQ ID NO:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   Nucl	de nucleotide eleotide insertion) ARCFSARSED PNGRNVLSQ
Sequence   Sequence	ARCFSARSED PNGRNVLSQ
23896 36264 A 26037 1162 3478 LVRFGLLPLAYS, RPKDECETCCIKY EIHQVFVLNGIOS NELASMGGLVDY AREAFSHSIDLA RYWLAEHINNT GYLAEHINNT GYLAEHINNT GLGRAPGSDORT GLGRAPGSDORT SGDIDNFPRDV AI DPILEPTHORRIL GYTRGVEPTTOPI GYTRGVEPTTOPI	PNGRNVLSQ
RPKDECETCCIK\ EIHQVFVLNGIQS NELASMQGLVD\ AREAFSHSIDLA RYWLAEHHNMT GYLAANTTILHL HSPLVIAEPGTI GLGRAPGSDQST SGDIDNFFRDVAI DPILEPTHNGRRL GYTPGVEPTTOPI	PNGRNVLSQ
RPKDECETCCIK\ EIHQVFVLNGIQS NELASMQGLVD\ AREAFSHSIDLA RYWLAEHHNMT GYLAANTTILHL HSPLVIAEPGTI GLGRAPGSDQST SGDIDNFFRDVAI DPILEPTHNGRRL GYTPGVEPTTOPI	PNGRNVLSQ
EIHQVFVLNGIQS NELASMQGLVD' AREAFSHSLDLA RYWLAEHHNMT GYLAANTTITLHL HSPLVJAEQFGTU GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRL GYTPGVEPTTOPI	
NELASMOGLVÖ AREAFSHSLOLA RYWLAEHENMT GYLAANTITLHL HSPLVIAEQFGTL GLGRAPGSDQRT SGDIDMFRDV AI DPILEPTHNGRRL GYTPGVEPTTGP	
AREAFSHSIDLA RYWLAEHINMT GYLAANTTILHI HSPLVIAEQFGTI GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHORRIL GYTPGVEPTTOP	
RYWLAEHHNMT GYLAANTTILHI HSPLVIAEQFGTI GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRI GYTPGVEPTTOP	
GYLAANTTILH. HSPLVIAEQFGTI. GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRI. GYTPGVEPTTDPI	
HSPLVIAEQFGTL GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNORRL GYTPGVEPTTGPI	
GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRL GYTPGVEPTTOP	
SGDIDNFPRDVAI DPILEPTHNGRRI GYTPGVEPTTOPI	NTLYPGRIDL
DPILEPTHNGRRL GYTPGVEPTTGPI	MMALRRHM
GYTPGVEPTTGPI	ELVDWFDAR
	CSTVRHPRM
	LGQGLANAV
I I I I GLAIAERTLAAQI	FNQPDHEIVD
HFTYVFMGDGCI	MEEGWFTD
DTAKRFEAYHWI	HVIHEIDGHD
POAVKEAILEAO:	SVKDKPSLIIC
RTVIGFGSPNKAG	
GEEEVALAROKL	
KEIYHAWDAREK	
NEKFAAYKKAHI	
MSGGLPKDWEK*	
ANPAKIATRKASI	
MLPELLGGSADL	
SVSLKEDPAGNY	
MTAIANGIAHHG	
MFVEYARNAARI	
IMVYTHDSIGLGI	
OLASLRLTPNFST	
AVGWKLAVERH	
ONLAQVERTPDO	
VLKDSGGKPDIIL	
QAAEKLAGEGRY	
AAGGDEDREKEI	
KQKGLGLAAGW	
ASQLPPPPTHPIPC	
QHLLSTLWTNVC	
GGWCMNLDMDI	
RRHWDTGGIKPH	
TLSEREEIRAGLS	
ALNRSPSTISREV	
KAVDANNRANRI	
DQNLPLRKLVLE	
OISGWLRRTKPRO	QKTLRISPETI
	NHLNIQ\HLA
YKTLYFRSREALI	NRNGERGPV
YKTLYFRSREALI	RTSVKRALGQ

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
1				sequence		
25898	56266	A	26039	797	1440	PAMRLTAMRCISMKSRLPASR
25070	50200	ľ.	20033	1.77		MOFCATVRWKYRCHREPTLSA
				l		QHGAFRSINPTPRNSRGNCWKK
		1				REMKWANWPIWCR*KN*RERS
		1				LSAICCASRK/TGQFVLPPARYH
į.		1		l		LRRSHSLRHGRRHTRKGERGTI
						NIVNGTPIHERSRNIDNRRSLGH
1		1				WEGDLVSGGVGTVIGVVTGVII
						FTVINYGLTYIGVNPYWQYIIK
		1				GAIIIFAVALDSLKYARKK
25899	56267	A	26040	687	1106	GSLSLTALLPDTAEREEIRAGLS
123077	50207	ľ`	200.0	007		AKMSI/RAIATALNRSPSTISRE/
		1				VORNRGRRYYKAVDAN/NRAN
				l		RMAKRPKPCLLDQ/NLPLRKLV
						LEKLNIQHLRRSHS/LRHGRRHT
						RKGERGTIN/IVNGTPIHERSRNI
						DNSALVTVLR
25900	56268	A	26041	1	2851	MKTLIARHKAGEHIGICSVCSA
25500	50200	ľ.	20011	ľ		HPLVIEAALAFDRNSTRKVLIEA
						TSNOVNOFGGYTGMTPADFRE
1						FVFTIADKVGFARERIILGGDHL
1	ļ					GPNCWOOENADAAMEKSVEL
						AVVIDLWSRAVIGWSMSPRMT
	l	l				AQLACDALQMALWRRKRPRN
	1					VIVHTDRGGQYCSADYQAQLK
		i				RHNLRGSMSAKGCCYDNACVE
						SFFHSLKVECIHGEHFISREIMR
	i				1	ATVFNYIECDYNRWRRHSWINS
1	1					LLSQKRNTQGRIEDGRQH
25901	56269	В	26042	1	1048	222411111421122211411
25902	56270	Ā	26043	323	1290	GTSMNTVGTPLLWGGFAVVVA
						IMLAIDLLLOGRRGAHAMTMK
l						QAAAWSLVWVTLSLLFNAAF
1		1				WWYLVOTE\GRAVADPOALAF
1						LTGYLIEKSLAVDNVFVWLML
1		1		Ì		FSYFSVPAALORRVLVYGVLG
}				ĺ		AIVLRTIMIFTGSWLISQFDWIL
1		l		ļ		YIFGAFLLFTGVKMALAHEDES
						GIGDK\RWCAGYA/VHLRMTDT
ł					İ	IDNEHFFVRKNGLLYATPLMLV
1						LILVELSDVIFAVDSIPAIFAVTT
1	i					DPFIVLTSNLFAILGLRAMYFLL
						AGVTKRFSMLKYGLAGILVFIG
	1	1	1	1		IKRLIVNFNLLQTRACLGGGWA
	1	1		l		FGETLIIKPGEYRMKTAGG
25903	56271	A	26044	28	96	
25904	56272	A	26045	1	777	
23,04	302,2	Ľ.	1200-13	ı	17.7.	

SEO ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25905	56273	A	26046	77	532	I KPSRPEISKGKSVKPAASRRARE
23903	36273	Ι^	20040	l''	332	CAVQALYSWQLSQNDIADVEY
1		1				
						QFLAEQDVKDVDVLYFRELLA
						GVATNTA\YLDGLMKPYLSRLL
l						EELGQVEKAVLRIALYELSKRS
						DVPYKVAIKEAIELAKSFGAED
		<del>  -</del>				SHKFVNGVLDKAAPVIRPNKK
25906	56274	A	26047	3	175	
25907	56275	Α	26048	85	440	YSSSSLWAARKRRQMVLSARR
	1					FATSDRVCRCVLVWSAGTSRA
		l				KSKSTGWLSMASKAIGVSS*TK
		1				TPTARRVSSSSLPCGMAIPLPIP
l		1				VLPIFSRVRIASKTT*GSSLSCFA
		_				ARSLMTS
25908	56276	A	26049	80	706	KLIQVAVVIGGGQPLGAFLCHG
						LAAEGYRFPVVDIQSDK\AANV
1			ļ.			AQEINAEYGESMAYGFGADAT
i		1				SEQSVLALSRGVDEIFGRVDLL
ļ						VYSAGIAKAAFISDFQLGDFDR
						SLQVNLVGYFLCAREFSRLMIR
1						DGIQGRIIQINSKSGKVGSKHNS
1			1			GYSAAKFGGVGLTQSLALDLA
1		1		l		EYGITVHSLMLGNLLKSPMFQS
						LLPQ*KTKLGIK
25909	56277	Α	26050	741	893	TGCSGKRSLQQRREERRRNPVQ
ŀ						KIRCTV*RVRNGRIRYCSPRAGF
						YSRYR
25910	56278	Α	26051	269	987	
25911	56279	Α	26052	1	1268	MDAKCDRSRFPWLWPTKRPRG
						CFATFVPIGIPYDQTKTHLHTLS
						LVAKRLADKTICRRLRAAQSDE
						ELYQIITDTEGTPDEARCEEKQY
1				l		MVLMIVSGRSGSGKSVALRAL
				l		EDMGFYCVDNLPVVLLPDLAR
1				l		TLADREISAAVSIDVRNMPESPE
1						IFEQAMSNLPDAFSPQLLFLDA
						DRNTLIRRYSDTRRLHPLSSKN
						LSLESAIDKESDLLEPLHGFPDY
						DTVGFSCKRRIDYVCRIKHSRRI
						RQVVLLNFAKSGAFSTTRGTDD
1						KTRRSLLVTL/VAYFLCAR/EFS
1						RM/MIRDGIHVRIIQINSKSGKV
		1		I		GSKHNSGYSAAKFGGVGLTQS
		1		I		LALDLAEYGITVHSLMLGNLLK
		1	l	1		SPMFQSLLPQYATKLGIKPDQV
	1					EQYYIDKVPFKRGCDYQDVLN
		1				MLLFYASPKA\SY\CTGQSINVT
25912	56280	A	26053	1 .	168	LKVFILVIFTLSRE*EHAMFGFL
1	1	ſ		I		FLC*FAENDGFQLHPCPCKGHE
			ŀ			LILFYGCIVFH
25913	56281	A	26054	2	253	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25914	56282	В	26055	319	3780	
25915	56283	Α	26056	513	762	
25916	56284	A	26057	375	550	GVGLCGRSSIRRNM*CK**G*/L SPKIALMACGRRHTRSLFMTSK DLSRMMRLQKEIRL
25917	56285	Α	26058	662	1033	EPKRASGCMWPVGAHCHHPLL LLACQQKLGPPSHQASSRS*NIQ TLDRLCMSSWIPQEHSSSQSWH RSCFLNVTRPWSFYSPVGKNR WMGPFWSFSLDALLLFFTLHSY VAWPVEMMALNLLG
25918	56286	В	26059	1	2034	
25919	56287	A	26060	369	515	HAKPPGGLGHCSLCPSHYSCIH G*KGPRYVSVSCSRGWKPEAT KAFMW
25920	56288	Α	26061	352	2631	
25921	56289	В	26062	10	351	
25922	56290	Α	26063	321	537	EPLDTGRGTSHTRACHGVGYW GRDSVRRYT*CK*RINGYSTPT WHMHEYVTNLHIVHMYPRTYS IIIKKMSD
25923	56291	A	26064	788	912	VHTHLSERTRKCLPPPAPS*WV TCHHGDCCLPTRLRAPQGP
25924	56292	Α	26065	1348	1799	
25925	56293	A	26066	606	2219	ATYPSAHYPDHNRGEFLWPSL GLGKELDITFWSSLYPFGSPVSA VSRELVRKFSLGGTVDSTGSLP VSGDISPVSDVA/ACTREPLRFR LQVGDRYITLMDLPGVGESGA RDTEV AALYREQLPRLDLVLW LIKADDRALTVDEHFYHQVIGE GQLSTAQKQNISRKICLLHELFQ PVHPVCAVSVRLQWGLKVMA EKMIKCLPREATSPVVSQLHPSF RTTVVREQARSDFGETVGAVL DSISAPFLIPAPVRAVIQAVRTT VVSFAASVTLLLLPLRSTPVEKS PTCLIPASETFPLLVVMLNPVAS LTLTLTSPVLDTSCPHISLSAAQP NLIQLSGNNNISFVVNRAVVTN VLNTMRTACNSQATIQIYNADI ARDFGTRGIFSINSGFSTVYSRRI GHQSPEVTGEAMALTLSQPSG GHGSPEVTGEAMALTLSQPSG DIDGLIAVANUTDTGLRIGGDARQ KAITAGYPVVDTDKCRIRLR RIRHEQCADENSYQNYNCERP
25926	56294	A	26067	543	741	
	1			4		

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mct hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25927	56295	А	26068	3	373	VYTGLKPRTIDAQYTPINVV/W KFLSLTHHAYSPLLVVINKAKF DGLSPEFQQALVSSAQEAGNY QRKLVAEDQQKIIDGMKEAGV EVITDLDRKAFSDALGNQVRD MFVKDVPQGADLLKAVDE
25928	56296	Α	26069		1107	MGAFTGKTVLILGGSRGIGAAI VRRFVTDGANVRFTYAGSKOL AKRLAQETGATAVFTDSADRD AVIDVVRKSGA*ILILKRRSISSA FNSRASPKTPIPAFTTRISNAPLL RTTSMTASLSALSVNTAVAPVS CARRLAASFDPA
25929	56297	Α	26070	39	254	
25930	56298	Α	26071	1432	1845	
25931	56299	A	26072	674	1614	AVIVVAILVSKSTGAWVAFSIR MPSITFSHNSVVAGVASARKDS SPSYGDPLESAIPKLNVKRSRSG LSKSLLTLTSCSTIWINWITGQT PIKPCSVTGSVYPKA WRSPSTL TTMTTR*PFTLPA/LDTFISRPAG CTYANECHAPEDSAITRINDVAAR PCNCAQCAALDCVSVFVTIRHS CSSVYSAPGILVAALQAGHKPV ALVGGATGLIGDPSFKAAERKL NTEETVQEWVDKIRKQVAPLP DRKNISPADSRLSPDGRYRGYV HPAPPIPDSHLIRHHRCVIYQQ CLAQFRLNGWAASRSQSICKI GCD MSSSCIEEVSVPDDNWYRIANE
25932	56300	A	26073		3476	MSSSCIEEVSYPDOWYRIANE FERRYLQEGSLGLGESYMDGW WECDRLDMFFSKVLRAGLENQ LPHHFKDTLRIAGARLFNLQSK KRAWIYGKEHYDLGNDLFSRM LDPFMYSCAVWKDADNLESA QQAKLKMICEKLQLKPGMRVL DIGCGWGGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGL DVTILLQDYKDLNDGPENKYSV QMEHYDRFNYDTYFAVVDR
25933	56301	A	26074	200	1100	
25934	56302	Α	26075	1	2061	
25935	56303	Α	26076	1	3294	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25936	56304	A	26077	11	2064	MNYSLKOLKVFVTVAOEKSFS
						RAGERIGLSQSAVSHSVKELEN
	ı					HTGVRLLDRTTREVVLTDAGO
1	l	I				OLAFRLERLLDELNNTLRDTGR
ŀ		1				YGATTERSARYSASLPAPTSGR
		l				SEPAALVQNSSSQPSSLKENIM
		l				KLRSVTYALFIAGLAAFSTFFLA
1	İ	l				\AOSIRCGYETSQADSOHSGAK
	l	l			1	KFNDLLOERPKGELKLKLFPDS
		1				TLGNAQAMISGVRGGTID\MEM
		1		l		SGSNYFAGLSPVMNLLDVPFLF
						RDTAHAHKTLDGKVGDDLKAS
	1	l				LEGKGLKVLAYWENGWRDVT
	l .	l				NSRAPVKTPADLKGLKIRTNNS
	i					PMNIAAFKVFGA\NPI\PMPFAE
		1				VYTGLETRTIDAOEHPINVVWS
						AKFFEVOKFLSLTHHAYSPLLV
	1					VINKAKFDGLSPEFOOALVSSA
						QEAGNYQRKLVAEDQQKIIDG
	i					MKEAGVEVITDLDRKAFSDAL
						GNOVRDMFVKDVPOGADLLK
						AVDEPGWAERDIWAFAPAFFY
		1				PLFISDFNRVRLEFVGHYODVC
		ı	ľ			EKPASTTLWLDVGRSSGLDLTY
		l				OTLNVKNDLSHFPVPFFDPSDN
		l				RTNTLPMVFAGAPDVGLOOAS
		l				AIVASWFGSRSGWRGQNFPVL
		l				YNOLPDRNAIVFATNDKRPDFL
		1				RDHPAVKAPVIEMINHPONPYV
	1	1	1	1		KLLVVFGRDDKDLLQAAKGIA
1	1	1		i		OGNILFRGESVVVNEVKPLLPA
		İ				GSOPVWSSSASESRCCFYA
25937	56305	Α	26078	I	480	LGNTKTVKGWLAQLPAKYHQ
23931	50505	^	20070	l'		RATCMFDRHGLLALLAGRFLA
					1	FVRTLLPTMAGISGLPNRRFQFF
					1	KAKLR\WLS*PTRIAAALAFMP/
		1				FMDDHHPRLMQTVILQILQRRG
	1	1	1		1	TGDRLKIMVERRYAHVGFCRQ
						LLDAQVFGVFILNPFQHAANQT
						EVSLATDORO
25938	56306	A	26079	1	2184	ETOLATDONO
23938	20300	IA_	20079	11	12104	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	l	09/340,217	sequence	or peptide sequence	detection, (~possible nucleonide insertion)
25939	56307	Α	26080	1429	2152	NLFREVVFPTHCPVCGSDVERV
						EGEAVARCTGALICGAQRKESL
				i		KHFVSRRAMDVDGMGDKIIDQ
						LVEKEYVHTPADLFKLTAGKLT
						GLERMGPKSAQNVVNALEKAK
	ł					ETTFARFLYALGIREVGEATAA
	ŀ	l .		1		GLAAYFGTLEALEAASIEELQK
		l l			1	VPDVGIVVASHVHNF\LPKKAT
	i .					AMSSASCWRKVFTGLRRSLSTR
	i i					KRLTARLLVKPWCLRAASGTP
		1		1		LKRASLLMFSGCFSHTSGLAMY
25940	56308	Α	26081	1	2448	
25941	56309	A	26082	125	741	AHLNRTRWKVCWIR*RKISPW
						AKRNTKTVKG\WLAQLPAKYH
		1				QRATCMF\DRHGLLALLAGRFL
						AFVRTLLPTMAGISGLPNRRFQ
	1					FFNWLSGLLWVSVVTSFGYAL
						SMIPFVKRHEDQCRNGVFGKR
						KGGIAAALILTRLRRRFVSSWK
						RFRELRRKSSQADDMNVFGILE
		1				DFTHQFIGGAFLRADISGAAKM
		<u></u>				SCLAKAQASSSMH
25942	56310	Α	26083	1066	1359	
25943	56311	Α	26084	256	952	RLKRCSTGKSMAVIQDIIAALW
1						QHDFAALADPHIVSVVYFVMF
						ATLFLENGLLPASFLPGDTLLIL
						AGALIAQGVMNFSGLRIAVLDP
						RNQVRGGGLSIFKGRWLGNPK
		1				TVKG\WLAQLPAKYHQRATCM
	1	ı		1		FDRHGLLALLAGRFLAFVRTLL
	1	!				PTMAGISGLPNRRFQFFNWLSG
	1	1				LLWVSVVTSFGYALSMIPFVKR
		İ				HEDQVMTFLMILPIALLTAGLL
						GTLFVVIKKKYCNA
25944	56312	В	26085	1	1290	

SEO ID	SEO ID NO	Mes	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25945	56313	A	26086	1	1839	MRCQNA WWIMQHSSGSERLSS
						VLLHFRRTNLADSNDRIQYHSL
		l				RFFDEDGAOWLVILGDVLNHG
						PRNALPDGYAPRKVAERLNEV
						AHKVIAVRGNLRQRVDQMLLI
						SRAINRLVASNWNRRSAQMRC
						PISGKNLAWIPVQLPVYWQNN
	İ					CRRLLMRSHRKHGSGTNLPGE
						LMAIKLIAIDMDGTLLLPDHTIS
						PAVKNAIAAARARGVNVVLTT
1		1				GRPYAGVHNYLKELHMEQPGI
l						YCITYNGALVQKAAD/GYDDY/
1						RF/LEKLSREVGSHFHALDRTT\
1		1				LYTAN\RDISYY\TVHEFLRCHQ
		1				FPLVVCDGGRMTPRAMFLFSSA
i	1					HILMPLNYHNSHINTLFPVAGT
						LMVEPTESESKVELDRFIDAML
						AIRAEIDQVKAGVWPLEDNPLV
		1				NAPHIQSELVAEWAHPYSREV
						VFPAALVTGGSRGIGRATALLL
						AQEGYTVAVNYQQNLHAAQE
						VMNLITQAGGKAFVLQADISDE
1						NQVVAMFTAIDQHDEPLAALV
1		1				NNAGILFTQCTVENLTAERINR
1						VLSTNVTGYFLCCREAVKRMA
						LKNGGSGGAIVNVSSVASRLGS
						PGEYVDYAASKGAIDTLTTGLS LEVAAQGIRVNCVRPGFIYTEM
		1				HASGGEA WTRRSR
25946	56314	A	26087	2	1275	VNFSPKSSQIHHALRTVAGRFA
		1				VKSIDYFWHDSCNASKRFHIWE
						SIMLELLFVIGYLVMLMVTGVS
İ		1				LLGIIAALVVATAIMFLGGMLA
		l				LMIKLLPWLLLAISVVWVIKAI
						KAPKVPKYQRYDRWQLAVRRS
1						PLLPDHTISPAVKNAIAAARAR
						GVNVVLTTGRPYAGVHNYLKE
						LHMEQPGDYCITYNGAL/VYRK
						AAGWLAPLAAKLLLKLMDELI
						GFLEKLSREVGSHFHALDRTTL
1						YTANRDISYYTVHESFVATIPLV
						FCEAEKMDPNTQFLKVMMIDE
						PAILDQAIARIPQEVKEKYPVLK
1			l			APNLQQPHGSSGSSFHREIFFSS
			l	1		RSEDKRRGGLVVSGISLLVVSA
1						GPWVRNANEPLGQLKTWFSLS
1	1		l			HTLTLTYTRAPACRLTSTQTEP
1		1				RARPCLSPLSSEPRDRSLTPRLG
L						QRFIYLAVQ
25947	56315	В	26088	1	1509	
25948	56316	Α	26089	1	1323	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
25949	56317	В	26090	I	5073	
25950	56318	Α	26091	249	531	CWAMRMDSKVGVITPIRMWSA
	1					SGPFAMGTLVPTFAAVTDIPTK
			l	l		SVTTCLRQICERWQAPSTR*SRF
				l	<b>!</b>	ASLSQPAPRFTPSPITLALVLLP
						ARRC
25951	56319	A	26092	3	1038	LVLFGVAETYPVANDFAAGAG
						AYVRGRYAAGVRAWPTIITRK
						TMKTLVVALGGNALLQRGEAL
		i				TAENQYRNIASAVPALARLARS
	ŀ					YRLAIVHGNGPQVGLLALQNL
						AWKEVEPYPLDVLVAESQGMI
						GYMLAQSLSAQPQMPPVTTVL
		l	ľ			TRIEVSPDDPAFLQPEKFIGPVY
						QPEEQEALEAAYGWQMKRDG
						KYLRRVVASPQPRKILDSEAIEL
						LLKEGHVVICSGGGGVPVT\ND
						GAGSESVIHKDLAAALLAEQIN
		1				ADGLVILTDADAVYENWGTPQ
İ						QRAIRHATPDELAPFAKADGSM
			1			GPNVTAVSGYVRSPVQMHHRQ
						FQPVIIHIATNQIDHHRRIIHHWL
25952	56320	A	26093	1	3639	MKRLIVGISGASGAIYGVRLLQ
						VLRDVTDIETHLVMSQAARQT
		l		l		LSLETDFSLREVQALADVTHDA
		1				RDIAASISSGSFQTLGMVILPCSI
					1	KTLSGIVHSYTDGLLTRAADVV
						LKERRPLVLCVRETPLHLGHLR
				ł		LMTQAAEIGGNTGEIDEEELES
			Ì		1	LLYAIAKGNVFNFQTILHLPVA
	1		1		1	VQNDTIDFYQMFARIWSSHPQ
				1	1	WLTLYLAQHRAVIIPDDAKLHR
				1	1	NLLRWYSAGRLDIPELLDYAQS
_	L	L	L			WRETEPDNEDAPY

SEQ ID	SEQ ID NO:	I Mar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
	1	<u> </u>			1.000	
25953	56321	Α	26094	I	1260	AWARQDRRLSVKQWGKPPVD
ĺ	1	1		ľ		ETIPAKEQVRILRKLFDRYYGE
	1	1				VAGRGDGFCSPHVARYVGRVA
	i	1				G*RPCRLGPGHPTNRTPFVAPL
		1				LEALDIAKYFSVVIGGDDVQNK
	İ	1				KPHPDPLLLVAERMGIAPQQMI
		1			1	FVGDSRNDIQAAKAAGCPSVG
	!					LTYGYNYGEAIDLSQPDVIYQSI
		1		:		NDLLPALGLPIAKIRNRKMTKPI
	ı	l				VFSGAQPSGELTIGNYMGCTEA
		1		İ		DRQFAFNFNNFVLIQLLTNGGP
	1	1				DRLGTTTPAGYTDLLVNYTYRI
		1				AFEGGGGQDFGLAAAIATLIFL
		1				LVAIMFPLLMVVAISLRQGNFA
,		1				TGSLIPEQISWDHWKLALGFSV
		1				EQADGRITPPPFPVLLWLWNSV
						KVAGISAIGIVALSTTCAYAFAR
l	ŀ	l				MRFPGKATLLKGMLIFQMFPA
		1				VLSLVALYALFAPRVRAALCY
25954	56322	Α	26095	I	3240	
25955	56323	Α	26096	494	792	ATRLRHGVTSVGGDGGLQLTV
Į.	l	1				MDKLDVILLMSV/NPGFGGQSFI
	į	1				PQTLDKL/REVRRRIDESGFDIR
		1				L/EVDGGVKVNNIGEIAA/AGA
		1				DMFVAGSAIFDQPDAR
25956	56324	Α	26097	1624	2390	RTSERRWHAKALLKLFSAHHA
		l				GFVCCKEEEERLATGKVGWLP
		i				VETLLAQQHIEGHYQVDPSLFK
	ı	l				PNADCPVRVSGMSMKDIGIMD
		l				GDLLAVHKTQDVRNDPLLVPL
		l				FTLIREGKLAANWPLEQDELLT
		l				RLOKSCDMTQVSADYNALFIG
		l				DECAVPPYRSAWVEGATEAEV
	1	l	1	l		RAFLSERGMPLADTPADHIGTL
	1	1	l		1	LLAASWLEDQSTEDESEALETL
	1	l				FKRGA/LPKSLCLWGKAPAPHG
		1				SPVGGFSKGPKTWAPHEGAS
25957	56325	В	26098		534	
25958	56326	Ā	26099	67	399	
~>>>٥	120250	10	20077	I * *	12	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25959	56327	Α	26100	8	1016	PESRRKAVMTQPVLDIQQLHLS
		1				FPGFNGDVHALNNVSLQINRGE
					į.	IVGLVGESGSGKSVTAMLIMRL
						LPTGSYCVHRGQISLLGEDVLN
						AREKQLRQWRG/ARVAMIFQEP
						MTALNPTRRIALQMMDVIRHH
		ı				QPISRREARAKAIDLLEEMQIPD
						AVEVMSRYPFELSGGMRQRVM
						IALAFSCEPQLIIADEPTTALDVT
						VQLQVLRLLKHKARASGTAVL
		l				FISHDMAVVSQLCDSVYVMYA
						GSVIESGVTADVIHHPRHPYTIG
						LLQCAPEHGVPRQLLPAIPGTV
						PNLTHLPDGCAFRDRCYAAGA
						QCENVPALTACGDNNQR\GAC
						WYPQQEVISV
25960	56328	A	26101	3	102	ISRLNTQQHFG*RTRQISPHSPQ
						GCSRCPLHS
25961	56329	A	26102	290	490	SSLNSCMAVWDKTRLIRQ*LV
		1				MWSY*SPSPCR*PAGYRHMKL
						RSTSLVLSTPSRLFLAVIPPVVVI
25962	56330	Α	26103	1	3255	
25963	56331	A	26104	119	634	
25964	56332	A	26105	1640	1770	HLDSNRRVHDSTCNWCCNLS*
						QRLLWSG*WSELCCSVPRQKR
						A

SEO ID	ISEO ID NO-	Met	SEQ IĎ NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25965	56333	A	26106	281	2108	RESLKQKVGGRPQLSPFPPPDS
		1			[ · · · ·	WALDPGGGRARETPRGVSNAT
i		l			i	KEPISVAQHGN/GGDKEIRRELK
		l				YYAHLGRRLKDWSGIPRYHGT
i		l				VETDCGTGYVYDVIADFDGKP
						SITLTEFAEQCRYEEDIAQLRQL
						LKQLKRYLQDNRIVTMSLKPQ
						NILCHRISESEVIPVVCDNIGEST
		l				LIPLATWSKWCCLRKQERLWK
		l				RFIAOPALAIALOKDLOPOATE
		l				ASGAENMASIASGNIARTDPDM
		l				LSIPLSKKICCFGDRIIEIPETIDO
1		1				PVRFWVLTGPVVDMGIYACYL
1		l				SSPQWGWYAERDAEIENETVR
		l				REVEELROASETDLOPGTIEYE
		l				RHRLTRAQADAQELKNARDSA
		l				EVVETAFCTFVLSRIAGEIASIL
						DGIPLSVQRRFPELENRHVDFL
		l				KRDIIKAMNKAAALDELIPGLL
						SEYNRADRQYAGGSRVAARFA
			Ì			ASPRVAVLSVITGLIPRHVCAPY
		l				LLCGDPCCLSTPEDMTPRFRRY
		l				AVRSGNRSTPGLDHRCDACOR
		l	l			SAYELADLRCRPPPSTLFLLPEA
						DKNDFSDALPAVADAMYAAPP
			1			RRKAAPSKPEKAVVSPLRSVRK
		l	l		ł	ARHGSVCSLRPDOYAVRNLPA
		l				YRSCSSPDLQFMVWCALA
25966	56334	A	26107	1	2880	THE COOK DE STATE OF THE STATE
25967	56335	В	26108	61	5101	
25968	56336	Α	26109	80	561	IRPLPPRFKTESRSLPGPCLQPGT
		ļ				FLWSRNRRVLGFPSMNGEDMG
		1			i	LLFLCSEWERSSEGWLCNREGG
		1				SGHSIEPHCCTFLHLTHRSLAFS
		1				LLAGVSCTCASSCKCKE\CKCTS
		1				CKKSECGAISRNLGLWLKVGR
		l				EPKAVPEVRASGEPAFLCPCRL
						SLPV
25969	56337	A	26110	Ĭ	277	
25970	56338	A_	26111	902	1006	
25971	56339	Α	26112	2	1265	
25972	56340	A	26113	409	525	
25973	56341	Α	26114	91	431	NHKPGNIDVARRIQRGFAGDQI
			1	I		GHLRPVERQCSPDKRRFIAADG
l		l		ĺ		REIRGKQRAGHIFQLLSRCLLQI
		1				LNHCQRRAAHFRFQLSNQRHQ
		1				QLLPV/HYHAAEREYPAGACLV
						RWLL
25974	56342	A	26115	3	71	
25975	56343	Α	26116	1	1212	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25976	56344	A	26117	ı	2786	MAAVIEQIRRAVLALVTGVVHI GDIPVVWDIVWNATAFIAVIII SILLDESGFEWAALHVILRWG YGFGRLPFNRIGLIRRITFRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLFGLVTFILLLNRSQNPAQDIQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQGGLKRVYHSPG APDIREFTRDAIP
25977	56345	A	26118	48	219	EIFSVVWIIMTRGDVYTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI PETCGHLWAYVWPSCAAVIGL
						YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25979	56347	A	26120	1	912	

3498

TCVCVRTYAYVRVRVRY RVRVCAYARTRVRNSLSI LTLATPIHHIRQEFFNIRG RRWKPDLAIGIDITPSCIDT DYSEVRINQOG/GTCLNY TLAGLITPPRLIRMLEDTA IPVQREVAPQVITETGYIC GWEIGFSPLALLLAFLCSI GDPDGLGVIAYQDTVRPP AISELNALAVKGVILTDD AAAIAGELGLEFKAGLLP KAAVTENOHAPLAMVGI APAMKAAAIGIAMGSGTI ETADAALTHNILRGLVQ ARATHANIRGNITIALGLI VTTLDDRVVAGSAGRYG GDSECVKIVAQGIROTDR DRSPRPSGERVRVGKGG QPLSTAFTNQTITRQSIRLI VFHKGISRVVAGSSAIISN CILRTPNCRRGFPISCTGE YGWORDGHAFVLLAFE LLPDALSYEDGAFISCGVV EGILRGEVSGSDNVLVVG GMMAMMLAKGRGAKRI MLPERLAMAKQLGYMDI LPDVVY*ISVARYSWM SELRTRVAAVAHTRTRAF TRTRTYAVRTHTHVCA RVRVETHARAHTR TRTRTYAVRATHTRHAG TRTRTYAVRATHTHVCA RVRVETHARAHTR LPAQQRMKGENWYRGT- TONLDIIRRYKAGVEYVILL YKODYSRMLDHVEKGA ACMPYPIEGASAFGVMA DKIEFVEKPANPPSNPNE LASMGTYPDADVLYVEL RDENSHDFGKDLIPKITE YAHPPFLSCVGDDPADF CGYAGNFMESPRSGLIR PAGPPLPLPAARSEAPKA ASVPSIAPARLEGVKTGIR PAGPPLPLPAARSEAPKA	SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25981 56349 A 26122 3 1180 SKLGTRRSVVWA*SPSTS CSTFSAGHSSMKRMSEI LPAQQRMKGENWYRGT: TQNLDIIRRYKAFYVILL YKODYSRMLDHVEKGA ACMPVPIELASAFGYMA' DKHEFVEKPANPSMPNE LASMGTVFDADVLYELL RDENSSHDFCKDLIPKITE YAHPPELSCVGDPDAFP CGYAGNFMESPRSGLIR PAGPPLPLARSEAPKA. ASVPSIAPARLRPVPDPVE AAEFITGGDFTPRLHGSG QHHOTTRSHLEGVKTGIR. FSGNPGGGIAHVNGVARI QCHQAWGQQYAARLRF SLQJAHRVDIHRFDVRQ 25982 56350 A 26123 16 543	25980	56348	A	26121		1857	MRVCARACVRTRTRMCVYAH TCVCVRTYAYVRVRVRYHVRA RVRVCAYARTRAYVRVRVRVHVRA RVRVCAYARTRAVRNSLSILPIG LTLATPHHHHIGEFNIRGIOPVL RRVKPDLAIGIDITPSCDTPDLH RVKPDLAIGIDITPSCDTPDLH DYSEVRINOGYGITCLNYHGR GTLAGLITPRLIRMLEQTALEIN IPVOREVAPOVITETGYIQLFLP GWEIGFSFLALLLAFLCSTSPG GDPDGLGVIAYQDTVRPNAAT AISELNALAVGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAYTELNGHAPLAMVGOGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIGI TADAALTHNHLRGLVGMIGI VTTLDDRVVAGSAGRYGGDG GDSECVKIVAQEIRQTDRNIER STEPRSPERSFERVYRGGGGEN QPLSTAFTNQTIRGUSILFSNOG CILRTPNCRRGPPISCTGEGKAA YGWQRDGGHAEYLLAEEKDLI LPPDALSYEDOAFISCGYGTAY EGILRGEVSGSDNVLVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDLYVPIGVARYSWMNGRID MLPERLAMAKQLGVMDHGY*I LPDLYVYN*IGVARYSWMNGRID SELRTRVRAYHTERARTCTR
CSTFSAAGHSSMKRMME  LPAQQRMKGENWYRGT TONLDIJRRYKAEYVVIL YKQDYSRMIDHYEKGA ACMPVPIEASAFGVMA DKIIEFVEKPANPPSMPNI LASMGIYVFDADYLYELI RDENSSHDFCKDLIPKITE YAHPPLSCVQSDPDAEP CGYAGNFMESPRSGLIR PAGPPLPAARSEAPKA ASVPSIAPARLRPVPDPVE AAEFITGOPTPRICHGSG QHHQTRSHLEGVKTGIR FSGNPQGGIAHVNGVARI QCHQAWGQQYAARLRFG SSON A 26123 16 543							TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
							SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFVDL LPAQQRMKGENWYRGTADAV TONDLIIRRYKAEYVVILACDH YKNDDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN KUIEFVERPANPESMPNDPSKS LASMGIYVFDADYLYELLEEDE ROENSSHDFCKDLIFKITEAGLA CGYAGNFMESEPRSGLIRVSCM PAGPPLLPAARSEAPKAAGTV ASVPSIAPARLRPVPDPVELVLV AAEFITGGDFTPRLHGSGFIDIR GHHQTRSHLEGWKTGIFELNH FSGNPOGGIAHVNGVARFGVK QCHQAWGGQVAARLRFQARGI SLQIAHRVDIHRFDARGA
125083 156351   A 126124   I   13387							
25765 50551 A 20124 1 2507	25983	56351	Α	26124	1	3387	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25984	56352	A	26125	1688	2234	LSVGKTFPVLVPAAFRKVSATG
						AAVPGTPSILALPSYSTTPFGVC
		l				TSASMNVPVLTLRIRTRVTGEV
						AAIKPFSMANAPTPDSILPOLGV
		i				VSTRCS*TITCANR*STSARGSL
		l				ERLIMATLL/WVAGTFD*SVWF
l		l				GHDTDVVTLYRFHEALCYSVT
İ		l				LRTPHRRVLRFKSQHPGELACFI
						SPVA
25985	56353	A	26126	905	4761	PPHNWMPSNATPGIAFVWCAY
		l				GAI/LPGDAPVPVVDDYRKVVR
		1				KDTKGLIARWKYFWMSVIALG
		ı				VAFALYLAGKDTPATQLVVPFF
						KDVMPQLGLFYILLAYFVIVGT
						GNAVNLTDGLDGLAIMPTVFV
						AGGFALVAWATGNMNFASYL
		1				HIPYLRHAGELVIVCTAIVGAG
					1	LGFLWFNTYPAQVFMGDVGSL
				İ		ALGGALGIIAVLLRQEFLLVIM
1						GGVFVVETLSVILQVGSFKLRG
	1	l				QRIFRMAPIHHHYELKGWP
25986	56354	Α	26127	1056	1373	
25987	56355	Α	26128	1	301	SSGTDAGRRYRPRQRPSKSRNN
		l				RRVNRQPAPQQSSRN/SLRPSTT
		l				SSPFSLPAVKLPSAP/V*SAGMR
		1				LAEVRRVDSAISTVDSR*CPTAS
		_				SFSTGSITVTL
25988 25989	56356	A B	26129 26130	362	595 1305	
25999	56357 56358	A	26131	1	2022	MISKRSERSFGYGVGLVRRQDF
23990	30338	A	20131	<b>l</b> '	2022	SSSEGFFNLHSLRIDINKCLGVRI
		l		1		STATSTMGIVLPEQIKLACNGIQ
	į.			l		RVALCGGDDYLTSVDSFDVMF
				1		CSRFGWQVRPSSFCSPVFTWVT
	İ		1			ENQQHLHRGKDNLSLKNNNSA
	ļ					CGAACGSLRGEKSDPPSARNNP
						SSQQGGKKESGQQPSLKDPHIL
						RHDSAHRPRKEKPROPVNASLV
						VKFWRVKCVCVHNDHKRPACS
		ļ				VVCVDGDTYCWTEAYPAMGL
		l	1			PTLRGPDSALGERPE
25991	56359	A	26132	3	236	T TEROT DOTE CERT E
25992	56360	В	26133	1	4638	
25993	56361	A	26134	1501	1914	SAFSRALTGRQHFNNCAFTRFS
1						NGAECLLYHVCQTAFLVARRR
			1	1		VGAAVGFSHIEIVIVPLHLLQQP
				1		LADLFVHVARRLSSTMGIRDQR
	1	1		1		PLPG*LLNNITRWRRSAPVDQT
1		1		1		HSQSAGFAVTPENAFVASSGPS
1				1		RHRHQR
25994	56362	Α	26135	561	698	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25995	56363	В	26136	14	2040	
25996	56364	A	26137	804	947	LPCHCSCPWDGDVQPSPTPRQ WT*GERLH*QSEALPGVCCAPG HGPL
25997	56365	A	26138		734	SVHIGHQFFQFQSTSLNICPPLH RLFIAFQMNIRRNAARHAKFQ RLQAQVSIFEDDMSRKIANRQA TAMLNAPPFEANIGHNVPFIGF EAVIRQHFARRLNAFFALLFR PFRLFCPFFGINANQRSQVRQPQ LPRLDITFQFWSWLSGGVDQRT VDIVCHQWSALDRKEYYPAE TTMPTALHSRLCIIVGKIKRPVI VLFREANQARVGLFEH*STAA RPFWSAAPAGPALPLRVANAPS
25998	56366	Α	26139	2	309	
25999	56367	A	26140	472	885	SAFSRALTORQHFNNCAFTRFS NGAECLLYHVCQTAFLVARR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHOR
26000	56368	Α	26141	1	2469	
26001	56369	Α	26142	1175	1435	
26002	56370	Α	26143	218	443	AMARWKMLCTKSPPCVCLPGY P\G*RLAGPHHHHEFPPPAGAAS TGPPIVQDHQSLAGRSRRHDDS RHLGRCHHH
26003	56371	Α	26144	1	2031	
26004	56372	А	26145	1419	1875	TFCSPPSQPGSLKRRLRAGAGN CPLYSTGNGPLQRAICCAQPT*L HGRVPSHVPATTSSFQLWSTTV GACIHRSMYIISRSRCPFDPKTK TATMLGITSFVMERCQLFILSRA FTSQQPTCYPTASSNTWPSST RHCQVINLHSNSMHISL
26005	56373	A	26146	218	441	AMARWKMLCTKSPPCVCLPGY P\G*RLAGPHHHHEFPPPAGAAS TGPPIVQDHQSLAGPRRHDDSR HLVRCHHH
26006	56374	А	26147	1196	1462	LNTLVVAVRDGLKMTTVIANN VTSVSVLKIARNVTRKTILPPAA AANVTPYWLIRTIC*KRRYD*K TRWYYAVAACLCNMGTTRKA NG

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid scquence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26007	56376	A	26148	581	957	APSDPKRDFPLPHGADSAMAE YDRCHRAVLSQGGQWPTALSA GDHAAYSLHAALVQPERRCHG RCPVRNRLHAFVCPHIPG*PRAG SHHHHEFPPPARAASTGPSIVQ DHQSLAGRSRRHDDPRHFGGC HHH TSWISFSRTTPSTVSPYSTVDAN GIIWSARNRLASVNNIASWLSFF SNPLYLAITEPNCRLMMRNGGS TPOPGGWLSCIRC*WAVCSCVD AASRFLPCRGARRSASPHPPRQ APRRCGALW*PASAETINCSSPC SRLPS*LRGCCFKVLTLPGRSAI
26009	56377	В	26150	1	3924	SQSTSTSASSSALWRPLVAGIG
26010	56378	Α	26151	597	856	
26011	56379	В	26152	1	2781	
26012	56380	Α	26153	2809	2989	RCGYVRE*LAKSLQSNHFQWR MPQHQTAYCRS*AWYRHVAH ERLPAQTDNRHQHADRWNG
26013	56381	В	26154	1	2802	
26014	56382	A	26155	4493	5470	IQRRNHRRDGWCLASLPAGTD HAGARAEAGSWHSGGPHRVY ARSVSTPFAPIVNTATSLKPVR QLLDAALKIDHRRTLPKYSFGT FRRWYRSVAAQQAYKDQVA FFHGCFVNYNHPQLGQDLIKVL NAMGTGVQLLSKEKCGVPLI NAMGTGVQLLSKEKCGVPLI ANGFTDKARKQAITNVESIREA VGVKGIPVIATSSTCTFALRDEY PEVLNVDNKGLRDHIELANRW LWRKLDEGQTLPLKPMTLKVV YHTPCHME*MGWTLY/TLELLR NIPGLE/LTVLDSQ/CCGIPPIRV VIHMFRQIEESGADLVVTDCET CKWJEMSTSLRCEHPITLLAQ ALA
26015	56383	Α	26156	2467	3465	

SEO ID	ISEO ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nuclcotide insertion)
			İ	sequence		
	L					
26016	56384	A	26157	5758	7019	LKEGLLEPLAVTERLAIIRWRRP
		l			1	TMNDTSFENCIKCTVCTTACPV
1		1				SRVNPGYPGPKQAGPDGERLRL
		1		l		KDGALYDEALKYCINCKRCEV
		1		ŀ		ACPSDVKIGDIIQRARAKYDTT
		l		İ		RPSLRNFVLSHTDLMGSVSTPF
		[			ŀ	APIVNTATSLKPVRQLLDAALK
		1				IDHRRTLPKYSFGTFRRWYRSV
		l				AAQQAQYKDQVAFFHGCFVN
		l				YNHPQLGKDLIKVLNAMGTGV
		l				QLLSKEKCCGVPLIANG\FTDK
		l				ARKQAITNVESIREAVGVKGIP
		l				VIATSSTCTFALRDEYPEVLNV
		l				DNKGLRDHIELATRWLWRKLD
		l				EGKTLPLKPLPLKVVYHTPCHM
1		l				EKMGWTLYTLELLRNIPGLELT
		l				VLDSQCCGIAGTYGFKKENYPT
		1				SQAIGAPLFRQIEESGADLVVTD
		1				CETCKWQIEMSTSLRCEHPITLL
26017	56385	В	26158	I	2247	
26018	56386	Α	26159	882	2372	HAVHESPPECRSNQQRPTRTCR
		1		l		TIIDIMEMYHALHVSWSNLQDQ
		ł				QSIDERRVTFLGFDAATEARYL
		l				GYVRFMVNVEGRYTHFDAGTH
				ŀ		GFNAQTPMWEKYQRMLNVWH
		l				ACPRFLFDLDGTLVDSLPAVER
				l		AWSNWARRHGLAPEEVLAFIH
		l		İ		GKQAITSLRHFMAGKSEADIAA
						EFTRLEHIEATETEGITALPGAIA
		l		i		LLSHLNKAASGVTNKGFLTVD
1		l		İ		EIRRVTRAFARLGTEKVRLTGG
		l				EPSLRRDFTDIIAAVRENDAIRQ
			ľ			IAVTTNGYRLERDVASWRDAG
				l		LTGINVSVDSLDARQFHAITGQ
		l				DKFNQVMAGIDAAFEAGFEKV
		l		l		KVNTVLMRDVNHHQLDTFLN
		1				WIQHRPIQLRFIELMETGEGSEL
		1		l		FRKHHISGQVLRDELLRRGWIH
1		1		l		QLRQRSDGPAQVFCHPDYAGEI
		1		l		GLIMPY\DKDF\CATCNRLRVSS
		l		l		IGKLHLCLFGEGGVNLRDLLED
				i		DTQQQALEARISAALREKKQTH
			1	i		FLHQNNTGITQNLSYIGG
26019	56387	Α	26160	68	399	NKVKPRGDSV/PGSPHSPRLLSP
						PPLPGLLLWR/PLEEPFSPPLHC
		1	l	l		GSPFLGWPRPGGRGLGG/PPHSE
		1		l		QPASLSLPPTPRAPVRPEPPRRA
1		1	l	l		PPPAPRRPVPSTTQGLRNASAP
		Ь	L		L	T.T. T. T. T. Q. D. T. T. T. T. T. T. T. T. T. T. T. T. T.

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26020	56388	Α	26161	207	479	PWSDGAGPLPSLPHPDGRG*SV
	1	l		1		NSPQVLL**GSGE/PRASDSPLP
	l	l		İ		QLCGVSPHRPTWGSALWGGEQ
						CTSEMGETIDPPGPHTFSKNFCF
				1		ELQ
26021	56389	В	26162	1	453	
26022	56390	A	26163	1	379	
26023	56391	Α	26164	1	1054	MFLQAAQKAWNPHLLLVRTQ
						AASTHGRRADPHVGRCGETPQ
	l	1	1			SWGKGESLALAPLSLTKAALEE
		i		ŀ		CSQISPSHQGTLLCLLILDLRTG
		ļ				KLSLEHTEEPSDVPSHLLYRWSI
	l .	1				SSAITEVFQALASSDSTSQPVNV
	1	1				HTKEDMKVQDIALVLPSRKSR
	1	ł				NACRTTTSTCKALLMROLAAR
ł		1				VILQNCVSKSSRGIHVPQKNLT
		1				LPVRGDSVLAGSPHSPRSLSAPF
	1	1				LPGLPLWRHLKSPSAHRCTVGC
	i	ŀ				PFLGWPRPEPAPSACREALAAF
	1	1				P/PGOGSGPAAR\OPEPPPPWA
	ĺ	1				PVQPESPRQAPPPAPRSPVPSTT
	Į.	1				OGLRSTGTKHRDWOAAPPAAP
	l	l		i		VRDPLGEASWAPESGGDVENL
26024	56392	A	26165	2	362	EMSRLYRSRDRD/GVCLO/IEVK
20024	30372	ľ.	20103	ľ	502	MVSRTEANIDDSLIGGNASAEA
	ı					PEGEGTESTVITGVDIVMNHHL
ŀ						OETSFTKEAYKKYIKDYMKSIK
į .	l					GKLEEORPDRVKPFMTGAAEO
		l				KHILANFKNYO
26025	56393	A	26166	35	359	KITE/KITKITTQ
26026	56394	A	26167	22	459	
26027	56395	В	26168	102	431	
26028	56396	Α	26169	85	674	RRRRLPSVAIMIILPGPSSSHDE
				Į.		MF\SDISKIR\EIADGVCAWKVE
l	1	l		1		G\KMV\SRTE\GTID\DSLIGG\NA
1	1	l		I		SAERPRGAKGTERHOLITGV\DI
		1				VMTP\HL\QETKFSQKEASKK\YI
		1				K\DYMKSIKRET*KNRRPEKSK
l			1			TFL*PGAAEQIKHILANFKN\YQ
1		l		1	1	FFI/GENMNP/DGMVALLDYP*D
		1				WVVTPYMIFF*GWV*KWEKC
26029	56397	A	26170	1	1640	
26030	56398	Α	26171	1	1527	

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
0.0001	Lecano	ļ	06170	121	2560	Increumny a vegy congressor
26031	56399	A	26172	61	2360	PGFCHPRKAYSSYGQRSKGSQK
		l				MKASSGRCGLVRWLQVLLPFL
		l				LSLFPGALPVQIRYSIPEELAKN
ŀ		1	ľ			SVVGNLAKÐLGLSVRÐLPARK
						LRVSAEKEYFTVNPESGDLLVS
		1				DRIDREQICGKQPLCVLDFDTV
l		1				AENPLNIFYIAVIVQDINDNTPL
1		1				FKQTKINLKIGESTKPGTTFPLD
ĺ						PALDSDVGPNSLQRYHLNDNE
	1	ı				YFDLAEKQTPDGRKYPELILKH
	1	1				SLDREEHSLHQLVLTAVDGGDF
		1			1	PQSGTTQIRIKVTDANDNPPVFS
						QDVYRVTLREDVPPGFFVLQV1
						ATDRDEGINAEITYSFHNVDEQ
		1				VKHFFNLNEKTGEITTKDDLDF
		1				EIASSYTLSIEAKDPGDLAAHCS
						IQVEILDDNDCAPEVIVTSVSTP
		l				LPEDSPPGTVIALIKTRDRDSGE
		1				NGEVYCQVLGNAKFILKSSSKN
		1		l		YYKLVTDGALDREEIPEYNLTI
				İ		TATDGGKPPLSSSIIVTLHISDV
		1	i	1		NDNAPVFQQTSYMVHVAENNP
		ŀ		1		PGASIAQISASDPDLGPSGQVSY
		1		1		SIVASDLKPREILSYVSVSAQSG
				1		VVFAQRAFDHEQLRAFELTLQ
		1		1		ARDQGSPALSANVSLRVLVGD
		1				LNDNAPRVLYPALGPDGSALFD
	1	İ				MVPRAAEPGYLVTKVVAVDA
						DSGHNA WLSYHVLQASEPGLF
		1		1	1	SLGLRTGEVRTARALGDRDAA
		1				RQRLLVAVRDGGQPPLSATATI
		1			1	HLIFADSLQEVLPDLSDRREPSD
26032	56400	A	26179	47	325	ATMRLSVCLLLLTLALCCYRA
				"		NAVVCQALGSEITGFLLAGKPV
		1				FK\FQLAQFKAPVEAVASNMEA
		1				INCVDTM\AYEKRVLITKTLGKI
		1			1	AEKCDR
26033	56401	Ā	26180	I	3747	
26034	56402	A	26181	2776	2874	
26035	56403	Α	26182	89	369	
26036	56404	Α	26183	382	555	
26037	56405	Α	26184	2	67	
26038	56406	В	26185	1	444	
26039	56407	Α	26186	1129	1275	
26040	56408	A	26187	61	313	WIPHQGYRWSCLPVPRCALAFL
1	1	1	l	1		SPWVVDGTGHRGAGGGAGWG
	1		l	1	1	GFGRTGAHG\GVGGSGMAGCR
1	1	1	l		L	SRAHSGGVGMTMTWQIIPEVP

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26041	56409	A	26188	61	433	WIPHRGCRWSCLPVPRGALAFL
						SPRVVSGTGRRGAEGGARRGG
					l	SGRTGAHGVGGRLRHGGLQVP
						SLAPREGSCTCGG\GSGAREEQ
		l		1		NLGFPREPRSGGGARGSDGICG
		l		i		MRVMFRKWILFCPSSR
26042	56410	Α	26189	297	599	
26043	56411	Α	26190	370	585	
26044	56412	Α	26191	222	799	
26045	56413	Α	26192	346	634	
26046	56414	В	26193	206	955	
26047	56415	Α	26194	281	549	
26048	56416	Α	26195	1981	2337	
26049	56417	Α	26196	267	770	TRVDMIHYGLRKGPGETPS*SL
						RSFRAGQTGASRARGLTLLSSH
ŀ						SSALRKGSPKHFCTLCWQTFLA
l	I					WCVWKVAFSPSRCQTQFDLGK
	1					STQWTLEILTDPKSHLFSRKQQ
						PQARAPAVFPAPLKGCHVGAR
						GSHCQGFQGCFRPSVAPLILGT
	1	1				DGFSLLEKLWTFKTC
26050	56418	Α	26197	165	374	RVTVQWL*YLRPRMP*N*PRPR
						SGKPFIDSTHSSHR*RQRNAVSL
ļ	l					FSPVMSALRRCSVHRRLPDGGV
l	i					VA
26051	56419	Α	26198	357	981	HWRGDVLRRSHRRTALQSRYF
İ						CGIYRSP/YKAR/MQIQFFDPQQ
İ						MEAAOKRLTEESDILNALENHO
						FAIWLOPOVEMTSGKLRGISKO
						LVGFTNRQNGATKLLVQYFTH
l	1	1	1	1		ROIDCAGTADOPNPAGKVDDC
	1			1		GVTGNVTDRQQGKQHGQAKE
	1			1	l .	NELONACAFORAEEHKORKYA
l	1		1	1		POTOVDTKELCIWRIGOTOFRH
1		1				QONRNORHAERTNHFGVR
26052	56420	A	26199	1	2601	
20032	150,20	1::		·	2001	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26053	56421	Α	26200	1	1236	MGPGDLPRGLATFWTELGLLS
						WARELARMPAVEMPPRSCPGR
		ĺ				SRLSCSIGVAMFYGDLTAEOLY
						SRAISAAFTARHKGKNQIQFFD
1		l				POQMEAAQKRLTEESDILNALE
1						NHQFAIWLQPQVEMTSGKLPG
						KSAAIMLPLSVNLSALQLMHPN
	İ					MVADMLELLTRYRIQPGTLILE
						VTESRRIDDPHAAVAILRPLRN
						AGVRVALDDFGMGYAGLROL
l			l			OHMKSLVRLTKSEVSSETDODE
						LPLAKVSEVDEAKROWLOGMR
1						HPVDTVTEPEPAEILAEFIROHS
						AAGQLVARAVFLSPPYLVAEEE
						LSVLLESIKONGDYADIACLTG
1		l			į	SKDDYYYSTQAMSENYAAMSL
i .						QVVEQDIFSPIAHAVRFECQTY
						PRPYKVAMLMQAPYYFQEAQI
		1		1		EAAIAAMDVAPEYADIRQGIVG
26054	56422	Α	26201	1	1161	`
26055	56423	Α	26202	1	1038	
26056	56424	Α	26203	1	1472	MVRLCIRLPIRVYAKVVDKNAL
		l				SLWMRERSDLWVQPKVDGVA
		1				VTLVYRDGKLNKAISRGNGLK
		1				GEDWTQKVSLISAVPQTVSGPL
1		1				ANSTLQGEIFLQREGHIQQQMG
						GINARAKVAGLMMRQDDSDTL
						NSLGVFVWAWPDGPQLMSDRL
		ĺ				KELATAGFTLTQTYTRAVKNA
		l				DEVARVRNEWWKAELPFVTD
		l				GVVVRAAKEPRIPPLATGPGRV
1						AGGLEISTCSSGCRSEGNEPGKI
i		1				SVVASLAPVMLDDKKVQRVNI
1		1				GSVRRWQEWDIAPGDQILVSL
		1				AGQGIPRIDDVCPSDPAILSDIVP
						SW/VTTQW/LKKRAVSSRMMK
	ļ	1				NQ/VKKGSETGYFDKDEARFQK
	1					EGFRVVPPAALRQGAFIARNTE
						LRPSYVNIGAYVDEGTMVDTW
						ATVGSCAQIGKNVHLSAGVGIG
						GVLEPLQANPTHEDNCFIGARS
		1	1		1	EVVEGVIVEEGSVISMGVYIGQ
		1	1		1	STRIYDRETGEIHYGRVP/AGKV
		L				DAKTRGKVGINELLRTID
26057	56425	Α	26204	240	455	RLHPPYYRGWIFEEVPVISMGV
		1	1	l	1	YNGQSTRIYDR/ETGEIHYGRVP
		1		1		AGSVVVS\KVDAKTRGKVGINE
			L	L		LLRTID

SEO ID	SEO ID NO.	Mar	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26058	56426	Α	26205	197	1043	YEKSLTMQQLQNIIETAFERRA
						EITPANADTVTREAVNOVIALL
		l				DSGALRVAEKIDGOWYTHOWL
		1				KKAVLLSFRINDNOVIEGAESR
				i		YFDKVPMKFADYDEARFOKEG
						FRV\VPPAA\VRQGA\FIARNTVL
						MPSYVNIG\AYVDEGTMVDTW
	ì					AT\VGSCAQIGKNVHLSGGVGI
						GGVLEPLQANPTHEDNCFIGAR
						SEVVEGVIVEEGSVISMGVYIG
i				i		OSTRIYDRETGEIHYGRVPAGS
			ŀ			VVVSGNLPSKDGKYSLYCAVIV
l						KKVDAKTRGKVGINELLRTID
26059	56427	A	26206	1	406	MGKKNWNTLGEGVCSCRMFL
20039	30427	I <sup>A</sup>	20200	1'	400	PDANTLAKNSACSAASAVOAA
						DRPDSQEAEALEHMAHSRCAL
						RCQTLVIVHVSLMRVSWYHSVI
				l		IVVPLTEPLLESLVRCRLRSRRD
	1					DVPVAPAVSATPRREP\SVLRIA
						ERTNA
26060	56428	Α	26207	1	2574	MWAFRGKRPVTLKILHVPITNL
1						RKNITSTRGLTKESSQGKLVRA
						QEEYTPAREIAKMG\GNPCRPG
						GIVFAGER*DVTSPYV*TSTRGL
						TKESSQGKLVRAQEEYTPAREI
						AKMGWQSLPARRYCLCWRKIR
l					1	RYITLRLNIAYAGGYKAPVEDI
						ALWMETDGACDHVDFTWNIPS
		1				KCQGPMDIVSRPVFWHAHGIV
		1		l		LFAGARNLNPTLTRIPPYLWLL
l		1				TLRTGYAAAGMQALALDSRGS
						PDAVVLSTQHSEEIDQ
2606I	56429	Α	26208	1	3771	
26062	56430	Α	26209	239	451	LPPTAWMSTTNLTSAMLSVRG
		l				NVPMTLPARRRVNLPSSLICTCF
		ł				HKPA*RISMPKPVW*KARIISGN
						STS
26063	56431	Α	26210	1	2079	
26064	56432	Α	26211	1573	2562	
26065	56433	Α	26212	275	643	SSRTALFTGSAVPGCAPPSGRSL
		l		ł		FPQCLQSKLARSFPIRCSRSGAA
		I		1		ILFRRLSFSPGTELILEDR/IVKRF
			1	1		MRENSRGPQVPAGLPMTEEQL
				1	i	KKLGGRQLRALGKLMPGEEE\S
	l		1		l	VLRIAERTNA

Sequence	SEQ ID NO:			SEQ ID NO:			Amino acid sequence ( X=Unknown,
Sequence   Sequence	NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
RGYPYVTREGTDADDPO AALGSHRVAGQPELFSIDE RDPHSASGAWTARYTVST ALVIANRLYTIEEEATTPSC ASSSTSSRGVDMCLRNLC YDATIPLTILIAADSMDEYN LSHVISQQRADDLTRQTA AEQFNLHLEPQTWYTDIDA VVKSQNNQWQYDKLVLA SAFVPPVGRERLMILTINSQ RACETQLRDARRVLIVGG SELAMDFCRAGKAVTLIDD VIKSQURQADDLTRQTA AEQFNLHLESQLQQLEKTDSS TLDRQRNIEVDAVIAATGL TALARRAGLTINRGVCVDE TISTDIPLALDCAEINGQR ARRVYGRFFGAAVWRQL LRYCAGGPALPECQNPFPF PEISTADERPSPSTDAASGG VALTTPEYWQRCRLA MDYMVPVGMDWLCRETA RVSIKKGSVVPLNPELVM RQRSTIVTPSGFKAGAFNFI EASNQTLGSTELVSLSCFKL GSQPLDFDTKKSYTLKVE VHIDPRFSGRGFKDTATV VEDADEPPVSSPTVLLEVI AALNSVIGQVTARDPDITS: LYRIPGDAKCVOPNREG LKAKPVEKAAPAPAAAP PTPAKPMGEQLALYRMAG DRQGRMDFTRQSAAEW AEEADIAWVLKTYGEERFA RAINVERNEGOPMTETKEL VAAATPVKDKFKHPATETI VRIWNSELEKIEQALKSS LAPGGRLSISSHSLEDRIV MRENSROQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALKSLLAPGGRLSISHSLEDRIV MRENSROPQVPAGLPMTEI KKLGGRQLRALGKLMPGE VLRIAERTNA  26060 56437 A 26216 27 791  26070 56438 B 26217 1 1638  TKKRQRGERHPDGGRGA LPRTSVDQRPLRCYTNIPAG ANG*GVFRCRAHASTTI- T*NESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA*GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA**GGKVEGTIT E**PESSERMA***GGKVEGTIT E**PESSERMA***GGKVEGTIT E**PESSERMA*****CANTENT*****CANTENT****CANTENT***CANTENT***CANTENT***CANTENT***CANTENT***CANT		sequence		09/540,217		or pepude sequence	deterion, (-possible nucleotide insernon)
AALGSHRVAGQPELFSIDE RDPHSASGAWTARYTVST ALVIANRLYTIEEEATTPSC ASSSTSSRQVDMCLRALCA YDATIPLTILIADSMDEVN LSHVISQGQRADDLTRQTA AEQFNLHIPPQTWYDTDID VVKSQNNQWQYDICLVLA SAFVPPVFGRELMILTINSQ RACETQLRDARRVLIVGG SELAMDECRAGKAVTLIDD SILASLMPPEVSSRQ-IGHELI GVHLLLKSQLQGLEKTDSC TLDRQRNIEVDAVIAATGL TALARRAGLTINRGVCVDE TSNTDIVALGDCAEINGQR ARRVVPGRFFGAVWRQL LRYCAGGPALPECQNPFFP TEISTADERRPSTDAASGC VALTTPETWQRCRLA MDYMVPVGMDWLCRETA RVSIKKGSVVPLNPELVM RQRSTIVTPSGFKAGFANFIL EASNQTLGSTFLYSLSCPKI GSQPLDFDTKKSYTLKVE VHIDPRESGROPFKDTATV VEDADEPPVFSSTYTLLEVI AALNSVIGQVTARDPDITSS LYRIPGDDAKCVGFNREGG LKAKPVEKAPAPAAAAP PTPARPMGGQLALVRMAG DRIQGMDFTRGGSAAEW AEBADIAWVLKTYGEBEFA ARAIVERNBEQPMTRTKEL VAAA TPVKDKFKHPATTI VRIWVNSELERIEQALKSS) LAPGGRLSISSHSLEDRIVW MRENSROPQVPAGLPMTEL KKLGGRQLBALVRMAG DRIQGRMDFTRGGSAAEW AEBADIAWVLKTYGEBEFA ARAIVERNBEQPMTRTKEL VAAA TPVKDKFKHPATTI VRIWVNSELERIEQALKSSL LAPGGRLSISSHSLEDRIVW MRENSROPQVPAGLPMTEL KKLGGRQLBALGKLMPGE VLRIAERTNA  26068 56437 A 26216 27 791  26060 56437 A 26216 27 791  26060 56437 A 26216 27 791  26060 56438 B 26217 1 1638  STKKQRGEIHHPDGHGIAQ LPRTSVDQRPLRQTNHPAG ANG*GVFKRCRAHSATT** E*NESSERNA*GGKVEGTI E*PRESSERNA*GGKVEGTI	26066	56434	A	26213	I	899	MGRTTRRDAAQAPGTRRSGDS
RDPHSASGAWTARTYUST   ALVIANRLYTIEEATTPSC     ASSSTSSRGWDCLRNLCN     YDATIPLTILIADSMDEVN     LSHVISQQGRADDLTRQTT     AEQFNLHLFPOTWYTDID-    VVKSQNNQWYDIDLTNLT     AEQFNLHLFPOTWYTDID-    VVKSQNNQWYDIDLTNLT     AEQFNLHLFPOTWYTDID-    VVKSQNNQWYDIDLTNLT     SILASLMPPEVSSRLQHRLI     GVHLLIKSQLQGLEKTDS     TLDRQRNIEVDAVIAATGL     TALARRAGLTINRGVCVDS     TSNTDIYALGDCAENGQR     ARRVVPGRFPGAVRWQL     LRYCAGGPALPECQNFPFP     TEISTADERPSSTDAASGC     VALTITPEYWQRCRLA     MDYMYPVGMWUCKETA     RQSTIVTPSGFKAGAFNFI     EASNQTLGSTELYSLSCPKI     GSQPLDFDTKKSYTLKVE     VHIDPPSGRQPFKDTATV     VEDADEPPVFSSPTYLLEVI     AALNSVIGQVTARDPDITS     LYRIPGDDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIVENSCOPNTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQNTTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCYVENTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCYVENTITICAL     LYRIPGDAKCYVENTITICAL     LYRIPGDAKCYVENTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCYVENTITICAL     ARAINSVIGQVTARDPTITICAL     CROSTITUTICAL     CROSTITUTICAL     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVICCT     ARAINSVICCT					l		RGYPYVTRPEGTDADDPOKDK
RDPHSASGAWTARTYUST   ALVIANRLYTIEEATTPSC     ASSSTSSRGWDCLRNLCN     YDATIPLTILIADSMDEVN     LSHVISQQGRADDLTRQTT     AEQFNLHLFPOTWYTDID-    VVKSQNNQWYDIDLTNLT     AEQFNLHLFPOTWYTDID-    VVKSQNNQWYDIDLTNLT     AEQFNLHLFPOTWYTDID-    VVKSQNNQWYDIDLTNLT     SILASLMPPEVSSRLQHRLI     GVHLLIKSQLQGLEKTDS     TLDRQRNIEVDAVIAATGL     TALARRAGLTINRGVCVDS     TSNTDIYALGDCAENGQR     ARRVVPGRFPGAVRWQL     LRYCAGGPALPECQNFPFP     TEISTADERPSSTDAASGC     VALTITPEYWQRCRLA     MDYMYPVGMWUCKETA     RQSTIVTPSGFKAGAFNFI     EASNQTLGSTELYSLSCPKI     GSQPLDFDTKKSYTLKVE     VHIDPPSGRQPFKDTATV     VEDADEPPVFSSPTYLLEVI     AALNSVIGQVTARDPDITS     LYRIPGDDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIQGRMDPTRGQSAAEW     AEEADIAWVLKTYGEBFF     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     DRIVENSCOPNTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCVOPNREG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQLALYRMAG     LKAKPVEKAAPAPAAAP     PTPARPMGPQNTTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCYVENTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCYVENTITICAL     LYRIPGDAKCYVENTITICAL     LYRIPGDAKCYVENTITICAL     ARAINSVIGQVTARDPDITS     LYRIPGDAKCYVENTITICAL     ARAINSVIGQVTARDPTITICAL     CROSTITUTICAL     CROSTITUTICAL     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVIGCT     ARAINSVICCT     ARAINSVICCT							AALGSHRVAGQPELFSIDELTR
ALVIANRLYTIEEEATTPSC				'			
ASSSTSSRQVDMCLRNLC VDATIPLITLAADSMDEYN LSHVISQQQRADDLTRQTA AEQFNLHLIPQTWVTDIDD VVKSQNNQWQVPJKLVLA SAFVPPVFGRELMI.TLNSQ RACETQLRDARRVLIVGG SELAMDFCRSKLQHRLI GVHLLKSQLQLEKTDS TLDRQRNIEVDAVIAATGL LRYCAGGPALBEQCONFFP TEISTADERPFSTDAASGC VALTITEPVWQRCRLA ARRVYPGRFPGAVRWCRL 26067 56435 A 26214 I 1264 MDYMVPVGMDWLCRETA RVSIKKGSVVFPLNPELVM RQRSTIVTPSGRCAGAANFI EASNQTLGSTELVSLSCPK GSQPLDFTIKSVTLKVE VHDPRFSGROPFKDTATV VEDADEPPVFSSFYTLEV AALNSVIGQVTARDPDITS LYRIRGQLALVRMAG DRIQGRMDFTRGSAAEW AEEADIAWVLKTYGEBFF, ARAIVERNREQPMTRTKEL VAAATPVKDKFKHPATRTI VRIWVNSELEKIEQALKSS) LAPGGRLSISFISLEDRIV MRENSRQPQVPAGLPMTE KKLGGRQLRALGKLMPGE VLRIAERTNA 26215 64 663 26068 56437 A 26216 27 791 260070 56438 B 26217 1 1638 260071 56439 A 26218 1 375 STKKQRGEIHHPDGHGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPDGIAQ LPRTSVDQRPLRPTHPAG						1	
YDATIPLITIANDSMDEYN   LSHVISQGQRADDLTRQTA   AEQFNLHLFPQTWYTDIDA   VVKSQNNQWQYDKLVLA   SAFVPPVGRERLMILTINSQ   RACETQLRDARRVLIVIGGG   SELAMDFCRAGKAVTLIDI   SILASLMPFEVSSRLQHRLI   GVHLLLKSQLQQLEKTDSK   TLDRQRNIEVDAVIAATGL   TALARRAGLTINRQVCVDS   TSNTDIYALGDCABINGQR   ARRVVGGRPGAVRWRQL   LRYCAGGPALPECQNPFPP   TEISTADERNPSTDAASGG   VALTTPEY WQRCRLA   VALTTPEY WQRCRLA   RVSIKKGSVVPPLNPELVM   RQRSTIVTPSGFRAGAFNFI   EASNQTLGSTELVSLSCPKI   GSQPLOFDTKKSYTLKVE   VHIDPRFSGRGPFKDTATV   VEDADEPPVSSRTVLLEVI   AALNSVIGQVTARDPDITS: LYRIPGDDAKCVQNREG   LKAKPVEKAAPAPAAAP   PTPAKPMGEQLALYRMAG   DRIQGRMDFTRQSAAEW   AEEADIAWVLKTYGEBFF, ARAIVERNBEQPMTETKEL   VAAATPVKDKFKHPATETT   VRIWVNSELEKIEQALKSS   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPRAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPRAGLPMTE   KKLGGRQLRALKSLMPGE   VLRIAERTNA   LAPGGRLSISSHSLEDRIVM   MRENSRQVPRAGLPMTE   KKLGGRQLRACKSLMPGE   VLRIAERTNA   LAPGGRCSTATT   LAPGGRC						i	
LSHVISQGGRADDLTROTT   AEQFNLHLIFQTWVTDID    VVKSQNNQWQYDKLVLA    SAFVPPVFGRELMITLNSQ    RACETQLRDARRYLIVIGG    SELAMDECRAGKAVTLID    SILASLMPPEVSRLQHRLI    GVHLLLKSQLQGLEKTDSC    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAATGL    TLDRQRNIEVDAVIAGCAENINGRO   TRITTEYWQRCRLA    MDYMVPVGMDWLCRETA    RVSIKKGSVVPLNPELVM    RQRSTIVTPSGFRAGAFNFI    EASNQTLISFILVISLSCPKI    GSQPLDFDTKKSYTLKVE   VHIDPRESGROPFKDTATV    VEDADEPPVFSSTYTLLEVI   AALNSVIGQVTARDPDITSI    LYRIPGDDAKCVQFNREGI   LYRIPGDAKCVGFNREGI   LYRIPGDAKCVGFNREG							
AEGPNI-LILPOTWYTDIDA VVKSQNNQWQYDKUVLA SAFVPPVGRELMI-TINSQ RACETQLRDARRVILIVGGG SELAMDECRAGRAVTLIDS ILASLMPPEVSSRLQHRLI GVHLLLKSQLQGLERTIDG TLDRQRNIEVDAVIAATGL TALARRAGLTINRGVCVDS TSNTDIYALGDCAENGQR ARRVVPGRFPGAVRWQL LRYCAGGPALPECONPTPP TEISTADERPSSTDAASG VALTITPEYWQRCRLA MDYMPVGWMUCKETTA RVSIKKGSVVFPLNPELVM RQRSTIVTPSGFKAGAFNFI EASNQTLGSTELYSLSCPKI GSQPLDFDTKKSYTLKVE VHIDPRSGRQSPKDTATV VEDADEPPVFSSPTYLLEVI AALNSVIGQVTARDPDITS: LYRIPGDDAKCVQPNREGG LKAKPVEKAAPAPAAAP PTPARPMGPQLALYRMAG DRIQGRMDPTRGQSAAEW AEBADIAWVLKTYGEBEF, ARAIVENNEGQPMTRTKEL VAAATPVKDKFKHPATRT VRIWVNSELEKIEQALYSMAG DRIQGRMDPTRGQSAAEW AEBADIAWVLKTYGEBEF, ARAIVENNEGQPMTRTKEL VAAATPVKDKFKHPATRT VRIWVNSELEKIEQALKSSI LAPGGRLSIISFISLEDRIV MRENSRGPQVPAGLPMTEI KKLGGRQLRALGKLMPGE VLRIAERTNA  26068 56436 B 26215 64 663  26069 56437 A 26216 27 791  26070 56438 B 26217 1 1638  STKKQRGEIHHPDGHGIAQ LPRTSVDGRPLCOTNIPIAA ANG*GVFRRCRAHAATT** E*NESAENAA*GGKVEGTI E*NESAENAA*GGKVEGTI E*NESAENAA*TGKVEGTTINPAATT** E*NESAENAA*TGKVEGTTI		İ		Í		I	
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VLRIAERTNA   VLRIAERTNA   VLRIAERTNA     VLRIAERTNA     VLRIAERTNA							KKLGGROLRALGKLMPGEEE\S
26068 56436 B 26215 64 663 26069 56437 A 26216 27 791 26070 56438 B 26217 1 1638 26071 56439 A 26218 1 375 STKKQRGEIHHPDGHGIAQ LPRTSVDQRPLRQTINIPPAG ANG*GVFKRCRAHSATT**  E*NESAENAA*GGKVEGTL							
26069   56437   A   26216   27   791     26070   56438   B   26217   I   1638     26217   I   1638     26071   56439   A   26218   I   375     STKKQRGEIHHPDGHGIAQ LPRTSVDQRPLRQTNIPPAGA ANG*GVFRCRAHSATT** E*NESAENAA*GGKVEGTI	26068	56436	В	26215	64	663	· Diditibiting
26070         56438         B         26217         I         1638           26071         56439         A         26218         I         375         STKKQRGEIHHPDGHGIAQ LPRTSVDQRPLRQTNHPAG ANG GVFKRCRAHSATT**           E*NESAENAA*GGKVEGTL         E*NESAENAA*GGKVEGTL			_				
26071   56439   A   26218   1   375   STKKQRGEIHHPDGHGIAQ   LPRTSVDQRPLRQTNIPPAG   ANG GVFKRCRAHSATT**   E*NESAENA* GGK VEGTL							
LPRTSVDQRPLRQTNIPAG ANG*GVFRRCRAHSAT** E*NESAENAA*GGKVEGTI					1		STKKORGEIHHPDGHGIAODRI
ANG*GVFKRCRAHSATT** E*NESAENAA*GGKVEGTI			l .		1		LPRTSVDQRPLRQTNHPAGL*Q
E*NESAENAA*GGKVEGTE		l		Ì	1		ANG*GVFKRCRAHSATT**KDI
					[		
		1			1		
CQWVALSCGRHERSSV							,

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		ocqueace.		
26072	56440	Α	26219	213	407	TTCCCTNLSIPLANKYRSLSPQS
		l				DWRLSMPR*NRYVQKAPARAN
						KTSPMKAPPANIALGVNVAR
26073	56441	Α	26220	1	1179	
26074	56442	A	26221	176	569	WPMRHTFSEAHAAQRAGGKNP
						GHDTADYATNAVHTEDIAGIIH
						PQQAFEHGNAPQARQTSYHAD
						NQRAANPNVAAGWRHADQTG
						NRARTRPQQ*RLTTQRPFTEDP
						AKNCRRRCDHSIHKCQCRDFIR
						RAR
26075	56443	A	26222	1442	2309	
26076	56444	A	26223	155	2929	HLHWFVFSGWFTVTRLAFGEG
1						NNFFGNINWLMLKNIELTAVM
						GSIYQYIHVAFQGSFACITVGLI
						VGALAERIRFSAVLIFVVVWLT
ĺ	l	l				LSYIPIAHMVWGGGLLASHGAL
						DFAGGTVVHINAAIAGLVGAY
						LIGKRVGFGKEAFKPHNLPMVF
1			Į.			TGTAILYIGWFGFNAGSAGTAN
					1	EIAALAFVNTVVATAAAILGWI
						FGEWALRGKPSLLGACSGAIAG
						LVGVTPACGYIGVGGALIIGVV
						AGLAGLWGVTMLNAC
26077	56445	A	26224	2	1064	
26078	56446	Α	26225	1849	2515	MEGHLWIRIDLSQSAVSHSVKE
						LENHTGVRLLDRTTREVVLTD
						AGQQLALRLERLLDELNSTLRD
		ŀ				TGRMGQQLSGKVRVAASQTIS
						AHLIPQCIAESHRRYPDIQFVLH
						DRPQQWVMESIRQGDVDFGIVI
					l	DPGPVGDLQCEAILSEPFFLLCH
						RDSALAVEDYVP\ALPLPEGSPL
						VVKRITPVVERQLMLVRRKNR
						SLSTAAEALWDVVRDQGNAL
						MAAA

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26079	56447	Α	26226	102	1655	RKOMNYSLKOLKVFVTVAQE
						SFSRAGERIGLSQSAV\SHSVKE
						LENHTGVRLLDRTTRAVVLTD
						AGOPLALRLERLLDELNSTLRD
						TGRMGQQLSGK\VRVAASQTIS
						AHLIPQCIAESHRRYPDIQFVLH
						DRPQQWVMESIRQGDVDFGIV
						DPGPVGDLQCEAILSEPFFLLCH
						RDSALAVEDYVPWQALQGAKI
						VLQDYASGSRPLIDAALARNGI
						QANIVQEIGHPATLFPMVAAGI
						GISILPALALPLPEGSPLVVKRIT
		ļ				PVVERQLMLINVIQTLRFAFIFR
						LSRRQHFAKVTPLLHRHGDYF
						VFIGFDYGTANCSVAVMRDGK
						PHLLKMENDSTLLPSMLCAPTR
		1				EACGRVDVIEVSKSKVRKNTY
						AMRYVAGQPAERILPPGSFASI
		ŀ				GQALPPGEPLSTEERIRILVWNI
		1				YKQQRAEWLSVLKNYGKDAH
		1		1		LVLLQEAQTTPELVQFATANYI
	1	1		1		AADHVPAFVLPQHTSGVMTLS
						AAHPVYCCPLRERKPILRLAKS
						ALVTVYPIFPYLSNS
26080	56448	A	26227	159	290	
26081	56449	Α	26228	562	774	VLRMIT*SKSQFAQDMCRNVLL
		1				INNFGRIQHDPAIFHFQRNEAVP
		l				LWTVSAQEVKKDFTSGLRHGS
		L.			100	VRGDL
26082	56450	A	26229	50	409	GYASQALILASIPAASRPSSARIS
		l		1		S*VPCGIKKSGRPMFSTGTGLR
		l		1		WAISTSFTPLPAPPIMAFSSTVTS
		1		1		ASWLAAISRINASSSGFTKRIST SVAFSDSATFAASSTNSRNAPPP
		1			l	SVAFSUSATFAASSINSKNAPPP
26083	56451	A	26230	405	626	V E.WI
26083	56452	A	26231	1	1528	
26084	56453	B	26232	1	1755	
∠0083	30433	Ь	20232	1'	11/33	

NO: of peptide sequence bod in USSN possed, 27 codon for peptide sequence codon for text amino acid sequence codon for te	sence ( Yml lak nown	Amino acid sequence ( X=	Nucleatide location of last	Nucleotide	SEO ID NO:	Met	SEO ID NO:	SEO ID
26086   36454   A   26233   152   2099   GNRLLVVSFIAFSKNS AMRIILGAPOAGKG EKYGIPQISTOMIA.								
26086 36454 A 26233 152 2099 GNRLLVVSFIAFSKNS AMRIILLGAPÖAGKG EKYGIPQISTÖDMLR. ELGKQAKDIMDAGK. IALVKERIAQEDCRN PRTIPQADAMKEAGII FDVPDELIVDNIVGRR RVYHKKFNPKVEGG ELTTRKDDQEETVRK QMTAPLIGYYSKEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAE AKVDGTKPQIVSEAEE AKVDGTKPQIVSEAEE AKVDGTKPQIVSEAEE AKVDGTKPQIVSEAEEE AKVDGTKPQIVSEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE								
AMRIILLGAPGAGKG EKYGIPQISTODMLR.  ELGQAKDIMDAGK. IALVKERIAQEDCRN PRTIPQADAMKESI FDVPDELIVDRIVGRI RVYHVKPPKVEGI ELTTRADDQETVRK QMTAPLIGYYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE GIGPQUSRAQGVDL GUIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVYKDLNDEAP FFTEHNATFPARSCVI DVKIEIGAIAMLYTGO SAVRYPRGMASGVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG				sequence				
AMRIILLGAPGAGKG EKYGIPQISTODMLR.  ELGQAKDIMDAGK. IALVKERIAQEDCRN PRTIPQADAMKESI FDVPDELIVDRIVGRI RVYHVKPPKVEGI ELTTRADDQETVRK QMTAPLIGYYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE AKVDGTKPQIYSKEAE GIGPQUSRAQGVDL GUIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVYKDLNDEAP FFTEHNATFPARSCVI DVKIEIGAIAMLYTGO SAVRYPRGMASGVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG								
EKYGIPQISTODMI.R. ELGKQAKDIMAGK. IALVERIAGEDCRN PRITPQADAMEAGI FDVPPELIVDRINGER RVYHVKTNPKVEGE ELTTRKDDQEETVRK QMTAPLIGYYSKEAE AKVDGTKRQTRGES HTIVNPDGVVCDCG VASLSALKKQARV TOLLDPEKLTTAQUIA WITSWVDRSANAIGL ILINIQUIAVGRSCAE ILINIQUIAVGRSCAE GIGPOVPERGEGE IGFGQLSRAQQCVDL GQIPVPNTGEPVDEG IGFGQLSRAQQCVDL GQIPVPNTGEVTGVTG VSLDNVKAIVEAAGL KTTVFVKDLNDFAPV FFTEHAATPFARSCVT DVKIELEIAIMLYTG SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNAIL PEAAKVAESLNAIL PLDEALILEMASHE NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG			2099	152	26233	A	56454	26086
ELGKÇAKDIMDAGK IALVKERIAQEDCRIN PRTIPQADAMKEAGI FDYPDELIVDRIVGRI RVYHVKPNPKVEG ELTTRKDDQEETVRK QMTAPLIGYYSKEGE AKVDGTKPQIVFRGSE HTIVNPDGVCDCGG VASISALKKQAKVW TQLDPEKLTTAQLIA WITSWVDRSANAIGL ILNINGJWLYGRSCAF TIIRQTGFNPFDRDGG IGFGQLSRAQQGVDL QQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNFAGEVPAD TOKKENEY								
IIALWERIAGEDCRM PRTIPQADAMKEAGII FDVPDELIVDRINGRR RVYHWKPPPKVEGG ELTTRKDDQGETVRK QMTAPLIGYSKEAE AKVDGTKPQIYRGSL HTIVNPDGVVCDCGR VASLSALKQARVW TOLDPEKLTTAQLIA WITSWVDRSANAIGL ILNINOJINLYGRSA TIIRQTGPNPFDRDIG IGFGQLSRAQQGVDL QQIPVNPKTGEVDAD QSLDNVKAIVEAAGL KTTVFVKDLNBCAPP FFTEHNATFPARSCVI DVKIEIGAIAMLYTGS SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMASHE NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG								
PRTIPQADAMKEAGII FDVPDELIVDRIVGRR RVYHVKTNPPKVEGR ELTTRKDDQEETVIK QMTAPLIGVYSKEAE AKVDGTKPQIYRGSL HTIVNPDGVCDCGR VASISALKKQARVW TOLDPEKLTTAQLIA WITSWVDRSANAIGL ILININGIWLYGRSCAE TIIRQTGFNPFDRDEG IGFGQLSRAQQVOL GQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFAPV FFTEHNAITPARSCVEL IGKGIVKRGEKLAIL PEAAKVAESINATLV PLDEALLEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG								
FOVPDELI/DRIVGRR RVYHVKFNPFKVEGB ELTTRKDDQEETVRK QMTAPLIGYYSKEAE AKVDGTKFQIYSKEAE AKVDGTKFQIYSKEAE HTIVNPDGVVCDCGR VASLSALKQARVW TQLDPEKLTTAQLIA WITSWVDRSANAIGL ILNINQIWLYGRSCAE TIIRQTGFNPFDRDEG IGFQUSRAQGVDL QQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFAP FFTEHNATFPARSCVI DVKIEIGAIAMLYTTO' SAVRYPRGMASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE, NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG								
RVYHVKFNPRVEG ELTTRADDGETVRK  QMTAPLIGYYSKEAE AKVDGTKFQIYRGSL HTIVNPDGVVCDCGR VASLSALKQARVW TQLDPEKLTTAQLIA WITSWVDRSANAIGL ILNINQIWLYGRSCAF TIIRQTGFNFPRDDGG IGFGQLSRAQQVDL QQIPVNPKTGEVPAD QSLDNVKAIVEAGL KTTVFVKDLNDFAPV FFTEHNATFPARSCV DVKIEIEAIAMLYTG SAVRYPRGNASQVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALLEMA ASHE, NAIMGGAGSQNVEVI VPVLNIGLPDFFIPQG								
ELTTRKDDQEETVRK QMTAPLIGYYSKEAE ARVDGTKPQIYRGSL HTIVNPDGVCDCGG VASISALKKQARVW TQLDPEKLTTAQLIA/ WITSWYDRSANAIGL ILNINGJWLYGRSCAF TIIRQTGFNPFDRDGG IGFGQLSRAQQGVDL QQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFAP FFTEHNATFPARSCVI DVKIEIEAIAMLYTGY SAVRYPRGNASOVEL IGKGIVKRRGEKLAIL PEAAKVAESINATLV PLDEALILEMAASHE, NAIMGGAGSGNVEVI VPVLNIGLPDFFIPQG	DRIVGRRVHAPSG	FDVPDELIVDRIVG						
QMTAPLIGYYSKEAE AKVDGTKPQIYRGSL HTIVNPDGVVCDCGR VASLSALKQARVW TOLDPEKLTTAQLIA WITSWVDRSANAIGL ILNINQIWLYGRSCAF TIIRQTGPNPFTRDEG IGFGQLSRAQQGVDL QGIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNFAPP FFTEHNATFPARSCVI DVKIEIEAIAMLYTGS SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	PPKVEGKDDVTGE	RVYHVKFNPPKVE						ļ
AKVDGTKPQIYRGSL HTVNPDGVVCDCGR VASLSALKQARVW TOLDPEKLTTAQLIA- WITSWVDRSANAIGL ILININQIWLYGRSCAF TIIRQTGFNPFNDRDG IGFOQLSRAQQVDL GQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFAPV FFTEHNAITPARSCVI DVKIEIEAIAMLYTO SAVRYPRGNASGVEL IGKGIVKRGEKLAIL PEAAKVAESINATLV PLDEALLEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	EETVRKRLVEYH	ELTTRKDDQEETVI						
HTITNPEQUVCDCGR VASLSALKKQARVW TQLDPEKLTTAQLIA WITSWYDRSANAIGL ILNINGJWLYGRSCAF TURQTGFNPFDRDEG IGFGQLSRAQQGVDL QQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFA FFTEHNATFPARSCVI DVKIEIGAIAMLYTTO' SAVRYPRGNASGVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	YSKEAEAGNTKY	QMTAPLIGYYSKE/						
VASLSALK KQARVW TQLDPEKLTTAQLIAA WITSWVDRSANAIGI ILNINQIWLYGRSCAF TIIRQTGFNPFDRDEG IGFGQLSRAQQGVDL GQIPVNPKTGEVPAD QSLDNV KAIVEAGI KTTVFVKDLNDFAPV FFTEHNATFPARSCV' DVKIEIEAIAMLYTG SAVRYPRGNASGVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALLEMA ASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	QIYRGSLYVSDQIG	AKVDGTKPQIYRG:				l		
TOLDPEKLTTAQLIA/ WITSWVDRSANAIGL IILNINQIWLYGRSCAF TIIRQTGFNPFDRDEG IGFGQLSRAQQOVDL GQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFAPA FFTEHNATFPARSCVI DVKIEIEAIAMLYTG SAVRYPRGNASOVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALLEMAASHE, NAIMGGAGSVNEVI VPVLNIGLPDFFIPQG	VCDCGRYGCLET	HTIVNPDGVVCDC				1		
WITSWVDRSANAIGL ILNINQIWLYGRSCAF TIRRGTGFNPFRDEG IGFGQLSRAQQGVDL GQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVEDLNFAF FFTEHNATFPARSCVI DVKIELEAIAMLYTG SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE, NAIMGGAGSAVNEVI VPVLNIGLPDFFIPQG	QARVWLKSQPVS	VASLSALKKQARV			ŀ			
ILNINOJNLYCRSCAF TIIRQTGFNFFDRDEG IGFGQLSRAQQAVDL GQIPVNFKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFAPV FFTEHNATFPARSCVI DVKIEIEAIAMLYTG SAVRYPRGNASGVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALLEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	TAQLIAAWQSGEP	TQLDPEKLTTAQLI.						
TIIRQTGFNPFDRDEG IGFGQLSRAQQSVDL GQIPVNPKTGEVPAD QSLDNVKAIVEAAGL KTTVFVKDLNDFA FFTEHNATFPARSCVI DVKIEIAIAMLYTTÖ SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESINATLV PLDEALILEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	SANAIGLSLYNFLN	WITSWVDRSANAIO						İ
IGFGQLSRAQQGVDL GQIPVNPKTGEVPAD QSLDNVKAIVEAGL KTTVFVKDLNDFAPV FFTEHNATFPARSCVI DVKIELAIAMLVTGV SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPGG	GRSCAFGENWLN	ILNINQIWLYGRSC						
GQIPVIPKTGEVPAD QSLDNVKAIVEAAGI KTTVFVKDLNDFAPV FFTEHNATFPARSCVI DVKIEIEAIAMLYTÖ SAVRYPRGNASGVEL IGKGIVKRGEKLAIL PEAAKVAESLNATLV PLDEALLEMA ASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPGÖ	FDRDEGPSVKATQ	THRQTGFNPFDRDF						
QSLDNVKAIVEAAGL KTTVFVKDLNDFAPV FFTEHNATFPARSCVI DVKIEIEAIAMLYTG) SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE, NAIMGGAGSCVNEVI VPVLNIGLPDFIPQG	QQGVDLGNMIITS	IGFGQLSRAQQGVI						
RTTVFVKDLNDFAPV FFTEIMATFPARSCVI  DVKIEIEAIAMLYTG SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFFIPGG	GEVPADVAAQAR	GQIPVNPKTGEVPA				ŀ		
FFTEHNATFPARSCVI DV KIEIGAIAMLYTTÖY SAVEYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESINATLV PLDEALILEMAASHE. NAIMGGÄGSVNEVI VPVUNIGLPDFFIPGÖ	VEAAGLKVGDIV	QSLDNVKAIVEAAG			1			l
DVKIEIEAIAMLYTGY SAVRYPRGNASOVEI IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALILEMASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFIPGG	LNDFAPVNATYEA	KTTVFVKDLNDFA			l			
SAVRYPRGNASGVEL IGKGIVKRRGEKLAIL PEAAKVAESLNATLV PLDEALLEMAASHE. NAIMGGAGSGVNEVI VPVLNIGLPDFIPGG	PARSCVEVARLPK	FFTEHNATFPARSC						
IGKGIVKRRGEKLAIL PEAAKVAGSLNATLV PLDEALILEMAASHE, NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	MLYTGYHYNDAP	DVKIEIEAIAMLYT						
PEAAKVAESLNATLV PLDEALILEMASHE NAIMGGAGSQVNEVI VPVLNIGLPDFIPPG	NASGVELTPLEKLP	SAVRYPRGNASGV						1
PLDEALILEMA ASHE. NAIMOGAGSOVNEVI VPVLNIGLPDFIFPOG	GEKLAILNFGTLM	IGKGIVKRRGEKLA				l		
NAIMGGAGSGVNEVI VPVLNIGLPDFFIPQG	SLNATLVDMRFVK	PEAAKVAESLNATI				l		
VPVLNIGLPDFFIPQG*	MAASHEALVTVEE	PLDEALILEMAASH				l		
	SGVNEVLMAHRKE	NAIMGGAGSGVNE				İ		
				1		l		1
I I I I ELGLDAAGMEAKIKA		ELGLDAAGMEAKI				İ		1
26087 56455 A 26234 935 1020			1020	935	26234	A	56455	26087
26088 56456 A 26235 145 373		i	373	145	26235	A	56456	26088

SMYIKQ SMYIKQ SMYIKQ VFISMV DKYVAY NVTSPSG FLERKSL GEAILHA ARCHYG PPEEEKG NPMGDL DIIPDVTF PEEEKG NPMGDL DIIPDVTF KSDQVI VKGLRY VKGLRY VKGLRY VKGLRY KKAVM
SMYIKQ VFISMV DKYVAY NVTSPSG ILERKSL GEAILHA PEEEEKG NPMGDL DIIPDYTF PSADIRA HIPEDIH WEWENLH KSDQVI VRGLRY PPLKNY
VFISMV DKYVAY NVTSPSG ILERKSL GEAILHA RCHYG PEEEKG NPMGDL DIIPDYTF PSADIRA IHPEDIH HEWENLF KSDQVI VRGLRY PPLKNY
VFISMV DKYVAY NVTSPSG ILERKSL GEAILHA RCHYG PEEEKG NPMGDL DIIPDYTF PSADIRA IHPEDIH HEWENLF KSDQVI VRGLRY PPLKNY
DKYVAY NVTSPSG ILERKSL GEAILHA IRCHYG PEEEKG NPMGDL DIIPDYTF PISADIRA IHPEDIH IEWENLF KSDQVI VRGLRY PPLKNY
NVTSPSG FLERKSL GEAILHA RCHYG PEEEKG NPMGDL DIIPDYTF PSADIRA HPEDIH HEWENLF KSDQVI VRGLRY PPLKNY
TLERKSL GEAILHA RCHYG PEEEKG NPMGDL DIIPDYTF PSADIRA HPEDIH EWENLF KSDQVI VRGLRY PPLKNY
GEAILHA ARCHYG PEEEKG NPMGDL DIIPDYTF PSADIRA HPEDIH EWENLF KSDQVI VRGLRY PPLKNY
RCHYG PEEEKG NPMGDL DIIPDYTF PSADIRA HPEDIH EWENLF KSDQVI VRGLRY PPLKNY
PEEEKG NPMGDL DIIPDYTF PSADIRA IHPEDIH EWENLF KSDQVI VRGLRY PPLKNY
NPMGDL DIIPDYTF PSADIRA IHPEDIH EWENLF KSDQVI VRGLRY PPLKNY
DIIPDYTF PSADIRA IHPEDIH EWENLF KSDQVI VRGLRY PPLKNY
PSADIRA IHPEDIH EWENLH KSDQVI VRGLRY PPLKNY
IHPEDIH EWENLF KSDQVI VRGLRY PPLKNY
EWENLF KSDQVI VRGLRY PPLKNY
KSDQVI VRGLRY PPLKNY
VRGLRY PPLKNY
PPLKNY
KKAVM
MSSLLY
IKAFSFG
PSERRIL
GAEHFO
PFTGEPL
QFGWRC
DGDPTL
RSQPWE
GTPNAG
CCCGPM
SRLIHH
MAAAR
TERAAM TALSAQT
GTLFTYA
ELIPLSK
/AVHINA
WSGRNA
MEFEDK
RIIANED
KTIDRT
VEEYRA
VHRVPR
ATVAPV
ERPSTTR
ERPSTTR VKTEPK
VKTEPK
VKTEPK STKAPA
VKTEPK STKAPA QTASPA
VKTEPK STKAPA QTASPA VĢSLKS
VKTEPK STKAPA QTASPA VGSLKS DNLNGW
VKTEPK STKAPA QTASPA VGSLKS DNLNGW RNGQP
VKTEPK STKAPA QTASPA VGSLKS DNLNGW
FACOUNT

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26091	56459	Α	26238	732	1025	HEAKRTGRSYWFTAV*WLRG
						WRRMVARQNAKNCWHGTFFR
						VARVSLPISAHASSTHLSGSAH
		l				YVPPSAYRNSRRYSRGLCRCRV
				l		SSCDAATGVVVPQ
26092	56460	Α	26239	1905	3087	RVCSCDAGTLHWLQNLRCGLP
						VWCDGSGGTSGDPQQRRGSEC
						TG*QSRSQ*MRPVQPS*RRPGV
	İ	l				YGGLPDS\WLICVDRNKLEQLT
						PEKRRQAKLRAMKPDEFAQIQ
						QAVITQMLQHPQTLGEEASKLS
		1				KDFDRGNMRFDSRDKIVAQIKL
		ı				VTPQKLADFFHQAVVEPQGMA
		l				ILSQISGSQNGKAEYVHPEGWK
		l				VWENVSALQQTMPLMSEKNEQ
		l				NLYDCGALFAPVTWTSGSAAF
	i	1			I	PRPLTVEELLVVTFTEAATAEL
		l				RGRIRSNIHELRIACLRETTDNP
		1				LYERLLEEIDDKAQAAQWLLL
	1	ĺ				AERQMDEAAVFTIHSFCQRML
		l				NLNTNECCFQRTTKTIHRDSFK
		l				STPRAAKSCSGLLPALAPSQISS
						NTPIQPLSRFKFSGVTSPTSAAS
26093	56461	Α	26240	1	2235	
26094	56462	A	26241	166	416	CHVVGPFRVRRNLISAQH\PLTL
		1		ĺ	1	NS\RHTTTRAARRLLRYFGTPR
		1			l .	YRHSIDIHMQLDMTTSRSLSSL
	1					RDQLHCRWLLPAERQAI

SEQ ID	SEQ ID NO:			Nucleotide	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or pepade sequence	decease, (~possible indecestate insertion)
26095	56463	A	26242	h .	2084	I Imlfplatsgamepfpflagtag
20093	30403	A .	20242	'	2004	ALVGGLONIGSGVLASLSAMLE
	1	ł				OTGOPGVVDDLNGIVDRAVLA
		l			1	AAGDADVASGAARLSARHRSI
	1	1			İ	VISSMGERCCFIRSRITRICGHW
1	l	ŀ	ļ			
	1	1				CPQGNEIPVVAVASHDTASAVI
	1	1				ASPLNGSRAAYLSSGTWSLMG
					ŀ	FESQTPFTNDTALAANITNEGG
						AEGRYRVLKNIMGLWLLQRVL
	1	l			ŀ	QEQQINDLPALISATQALPACRF
		l				IINPNDDRFINPETMCSEIQAAC
	1	l				RETAQPIPESDAELARCIFDSLA
		l			ĺ	LLYADVLHELAQLRGEDFSQL
ļ	ŀ	l				HIVGGGCQNTLLNQLCADACG
	l	l				RVIAGPVEASTLGNIGIQLMTLE
ļ	i i	l			ľ	ELNNVDDFRQVVSTTANLTTFT
	ŀ					PNPDNSLYTTDKGALRMTTQL
		1			Ì	EQAWELAKQRFAAVGIDVEEA
						LRQLDRLPVSMHCWQGDDVSG
	1	1				FENPEGSLTGGIQATGNYPGKR
	1	1				VMPVSYVPIWNSTLSLSGSNWF
		1				NRKALGSPARYDVLPKWWRN
	1	l			1	VVKPTRTRLYIGIAFYKVGEPS
	1	l			*	KIEPDWMINGGVPELKKQLDL
1	İ	l			İ	NDAVPEISGTILFREDYRNKPQT
	1	1				QQAADPPIRAKAAEIAVAHAH
	1	l				YLSIEFYRIVRIDPHAEEFLSNEQ
	1	1				VERQLKSAMERWIINVLSAQIR
1	1	1				PQPAVT\HYRGLATVEMPVATG
-		l				RYPTTRY\GLVELEPKTGRKHQ
		1				LRRHLAHLRHPIIGDSKHGDLR
						QNRSGAEHFGLQRMER
26096	56464	Α	26243	1	2871	
26097	56465	A	26244	690	824	
26098	56466	Α	26245	950	1484	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
26099	56467	Α	26246	1	2625	MVAFYRHAGRMWPGIALSCSL GNIAASILLFSTSSLNMTWTTINI
	ŀ					VEAVVGAVLLRKLLPWYNPLQ
	l				ŀ	NLADWLRLALGSANSAGVNIS
						TATVCRQCEDAPCANVCPNGAI
	ŀ					SRDKGFVHVMQERCIGCKTCV
	i					VACPYGAMEVVVRPVIRNSGA
			l			GLNVRADKAEANKCDLCNHRE
						DGPACMAACPTHALICVDRNK
						LEQLSAEKRRRIPGNIRRIRSGR
						YRRPVTAGCDAVVSGRAGYAI
						HDGGNNSMAKNTSCGVQLRIR
						GKVQGVGFRPFVWQLAQQLSH
						GSRMRDGTCNLKYDEYSRSGS
						MQYNPLGKTDLRVSRLCLGCM
						TFGEPDRGNHAWTLPEESSRPII
		1				KRALEGGINFFDTANSYSDGSS
						EEIVGRALRDFARREDVVVATK
						VFHRVGDLPEGLSRAQILRSIDD
				ŀ		SLRRLGMDYVDILQIHRWDYN
						TPIEETLEALNDVVKAGKARYI
		1				GASSMHASQFAQALELQKQHG
						WAQFVKSDENDAPDRQSGSTG
		1				SQCKNCGADTEPQVAAGPGLS
		1		ļ		ELNPVHCPHLHYRAHFRADRH
		l				SVACSLLDTPVTGHQVAPTYRQ
					1	QVPRAGQVHDPSKHTRMPCEN
		1				IDPVRTIIRRISDPPVPASATLGA
-		l				SKASRIRPRRSHSIPEITAKSRKP
		l	ŀ			GGQPKWQVICWLDRDEKVVV MOTVRDOIGOHVFTAHRLDRP
		l				TSGVLLMGLSSEAGRLLAQQFE
2//00	*****	ļ	0.00.10		1033	13GVELWIGESSEAGKELAQQFE
26100	56468	Α	26247	1	1833 517	MRNKLSFDLOLSARKAAIAERI
26101	56469	Α	26248	l¹	317	AAHKIARSKVSVFLMAMSAGV
						FMAIGFTFYLSVIADAPSSOALT
					ŀ	HLVGGLCFTLGFILLAVCGTSLF
		l				TSSVMTVMAKSRGVISWRTWL
						INALLVACGNLAGIACFSLLIWF
						SGLVMSENAMWGVAV\YTAPR
26102	56470	<b> </b> _	26249	3117	3527	AKCIIHLLNLSASALCAI EAVHRLARYRDAPRRS**SPLL
26102	30470	Α	20249	3117	3341	CASVYP*LEQVPLQAQAVVPLR
		l				VLQAGKPVVPVAVLNAQAAAL
		ı		1	1	
		l	1	1	1	ARPVAKLAAATAVQAAADRQ
1		l				AAAPAALDAEHVAAVPALQAA
		1			1	AGPVDAAAQTHKAVGTGVAA
	L	L			L	TDEQPHAPER

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26103	56471	A	26250	2	563	STTSSTTAFSATTAGTPSTONTP SASPIWRRPNFWARKVYLLHW FCHROPSKEVLFHLALYRNNPR CKAVVHLHSTWSTALSCLOGI DSSNVIRPFTPYVVMRMGNVPL VPYYRPGDKRIAODLAERETH NHAFLLANHGPVVCGESLQEA ANNMEELEETAKLIFILGDRPIR VITAGEJELRS
26104	56472	A	26251	2	1481	PENQINKLKQAIPADYRSHQKC VNQPSSPTITPRIFAITVITDERG YATGSAGNISL/LLPDGNILLAT PT/GSCLGWILDPGNFSKVAADG EWL/SGOKPSK/EVLFHILALYR/ NNPRCKAVVHL/HSTWST/ALS CLQGLDSSNVIRPFTPYVWMR MGNVPLDLAELA/DNQAFLL ANHGPVVCGE/SLQEA ANNME ELEETAK/JEI-GDRPIRYL/TAG VCPLAKMLNGTGQYLSIKRCT NNRSVRGTCSAPRAGFKGYGL LYSYHRASACADSTTLTVLISY THLLVNSYSTVPPLEGSCTOP SPSFPTRVSDDHNRDFFFLLSPC GLLQWLAQCIRQVGJQLDFGCV GATSSPGAISFEQTVNARSHVL RVTLTLGLTRPMLYYTGSLKWI NICILIPISLKPRTYJELAQFT ANTICLTRPMLYYTGSLKWI NICILIPISLKPRTYJELAQFT ANTICLTRPMLYYTGSLKWI NICILIPISLKPRTYJHLAQFT ANTICLTEPMLYYTGSLKWI NICILIPISLKPRTYJHLAQFT ANTICLTEPMLYYTGSLKWI NICILIPISLKPRTYJHLAQFT ANTICLGRAFT
26105	56473	A	26252	1	413	
26106	56474	Α	26253	3	247	
26107	56475	Α	26254	300	665	
26108	56476	Α	26255	1	1854	
26109	56477	Α	26256	1	1611	
26110	56478	Α	26257	942	1040	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
26111	56479	A	26258	1616	3678	PLAKTGRQREQLAGLAK/AHPS
20111	30473	n	20230	1010	3070	LTLHODPVYVTRADAPVAGKV
		1				ALLSGGGTEHEPMHCGYIGOG
		1		i		MLSGACPGEIFTSPTPDKIFECA
		1				MOVDGGEGVLLIKNYTGDILN
		1			1	FETATELLHDSGVKVTTVVIDD
		1		l		DVAVKDSLYTAGRRGVANTVL
	:	ı				IEKLVGAAAERGDSLDACAELG
						RKLNNOGHSIGIALGACTVRSA
			ŀ			GKPSFTLADNEMEFGVGIHAIL
						KGDIPEAEAILASIKPAGVVSRA
						DVVLPNOFOALRKSFIPERPVP
						VMVTRLFELPVQISLGVYSLER
		1				PANPOPIAYLVLOPRRKANNON
						ASTSAIIRATIGEPISCSVPSRGC
				l		EGGISVAETVPAMIIAIGITISEG
						LDARYRHVNSEHDPSDROAKF
						EWRYFGNLGKTVNDWRKNNK
1						ADIKEDGNRRCRHTNOPHCRIE
		l				AVEYDDGRLCPLHGAHRGQSS
						DGELVKPTVKTQSLAVHYSIGK
	1			l		LRHRPNHGAVYYORLRSGMGL
						MNAFDSQTEDSSPAIGRNLRSR
						LARKKLSEMVEEELEQMIRRRE
ĺ		l				FGEGEOLPSERELMAFFNVGRL
		l				RAGSVKTQRSGANKQRRTRCV
		l				SRPSADTIIGELSGMAKDFLSHP
		1				GGIAHFEOLRLFFESSLVRYAA
		1		l		EHATDSRDPRYRPKFYSISRSVP
	İ	l				VSDNITLOOLLISLNDOPARCK
	Ì	l				PSARCRLHGSHTSRYECNHRHG
26112	56480	A	26259	185	775	IPEIFSGETHLKVSTLSKPTFSISS
120112	50 100	ľ.	20257	1.05	1,,,,	LIRCTTRFSSQLSLGIATMSHRK
		l				RVISALKSLSRLSANSLVFANQ
		1				VERSSLTNLGCTRCSG*SLFWO
		l	1	1		RPALR*PFGLCPTVALTYLIVSP
		l	1	I		EW*KAVSVKCWRNRRLTLMTS
		1	1			PICTNSGTLTTAPVDRVAQVTF
		l	1			OSPECLOHMRLTIALRYFRVAL
		l				SRRLLVYASVCFTFSG
	l	1_	l			SKKLLV I ASVCF IFSU

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26113	56481	A	26260	301	1313	RLEHDGVCLHRANHRYPGCRL
						HLDYVEPQLQHDDALRAAVM
		l				MFKQYLQVTKPGIIFGNLISVIG
		l				GILLASKGSIDYPLVIYTLVGVS
		l				LVVASGCVFNNYIDRDIDRKME
		1				RTKNRVLVKGLISPAVSLVYAT
		1				LLGIAGFMLLWFGANPLACWL
	i	1		ł		GVMGFVVYVGVYSLYMKRHS
	ì					VYGTLIGSLSGAAPP\VIGYCAV
	ŀ	1				TGEFDSNAAILLAIFSLWOMPH
		1				SYAIAIFRFKDYQAANIPVLPVV
l				1		KGISVAKNHITLYIIAFAVATLM
						LSLGGYAGYKYLVVAAAVSV
						WWLGMALRGYKVADDRIWAA
	1	l	ľ			QSCSGFSIIPITALSVMMSVDFM
		l				VPDSHTLLAAVW
26114	56482	Ā	26261	3631	4078	CFLNFKTLLLVHLFRRVFLRIRL
20114	30482	l^	20201	3031	4078	RHRKLHPVGLGGPVNKAAYAF
						CLGAMANGVYGPYAIFASVKM
	1	l		ŀ		VSAFTVTASTMLAPR\WLLGLA
	1	l	1			GITEGAIPMAIEDPLRVIGSFVL
	1	l				GSMVTGAIVGAMNIINRTLRVE
						ASVTSAQIVQTIIRLRR
26115	56483	A	26262	814	2126	CTGCRKQRLPVVQGFAAGLAA
20113	30483	l^	20202	014	2120	NMIGSGFLGAVVGGLIAGYLM
	1	i				RWVKNHLRLSSKFNGFLTFYL
						YPVLGTLGAGSLMLFVVGEPV
	1					AWINNSLTAWLNGLSGSNALL
1		1				LGAILGFMCSFDLGGPVNKAA
		ı				YAFCLGAMANGVYGPYAIFAS
	1	l				VKMVSAFTVTASTML\APRLFK
		l				EFEIETGESTLLLGLADITEGAIP
		l		i		MAIEDPLRVIGSFVLGSMVTGA
	l	l				IVGAMNIGLSTPGAGIFSLFLLH
	İ	ı				DNGAGGVMAAIGWFGAALVG
	1	1				AAISEGKRIFRYRDLIIVNSNOL
	1	1				FLHDHRFPRWEGLESVFFLLAA
1			I	l		FQQDVGIWPPLGAMLGLATAV
l				l		VLGFLLYWGGIRLNLGAFFKW
		1		l		TSLFILFVAAGLAAGAIRAFHEA
				I		GLWNHFQEIAFDMSAVLSTHSL
				l		FGTLMEGIFGYQEAPSVSEVAV
		ĺ		[		
26116	56484	A	26263	1	525	WFIYLIPALVAFALPPRAGATAS
26117	56485	A	26264	1	700	
26118	56486	A	26265	1	1428	
26119	56487	A	26266	254	475	RDOLVSELNOMLV*KSAFRMA
	,				l	ALITSRWPMVTHWFREVRRGN
l	1	1				WROFLPALTLLVRLSLMLMGR
		1				OAILRSRRNY
		∟	L	L	l	Aurenouna.

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
26120	56488	A	26267	1	1657	MLIQRRRLAFDRAKHRRAEML
		1				AQRARGEEEAHHHSSPEGAIEV
						DESEVDLDAISAQSLRLVRSILM
1						LIALLSVIVLWSEIHSAFGFLEN
						SLWDVTSTVQGVESLEPITLGA
	ŀ					VLIAILVFIITTQLVRNLPALLEL
						AILQHLDLTPGTGYAITTITKYL
l	ŀ					LMLIGGLVGFSMIGIEWSKLQW
						LVAALGVGLGFGLQEIFANFIS
						GLIILFEKPIRIGDTVTIRDLTGS
					l	VTKINTRCHTHRRQQLLLQQA
						ATSSADVIYLGEAVCSKRRATK
	İ					VGDWLEMAKSLAGSGKOIVLS
	İ				i	TLALVQASSELGELKRYVENGE
	İ					FLIEASDLGVVNMCAERKLPFV
	ľ					AGHALNCYNAVP\LKILLKQGM
	ŀ			l		MRWCMPVELSRAWLVNLLNQ
						CDELGIRNQFEVEVLSYGHLPL
					ĺ	AYSARCFTARSEDRPKDECETC
	į.					CIKYPNGRNVLSQENQQVFVLN
						GIQTMSGYVYNLGNELASMQG
İ	i					LVDVVRLSPQGTDTFAMLDAF
	i				ŀ	RVNENGAAPLPLTANSDCNGY
						WRRLAGLSLRQIKTCLIFLLCQF
						RGRRPYRTRAMPPILTMPANSP
26121	56489	A	26268	482	605	
26122	56490	Α	26269	1	298	MWPGMVTHAVRIPLHNDTVTL
						SDNFQPFAGTDAMTITRPLEML
	ŀ	l				RDGKCPQPDWISSEGACAGNA
						TDSPHPFELKAGKTITLEDGRQI
	i	1				NGADYLAAPVPGKALAIFGDT
	ł			1		GPCDAALDLAKGVDVMVHEA
						TLDITMEAKANSRGHSSTRQAA
						TRESELFRYTVKHSLIFASVIGII
	1					TLLQASTKIYTPGRKEQGEPMT
				ĺ		PRRTPARF*IKSGQNNHAGRWK
l	1			l		AD*RRRLLSCSSAR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26123	56491	A	26270	1	1707	MTRDGLANKALAVARTLADSP
20123	120131	ı	202.0	·		EIRQGLQKKPQESGIQAIAEAVR
						KRNDLLFIVVTDMQSLRYSHPE
						AORIGOPFKGDDILKALNGEEN
						VAINRGFLAQALRVFTPIYDEN
						HKOIGVINDSRWSIIWSVLFGM
						LVGLIGTCILVKVLKKILFGLEP
			1			YEISTLFEOROAMLOSIKEGVV
						AVDDRGEVTLINDAAQELLNY
						RKSODDEKLSTLSHSWSOVVD
						VSEVLRDGTPRRDEEITIKDRLL
	1					LINTVPVRSNGVIIGAISTFRDKT
						EVRKLMORLDGLV/NLC*RTS*
						TIPLRAHSPQSKSAIYHEIAP*NA
			ĺ			PAFYRRKCHCADIFLPYF*TCR\
		ļ				RDRAMSAYLRYIVQKADSSFL
						YDKYQNQSIAAHVMRALAAEQ
		1	İ			SEVSPEORRAICEAFESANNTH
		l		İ		GLNLTAHKYPGLRGTLQTAST
		1				DCDTIVEAAALLPAFDQAVEGN
	1					RHQDDYGSGLGMAEEKFHYYL
	1				ł	DLFRAVGDGHNSKEDATFGLG
		l	ŀ			WRVNGNATMTPTFGTLASPQT
		1				YGHTGWTGTVTVIDPVNHMTI
		l	l			VMLSNKPHSPVADPQKNPNMF
						ESGQLPIATYGWVVDQVYAAL
26124	56492	A	26271	257	817	TSSRCISLRTSVLSLKVEMAPMI
						TPLLRTGTVLISNSRSLIVISSSR
						RGVPSRNTSETSTTCDHEWLSV
			ŀ			DSFSIVLRLTVIQQFLCGIVDQR
			l			DLAAIVHGNDAFFDRLQHGLA
					•	LLKQRGDFVGFQAEKDFFQYL
						NQNAGANQSDQHAK*Y/LTR*C
				i		SSDCH*SVGSHGLTQGRSPPRQ
			l			FVYDFHRRWG
26125	56493	Α	26272	I	2700	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
1		1		sequence		
2612 <b>6</b>	56494	A	26273	1	1038	MGCLDLGDGRAGSVARYFRRY
		1			ļ	RPPCDA ALDLAKGVDVMVHEA
1		l				TLDITMEAKANSRGHSSTRQVL
1		l				KKILFGLEPYEISTLFEQRQAML
						QSIKERSRRHRLPKEKKIMTPTI
	ŀ				1	ELICGHRSIRHFTDEPISEAQRE
		l		ł		AIINSARATSSSSFLQCSSIIRITD
İ		l				KALREELVTLTGGQKHVAQAA
	ŀ	1				EFWVFCADFNRHLQICPDAQLG
1		1				LAEQLLLGVVDTAMMAQNALI
1		1				AAESLGLGGVYIGALRNNIEAV
1						TKLLKLPQHVLPLFGLCLGWPA
						DNPDLKPR\LPASILVHENSYQP
		l				LDKAALAQYDEQLAEYYLTRG
ļ			l	1		SNNRRDTWSDHIRRTIIKESRPFI
		1				LDYLHKQGWATR
26127	56495	Α	26274	I	1338	
26128	56496	Α	26275	2	375	HSDPEASGPLTRLRAMEQRRVT
						DFFARRRTPGSVPSTDRR*TIVR
						MIPCTSSGRRTKAMVILRTSLV
1						NPASNE/CATELFNALDVSIQNP
1						RMIISP*IQHRTELSGSPLVAVG
						RMCSLTPRVIFEH
26129	56497	Α	26276	219	767	RFTQGKGPINNPAVIRPLDFPQN
i		1				GSRPLANQ\IFTTSLKVGDYFGK
		l				RHKDVLRAIRNLKCSDDFTQRN
		l				FAPIDFIDKNGDVQPMYNITRD
		l				GCMMLVMGFTGKTAAAVKEC
1		1			1	YINAFNWM\AEQLNRRMAMGE
		1			Į.	ELQHRYAIKETRSKLKGTIG\TR
		1				LMNERKKEKRVLELEHEHIMQ
						VTQPELLIG
26130	56498	A	26277	16	104	HICQSAPL*RGSSGLNGYGQYR
						PAGFLDG
26131	56499	Α	26278	3	399	
26132	56500	Α	26279	1112	1831	TGIRNCAPLSLTWKSKTANRKV
		1				RCGHIRYPLADGAKTSDGKDY
						LVVATTRPETLLGDTGRSRLTR
						KIRVTKELIGKYVILPAGTAPGV
						RQGPVWMPGDEVKKVTCKNG
		1	l	1	I	VVNEIWTRNHADIPLRPRFAVL
		1	l		I	ASGSFFSVGLVAERNGIREPILG
		1	l		l	LDVLQTATRGEWYKGDFFAPQ
		1	l	1	I	PWQQFGVTTDET/LRPSQAGQT
		l			1	IENLFAIGSVLGGFDPIAQGCGG
		l				GVCAVSALHAAQQIAQRAGGQ
26133	56501	Α	26280	3	790	
26134	56502	Α	26281	334	609	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
26135	56503	A	26282	1	1338	I MTRHYGAEATNALLPGKASKH
20133	30303	^	20202	1'	1550	QIVGCGVNALSDLDPRRPDKTR
						SVASGIGAALLLRLIKTLADDL
ŀ	İ				l	ONLTDLSVFNGERYKDAOHVV
		1				IRAAGEKNQAFIAGARHDLGGE LGVGLVWIPASKVNGIMGPSPV
1						WLTFRVSNIAGESAEGLLVTKP
						KNYDQVPANKPIVDAIKAKKQ
		1	ľ		ŀ	DPSGAFVWTTYAALQSLQAGL
l		1				NQSDDPAEIAKYLKANSVDTV
		1			İ	MGPLTWDEKGDLKGFEFGVFD
1		1				WHANGTATDAKRYCANVKGV
						NPDTQEPSPSGVKVNDPKVDER
						LIRQEAGMVFQQFYLFPHLTAL
		1			İ	ENVMFGPLRVRGANKEEAEKL
		ı			İ	ARELLAKVGLAERAHHYPSELS
l						GGQQQRVAI\ARALAVKPKMM
		ŀ				LFDDPTSALDPELRHEVLKVMQ
		l				DLAEEGMTMVIVTHEIGFAEKV
		1				RSRLIFIDKGRIAEDGNPQVLIK
						NPPSQRLQEFLQHVS
26136	56504	A	26283	1170	1575	DPPVLVQRDANSTVRFPHASAS
		1				ADPAGDIPPIF\AQAAGADLVY
		1				VGVEPPKPKAEVILVAEYSPIKT
	ŀ	1				VADLGCPLHVQKVSRYPPEFTQ
ł		1				VITPVQCYVTIDALGQYAAWT
		ı			i	RANMTYRPGSNIIQNLGNDIRL
		_				RTVQ
26137	56505	Α	26284	3	1351	RTAPETPNQRPATLDSGILGGYI
		1			Į.	APDNLTITFIGGHSLFDERFCLA
	ŀ	1				HRCQKAAEDDAFPHDSLDAAS
		1			i	LLEYAREKLNGLDVEVYHWNL
		1				QNFAPEDLLYARFDSPALKTFT
		1				EQLQQADGLIVATPVYKAAYS
	ŀ	1	l			GALKTLLDLLPERALQGKVVLF
		ı				LATGGTVAHLLAVDYALKPVL
		1				SALKAQEILHGVFADDSQVIDY
		1				HHRPQFTPNLQTRLDTALETFW
		1				QALHRRDVQVPDLLSLRAPKP
		1				KAEVILVAENSPIKTVADLKGH
		1			I	K/VAFQKGS/SSHNLLLRA/LRQ
	1	1			1	AGLKFTDIQPTYLTPADARAAF
		1				QQGNVDA WAIWDPYYSAALL
		1	1		l	QGGVRVLKDGTDLNQTGSFYL
	1	1				AARPYAEKNGAFIQGVLATFSE
		1			1	ADALTRSQREQSIALLAKTMGL
	1	1			1	PAPVIASYLDHRPPTTIKPVNAE
		1			l	VAALQQQTADLFYENRLVPKK
		1	1			VDIRQRIWQPTQLEGKQL
		_			·	, , , , , , , , , , , , , , , , , , , ,

			Nucleotide	[Nucleotide location of last	Amino acid sequence ( X=Unknown,
of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
56506	A	26285	364	1937	KLSGRHCTAAMFRFLTFCLCEG
					MPMRNIIKLALAGLLSVSTFAD
					AAESSPEALRIGYQKGSIGMVL
			1		AKSHQLLEKRYPESKISWVEFP
					AGPQMLEALNVGSIDLGSTGDI
	İ				PPIFAQAAGADLVYVGVEPPKP
		l			KAERILVAENSPIKTRTDLKGH
					KGAFQKGFSSHNLLLRALRQA\
					GLKFTDI\QPTYLEPRWRPRAA\
	1		1		FQTRGTVDA\WAIWDPYYSAA
					LLQGGVRVLKDGTDLNQTGSF
	1				YLAARPYAEKNGAFIQGVLATF
					SEADALTRSQREQSIALLAKTM
ĺ	İ				GLPAPVIASYLDHRPPTTIKPVN
					AEVAALQQQTADLFYENRLHY
1	l			ļ.	SEYCRPMVSVGNWFLDGSHSV
					FSYDALDRLVQQGGFDGRTQR
l			l	l	YHYDLTGKLTQKQWQYDGHG
				ŀ	WLTDISHLSEGHRVAVHYGYD
					DKGRLTGECQTVENPETGELL
					WQHETKHAYNEQGLANRVTP
					DSLPPVEWLTYGSGYLAGMKL
					GGTPLVEYTRDRLHRETVRSFG
					SMAGSNAAYEMTSGTELIDLC
56507	Α	26286	511	1152	SVRFNIVFHFMRLLRFCCVLDH
	l				LICFTSPVNTFLRYNAFTLCNGE
	l	1			FGMSHPALTQLRALRYCKEIPA
l					LDPQLLDWLLLEDSMTKRFEQ
i					QGKTVSVTMIREGFVEQNEIPE
					ELPLLPKESRYWLREIL\LCADG
					EPRLAG\RTVVPVSTLSGPELAL
					QKLGKTPLGRYLFTSSTLTRDFI
			-		EIGRDAGLWGRRSRLRLSGKPL
	1				LLTELFLPASPLY
56508	В	26287	184	415	
56509	A_	26288	15	87	
56510	Α	26289	78	157	CKRYGKARDTG*QPRTQKCTC CELDE
	56507 56508 56509	56506 A  56507 A  56508 B  56509 A	56507 A 26286  56508 B 26287  56509 A 26288	Sequence   99/40,217   codon for peptide	1937   1937

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		-
26143	56511	Α	26290	1	1817	MTSAISLGSRCSGRIPSDIIGSNL
		l				DITAFNWQPDLLTIWHRQLHLH
		l				LTRLDGGGHFYRQEVHLWRTD
		İ				KSGDKRRPQGDPKTTGITAKVI
		i	Į			NVRSTKLVGLPHRITATRWKR
		1			l	KRSRMLHTNTGKLVFNNRDQK
						RCTRKVMFDKALKLLDEAERL
				1		GSTSARSTIYQQCKRQGVITPHS
		l				ADFATTVRLLAHLSQERLGKLQ
		l				DSIYISLTDHCQFAIKRFQQNVL
				ĺ		LPNPLLWDIQRLYPKEFQLGEE
		l				ALTIIDKRLGVQLPKDEVGFIA
						MHLVSAQMSGNMEDVAGVTQ
						LMREMLQLIKFQFSLNYQEESL
			1			SYQRL\VPHLKFLSWRILEHASI
						NDSDESLQQAVKQNYPQAWQ
		l				CAERIAIFIGLQYQQLGLTQPAV
l	1					SKIINDIEDYFGVELVVRKNTG
			İ			VTLTPAGQLLLSRSESITREMK
İ		1				NMVNEISGEKNPGEGSEKELET
	1					VYVQAVGAHWEGNQVWLILA
						GGALFAAWPRVYAAAFSGFYV
1						AMILVLCSLFFRPLAFDYRGKIA
ļ						DARWRKMWDAGLVIGSLVPPV
						VFGIAFGNLLLGVPFAFTPQLR
				1		VEYLGSFWQLLTPFPLLCGLLS
		l	1	l		LGMVILQGGVWLQLKTVGVIH
			İ			LRSRVRIPCDLHIYAQMA
26144	56512	Ā	26291	557	808	
26145	56513	Α	26292	8	274	
26146	56514	Α	26293	523	1851	
26147	56515	Α	26294	1	589	

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
		<u> </u>				
26148	56516	A	26295	11	1848	MDLSTPERGSPYPRLLPCGDPL
						GETIVAIDQEAKPSTEDLGNKK
						ETKYIKLKVIRWDNSDFNFLYS
						NYERIRARTTKKEDSATNVPVT
						FEKHGSHAVVYARRSATVLTD
				l		RNKEAPRVPQGGYMVSFVDIPE
				l		ALTQGETVAEAMEAAKDALLT
				ł		AFDFYFEDNELIPLPSPLNSHDH
				i		FIEVPLSVASKVLLLNAFLQSEI
						TQQELARRIGKPKQEITRLFNLF
						HATKIDAVQLAAKALGKELSLI
						CLMDILNLNKHISGQFNAELES
						RTQVMTLGGMVDKQLSDAITA
						IHNQDSDLAKRVIEGHKNLNM
				l		MEVAIDEAR/C*AIIAKHQS\TAS
						D\LRLVMVI/SKTIAEMERIG\DV
		Į				GRNKICRTALEKLSQQHQP*VV
	1					S\LE\SLDRHTIQMLHDVVKAFA
		1				RMDIDETAKCQIFVEYVLKPKV
		1	1			IWLLCFANIFLYVVRIGIDQWST
						VYAFQELKLFKAVAIQGFTLFE
						AGALVGTLLWGWLSDLANGR
		1			İ	RGLVACIALALIIATLGVYQHA
					į	SNEYIYLASLFALGFLVFGPQLL
					1	IGVAAVGFVPKKAIGAADGIKG
		l				TFAYLIGDSFAKLGLGMIADGT
1		i				PVFGLTGWAGTFAALDIAAIGC
1					1	ICLMAIVAVMEERKSAARKKFS
26149	56517	Α	26296	395	1428	TSATATSTFALPRGGGYLVVSE
ı					i	WVVLRFTDIFLRIFPCDNGRTIL
į.					1	RFGIFRMLMIVAIETQQFPVTAI
						FRVIGMVVINVVNASEETNRRL
		1				HHRSLRLIOECVMDSLNLNKHI
						SGOFNAELESIRTOVMTMGGM
		ľ				VEQQLSDAITAMHNQDSDLAK
		1				RVIEGDKNVNMMEVAIDEACV
		1				RIIAKRQPTASDLRLVMVISKTI
		1				AELERIGDVADKICRTALEKFS
		1				OOHOPLLVSLESLGRHTIOMLH
		t				DVLDAFPRMDIDEAVRIYREDK
1		1			l	KVDH\EYE\GIVRQLMTYMMED
		1			l	SRTIPSVLTALFCARSIERIGDRO
1		1		I		ONICEFIFYYVKGQDFRHVGGD
1		1		1		ELDKLLAGKDSDK
26150	56518	A	26297	667	1002	DEDITED TO TO TO TO TO TO TO TO TO TO TO TO TO
26151	56519	В	26298	1	1716	
20131	100017	10	20270	ı <u>.                                    </u>	1	L

C=Unknown,
e nucleotide
eotide insertion)
GKKGDHFSV
.GGIIVSLIISS
TKEWDAPN
VTSFIALLIA
APGWLKRP
/YGMWGLFIF
NIMSNIPIVG
AGVILAIMII
QTPVMMKES
VRIVLPFTKN
LGETMAVTF
YMPGNSITSA
VAALMELG
KFMIMRRIA
FWLIWILMST
TEMTPPPNTE
LLILWATVY
TI
GLTATTAALA
SIDIAMYEV
YFNGGEMCP
CGLYQCAD
GAIDPILNECF
IPEGTQLIHRI
AWLATHTIA
AKVLTVPEL
QWQTMDGR
NPGQIWRG
KNIGYSENDI
MDRGAMDII
LADVYGHKT
YSYLELNOEI
KGDKVALHL
AKIGAIMHE
AFELTP*SGK
*ASPACSSEK
SVRSWAHFS
t towns
KGI AKI AFE *AS (SVI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26154	56522	A	26301	2	1021	TPGNNVDSIFLAFFLNOFLTLGY
		1				IMGKTISIKVLFGIYLLLMAAKV
		l				FAFSCNVDGGINGAGTTSVYV
						NLDPVIOPGONLGVDLAHHISC
1						WNGDGGWYDTDHMNLVQGS
1						AFAGSLOSYIGSLYWNNVTYPF
					i	PLTTNTNVLDIGDKTPMPLPFK
				i		LYITPVGAAGGVVIKAGEVIARI
l						DMYKIATLGSGNPSNFTWNIIT
ŀ		1				NNNAVMPTGGCTVDSRNVTVD
						LPDFPGSAEIPLGVYCSSEOKLS
		1				FYLSGATTDSSRQVFANTAPDA
		1			1	TKASGVGVTLMQRQLAGINDS
				1		HLLHYLDDEVWDNDYLATPHF
				ŀ		LLKSAILRSMNDALMTRVTGE
						KNGOVRLEEIER
26155	56523	A	26302	522	714	
26156	56524	A	26303	1	976	STCSSRSHLHLIQASPILPNYVA
		1				TAVAARIIADVQGISDTCVIAQP
		l				SPPHPGALRTLVFTTDEPETPQP
		l				PGAAGFQLVQKKQVQLHNVLY
		l		l		VMTPHAFAQGTVTIYLPGEQQT
		1		1		LSVAPLKNVVQLVTQQHLRDR
	ŀ	1				LWWPGAFLTDFAAKVKALKD/
						YPNHVMAQRASGEAEADDDV
		1			1	AATIKSVRQQLLNLNITGRLPV
i		1				KLDPDFVRVDENSNPPLVGDYT
		1		1		LYTVQRPGTEQGSFKVKRARA
		1			l	RVRQTRAPLFGPKSPAPEHMES
1						ELEFELIGPSKSTSGNPRGLRSE
İ						RPVLFCLYPEMPTAAARAILIAE
		1				EQSREVKIALVVLDRLQRE
26157	56525	Α	26304	1	1701	
26158	56526	Α	26305	1839	2038	ARSGCFVRQSCPRGRCSKNRR
				1		WRDPYDHYPARPAYCP*R/WC
İ				1		M*LSTLATPKKVSPCKPAPAAH
		<u>_</u>				RWR
26159	56527	A	26306	1	3270	
26160	56528	Α	26307	1962	2049	
26161	56529	A	26308	94	942	
26162	56530	A	26309	879	4104	TARELOVOORDUITROTACUDA
26163	56531	A	26310	879	1367	TASELGKSCSRDHTPCTASVRA
		1		1		LYYARLRHAPANDPGEDGWAL
				1		AAKPPALPPRNSLNSQAIFRDKP
				i		NLPHRSPATYRQTERG*DTRSE
						FHA*TDAIPVATRARAGEFCRQ
l		1		1	1	MFWGEDQADEQPA**ACCHRK
l		1		1	1	*PVPK*DLAMLRAPPRMDSPPD
		<u></u>	L	l	L	ASRTSDLHN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \= possible nucleotide insertion)
				sequence		
26164	56532	Α	26311	1203	1911	SRPAYHPAPREFQRQWRQDPAP
l		1				GLAITPGQQLFITIKLWNDDH\K
		l				RPREALLDSLKKLQLDYIDLYL
l		1				MHWPVPAIDHYVEAWKGMIEL
l		l				QKEGLIKSIGVCNFQIHHLQRLI
l		l		1		DETGVTPVINQIELHPLMQQRQ
l		l				LHAWNATHKIQTESWSPLAQG
	ŀ	1				GKGVFDQKVIRDLADKYGKTP
1		l				AQIVIRWHLDSGLVVIPKSVTPS
		1				RIAENFDVWDFRLDKDELGEIA
		1				KLDQGKRLGPDPDQFGG
26165	56533	Α	26312	3	793	
26166	56534	Α	26313	181	336	
26167	56535	В	26314	1	374	
26168	56536	A	26315	591	679	
26169	56537	A	26316	937	1395	YRLAAGSCGIRRRNRHCQRRPG
						RNSKRLIALISAIGMSIFLQNYV
						SLTEGSRDVAPSSVPLTPASLLI
ł	İ	l				AGSPPH*TISRLSGPLLREIMLK
	!					QLYHCGKSLTNLPIREILRM*G*
						LTGEEIELARGDFHIRDIWHRA
						VTNTAHKTGITQAQHRH
26170	56538	Α	26317	627	878	VVEWFEPLICVNGWESKWPVL
						LSE**PETVGTNCDSSN*IPASLN
		1		1		TSYTGLMAFDAIMVAVPTS*TC
		<u></u>				KIRRRVAGTKCGNPRA
26171	56539	A	26318	125	3078	IYTVEIQNLGFAFVTGENTTGIN
						SGTISLLQNGKDPAPSPIVLLAT
		l				NGGSATNAGTITGKVTEQHSVF
		l	1			NKYSTGTSNSFIFNNDVSSITGL
		l				VAQSNSTIINTDSGIIDLYGRGS
		1				VGMLAIADSTAENQGKITLDSM
		1				WVDANDTTAMRDIASNSAIDF
	1	l				GTGVGVGTDRYRGGRKNAPAF
		l			1	N\QLGGVITIYNAGAGMAAYG
	İ	l				ASNTVINQGTINLEKNGNYDDS
		l				LAANTLVGMAVYEHGTAINDQ
						TGVININVGTGQA
26172	56540	A	26319	205	419	
26173	56541	Α	26320	1829	2903	AWKVSHCAARPSFSRRWRGEK
		1		l	I	CTAGRRSQQFSARSTLKPMPSP
	1			1	I	R*SSMHRR**MPSASCALRLPIP
		-		1		PAAAQSSHQSKKLRTSDNASPV
		<u> </u>		l		AAARPVRPIRWT

SEQ 1D	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
		_				
26174	56542	Α	26321	402	1781	QRTTGAERYVPHHQPCPPASSL
						SAGPRG\LHPAKVQEGVDIAIEN
						DVIVAIGDALTQRYPDASFKEM
						HGRIVMPGIVCSHNHFYSGLSR
1			l			GIMANIAPCPDFISTLKNLWWR
		l				LDRALDEESLYYSGLICSLEAIK
		l				SGCTSVIDHHASPAYIGGSLSTL
		1			ŀ	RDAFLKVGLRAMTCFETTDRN
		l				NGIKELQEGVEENIRFARLIDEA
	ļ	1				KKATSEPYLVEAHIGAHAPFTV
		1				PDAGLEMLREAVKATGRGLHI
1		l				HAAEDLYDVSYSHHWYGKDL
1		1				LARLAQFDLIDSKTLVAHGLYL
						SKDDITLLNQRDAFLVHNARSN
						MNNHVGYNHHLSDIRNLALGT
		1				DGIGSDMFEEMKFAFFKHRDA
						GGPLWPDSFAKALTNGNELMS
		l				RNFGAKFGLLEAGYKADLTICD
		1			1	YNSPTPLLADNIAGHIAFGMGS
		1				GSVHSVMVNGVMVYEDROFN
		l				FDCDSIYAOARKAAASMWRRM
26175	56543	A	26322	284	340	
26176	56544	Α	26323	113	646	WTLVPNWNNTQPYLGLFF*FIR
						DFADFGTTIKQDFRLLGQTSVD
	1	1		1		RLLQLSQGQAVKGNQLLPVSL
1		1				VKRKTTLAPNTQTASPRALADS
		l				LMQLARQVSRLESGQRSDSSLR
		ŀ				EKKITKKHTKKRTASLILHAMI
						CCRSLNSSKTKNTKCLNSINOR
						LKILSLOKDLMCGTAGRCKTLT
		İ				EO
26177	56545	A	26324	1	582	` _
26178	56546	A	26325	3	947	OTOEWSGSATFTSDGKIRLFYT
						DYSGKHYGKQSLTTAQVNVSK
1						SDDTLKINGVEDHKTIFDGDGK
						TYONVOOFIDEGNYTSGDNHT
						LRDPHYVEDKGHKYLVFEANT
i		l				GTENGYOGEESLFNKAYYGGG
1		1				TNFFRKESQKLQQSAKKRDAEL
		1				ANGALGIIELNNDYTLKKVMKP
		1		l		LITSNTVTDEIERANVFKMNGK
1		1	1	l		WYLFTDSRGSKMTIDGGATQA
		1		l		FAKENNOKAYKETYGVSHITR
1	1	1		I		HDMLQIPKQQQNEKYQVPQFD
		1		l		OSTIKNIESAKGLDVWDSWPLO
		l				NADGTVAEYNGYHVVFALAGS
		l				PKDA/G*HINLHVLSK
	L	<u></u>	L	L	<u> </u>	LVDWQ_HINFUAF9K

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
i	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26179	56547	Α	26326	2	223	RIPIKNIESAKGLDVWDSWPLQ
						NADRTVAEYNGYHVVFALAGS
[			ĺ			PKDADDTSIYMFYQKVGDNSID
l					İ	SWKNAGRVFKDSDKFDANDPI
	1		l		1	LKDQTQEWSGSATFTSDGKIRL
	1	1				FYTDYSGKHYGKOSLTTAOVN
						VSKSDDTLKINGVEDHKTIFDG
		1				DGKTYQNVQQFIDEGNYTSGD
						NHTLRDPHYVEDKGHKYLVFE
						ANTGTENGYQGEESLFNKAYY
İ		l l				GGGTNFFRGATOAFAKENNOK
						AYKETYGVSHITRHDMLQIPKQ
	1	1			ŀ	OONEKYOVPOFDOSTIKNIESA
		ı				KGLDVWDSWPLQNADGTVAE
	İ	l			İ	YNGYHVVFALAGSPKDA/G*HI
1		1				NLHVLSKGRRQLNRQLEKRGP
26180	56548	Α	26327	1	803	MLEDPRKGLETPSPVSHNLHFQ
	İ	1			ĺ	FHLGPLLPGSPMKKWPALVVT
						GSKSPKLESYKHFQKIWDMHG
		ļ				EPSKREEGAGLTVNQHIPNGAS
	1	l				TCNEGPORLEALGARIPMAAGF
	į.					SSSKPTLVTPRRAYRADLRLEG
					1	YWGCQGVPGGPLVAQGGATQ
						AFAKENNQKAYKETYGVSHIT
						RHDMLQIPKQQQNEKYQVPQF
	İ	1				DQSTIKNIESAKGLDVWDSWPL
						QNADGTVAEYNGYHVVFALA
						GSPKDA/G*HINLHVLSKGRRQ
		l		1		LNRQLEKRGPCL
26181	56549	Α	26328	2	439	
26182	56550	Α	26329	1	1084	MVIAAMETQLSNGPTCNNTAN
		1				GPTTINNNCSSPVDSGNTEDSK
1		1				TNLIVNYLPQNMTQEELKSLFG
						SIGEIESCKLVRDKITGGATQAF
1						AKENNQKAYKETYGVSHITRH
		1				DMLQIPKQQQNEKYQCDNLKT
		1				CHTSHGSVMAETAVINHKKRK
		1				NSPRIVQSNDLTEAAYSLSRDQ
		1				KRMLYLFVDQIRKSDGTLQEH
		1				DGICEIHVAKYAEIFGLTSAEAS
1						KDIRQALKSFAGKEVVFYRPEE
1				1		DAGDEKGYESFPWFIKRGATQ
1			1	1		AFAKENNQKAYKETYGVSHIT
1						RHDMLQIPKQQQNEKYQVPQF
						DQSTIKNIESAKGLDVWDSWPL
1						QNADGTPERR**HINLHVLSKG
						RRQLNRQLEKRGPCL
			L			

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26183	56551	A	26330	34	1949	MGYLNNVAGYREDLLANRAIV
20110						KHGNFALLTPDGVVKNIIPGYE
						NCDATILSTPKLGASFVDYLVT
						LHONGGNOOGFGVEGIETFRY
						VISGNITAKAEGKTYALSEGGY
						LYCPPGSLMTFVNAOAEDSOIF
						LYKRRYVPVEGYAPWLVSGNA
l						SELERIHYEGMDDVILLDFLPKE
						LGFDMNMHILSFAPGANHGYIE
}						THVQ\EHGGATQAFAKENNHK
İ						
		1				AYKDTYGVSHITRHDMLQIPKQ
1						QQYEKYQDTHDTPYCEPLPGET
						RLWGDTDVIGLFDAETDMNDV
			1			VAILENHPLLGAGFAHKIEQLE
				l		DKDWEREWMDNFHPMRFGER
		l		l		LWICPSWRDVPDENAVNVMLD
						PGLAFGTGTIQTLSVPAMLDSS
				ŀ		THTRRMRSTLNLYEITRMSTVS
l				l.		TSEHSMTYTLVQVDMKEAQKP
		l				DTASYRTFNEFFVRPLRDEVRPI
1				l		DTDPNVLVMPADGVISQLGKIE
		1				EDKILQAKGHNYSLEALLAGN
1						YLMADLFRNGTFVTTYLSPRD
1		l		l		YHRVHMPCNGILREMIYVPGD
		l		l		LFSVNHLTAQNVPNLFARNERV
		l				ICLSDTEFGPMAQILVGATNGG
		l				SIETPESEGATVDESFVVGGPVG
		l		l		DFELLLCHGTVCVVGKMRDLIL
		l		l		QLSKSSIYSTKPPSRQVSVMLC
26184	56552	Α	26331	1	145	LRLGLLYGRRFVPPP*YALLNK
		l			1	DSSPWYPFSVPVLASKTRYLWL
		l		l		LSPT
26185	56553	В	26332	1	3090	
26186	56554	Α	26333	3	832	
26187	56555	A	26334	I	3258	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
26188	56556	A	26335	184	2324	ENRVRLFVLIVFQDLPTCYVNH NFVCTAADTFTTDITPKAGDAR LIGIAQTVRHLEDPMRAWKSHH KSCEILDPHRAPVKENTHEK INISDPAAGAVARIRYEGVLSVC RASASAYVSRSRTITVACWYVS TROYTGA TIGVKRQHRHARLFS GDGAPGFTGKRDIRQLRRLVR IQIQRTFFAAVLHVPTPWSRAID AAALLTVIDVKVLTACACQAC RTLALRVAQVIDRCSNPGDIMS SVARRYWFISRWSAKRDCAVS YDQDPGQAQRSCRSCLVAVDR GLWLSAYCRSUMTOTLPPDV PRILPNASSPSRLRCLQHLGNYR LLDLRKLIWLHRSQPSLCGWEK RLVKDLTRIQDTGRAKELIGAT ATLEFRLVNTNVDQAAAASGR VPGDSEVKQTREGGPVVLVKR RLYNDLTRIGDTGRAKELIGAT ATLEFRLVNTNVDQAAAASGR VPGDSEVKQTREGGPVVLVKR KPMATLPVEYKDSGKKDANG RAVLVKQEEVIIIANIQSRLGNS FRITGINNPNEARQLSLLRAGA RAVLVKQEEVIIIANIQSRLGNS FRITGINNPNEARQLSLLRAGA GLIATSALIANILLIVGIMSLLPG GLEACLAGLLVSILEMIFYKKF GLIATSALIANILLIVGIMSLLPG ATLSNPGIAGIVTLAVAVDAN VLINERIKEELSNGRTVQQALDE ATLSNPGIAGIVTLAVAVDAN VLINERIKEELSNGRTVQQALDE
26189	56557	A	26336	1	369	AVGTGAIKGFAITTGIGVATSM FTAIVGTRAIVNLLYGGKRVKK

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
26190	56558	A	26337	1	1316	MNGLLDSDSDSLSSCOORVKA
20150	30330	Ι΄.	20337			RLHEILQKDRDFTAEDYEKVES
						RIYHFARLSVGGYTADSSLTLK
	1					VYLOLMKAPKKRRGEVNVGT
						VVAFIKGGFPVVKKDYFRPAA
		1				DGSSALCRFFPTGNVHDOSDPO
						KVTDGAVVPVQPTDGPGLRCL
						RRARGCGAGRQGREQAQDCG
						AEIQAEAASRASRVQEGSYPRP
						PNGPFSTDLTGLMOFTKLLVLK
						VESOLTRRIRKCHNLREANIREE
		l				LRFFNCTNVALRTGVOFNRRPD
						SPGYSRGVLSPERHVRTRLYFT
1		1				SESHVHSLLSILRYGALCNRGG
				ļ		TLCCRAIHTLHRHTIVLNGVTV
		1				TLNLVQLTFYGNVSEIIRHQCQ
						LTRHGNHPLPLTAIQGIALFSDN
						OAAYRFRADORTLRPFGLPVAR
		1				OPVRRGGFHDIVIVFDFGTARO
			İ			QQE/LRLQLRVFSSFVLHEKKR
26191	56559	А	26338	2	1415	``
26192	56560	Α	26339	1434	1667	KRTDWRDRVAFRCRSIAESG*R
						QAIAKELELTASAEILLWDDYF
						APGYGVPNDEGMEAVKLLARL
						EGILLDPAVRLR
26193	56561	Α	26340	1	1671	
26194	56562	A	26341	1067	3947	FCTVPNAVYIGGPGFGARHNAS
		1				NSLKDIAELVPFAHRYGAKIFV
		1			l	TLNTILHDDELEPAQRLITDLYQ
		1				TGVDALIVQDMGILELDIPPIEL
		1				HASTQCDIRTVEKAKFLSDVGF
						TQIVLARELNLDQIRAIHQATD
		1				ATIEFFIHGALCVAYSGQCYISH
		1				AQTGRSANRGDCSQACRLPYT
	1	1				LKDDQGRVVSYEKHLLSMKDN
		1			i	DQTANLGALIDAGVRSFKIEGR
		1				YKDMSYVKNITAHYRQMLDAI
		_				IEERGDLARASSG
26195	56563	A	26342	182	881	HAEPLPYRGLLLKLGESRGCLL
						PASLPFSLQEFFYSGPREELAQK
		1			1	TLLVSVWDYDLGTADDFIGGK
	l	1				CDPADQDVVHTALRE\TREELG
	1	1				LAVPEEHVWGLLRPVYDPQKA
		1				TVVPVLAGVGPLDPQSLRPNSE
		İ			1	EVDEVFALPLAHLLQTQNQGY
		1				THFCRGGHFRYTLPVFLHGPHR
	1	1	1			VWGLTAVITEFALQLLAPGTYQ
		1	1		1	PRLAGLTCSGAEGLARPKQPLA
		_				SPCQASSTPGLNKGL
26196	56564	Α	26343	237	338	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26197	56565	A	26344	279	533	IHLRRILQRGQ*PRQRWRERCC ESGRGTSGPGSSQ*LTGSPQECC TPAGETGPRAHSPQ*SCWCHCC TPQGRQSICTRTSHRTA
26198	56566	A	26345	126	303	LLLSYGVGASHQSLECHHRSNH GSLWMHSKRCAGGKIRVGTPE CQ*SALERPGLPPLC
26199	56567	A	26346	368	746	SLLHTTSRAPEGPSRYPGPGPPS AATKGQRTRRPLCARPP/PGLPD APL/SPAAPTPTLPLPCPRVAQP AHGPPSASALSSWENRPCCHE LAAKPPEQAARRGHARTPTAG PAPPGRRAALSGSQFP
26200	56568	A	26347	79	159	SFLGVSRRGGFGRVTGQ*WRE GQQINK
26201	56569	Α	26348	1	3369	
26202	56570	А	26349	3	529	MELAKVVKSHPSAKMVLCIAT DDSHSLSCLSLKFGVSLKSCRIT LLENAKKHHVEVVGVSFHIGR GCPDPQAYAQSIADARLVFEM GTELGHKMHVLDLGGGFPCTE GAKVRFEEIASVINSALDLYFE GCGVDIFAELGRYYVTSAFTVA VSIIAKKEVLLDQPGMEEENCS
26203	56571	Α	26350	146	502	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
			<u> </u>			
26204	56572	A	26351	3	2212	MKRSRCRDRPQPPPPDRREDGV
						QRAAELSQSLPPRRRAPPGRQR
						LEERTGPAGPEGKEQPPALASQ
						SAEIAASARLPPRLGRLLGFQK
						ACRCWSLNPHILMALLRSLVPP
						DKKHPQVWRGRPPLHLAPNVG
						LFSRVKVRSSVVIEDKSMRDSR
						RGLSQRRRRRKKKKRGSSSKK
	İ					KKRRKKRKKKKKKKKRKR
						RKKKKKRKNKRKKKKKEEK
						KEEEEERRKKEEEDEEGRGRGR
1						RKRKRKKRKKRRSRKKKETAA
1						AAAAGERLGKWWPGECPVEC
	1				-	VAYFLRRRLQQRLHPARQLLL
1	ŀ					QGMAGYLSESDFVMVEEGFST
İ						RDLLKELTLGASQATTDEVAAF
						FVADLGAIVRKHFCFLKCLPRV
						RPFYAVKCNSSPGVLKVLAQL
		1		1		GLGFSCANKAEMELVOHIGIPA
		1				SKIICANPCKQI\SQIKYAAKHGI
		i				QLLSFDNEMELAKVVKSHPSA
		1		l		NFHIGSGCPDPQAYAQSIANAR
				l		LVFEMGTELGHKMHVLDLGGC
						FPGTEGAKVRFEEIASVINSAL\
	ĺ					DLYFPEGCGVDIFAELG\RYYV
				l		TSAFTVAVSIJAKKEVLLDOPGR
1		l				EEENGSTSKTIVYHLDEGVYGIF
					i	NSVLFDNICPTPILQKSSTKSLR
		1				TTIGEAFERLHRLLRERQKAML
						EELEADTARTLTDIEQKVQRYS
						QQLRKVQEGAQILQERLAETDR
		l				HTFLAGVASLSERLKGKIHETN
26205	56573	A	26352	1	860	MKKEDAFLKAFYIVHGKWNCV
20203	30373	ľ.	20332	ľ		KGSLTRTPCCCTNCLAGGIWC
						MRVQIFQLENKVLPGFPWACR
			ŀ			VDLYGOIGFDAAAOCLSLSVSK
				1		AEPLVKKAPPELREQLARKTLS
						SDNLKYLFDNKDIMKVKQSKK
						,
	l	1				KKEHSFRKNNGCIKIIAFSDHAE
1	ĺ					DFRKLGCEVLGISVDSQFTHLA
				1		WINNPQREGDLGPLNIPLLAEV
	l	1	l			ASGLSEDYAVLKTDAGIAYRG
	l	1	l			RFISDGKGVL/SQITVNDLPVGR
1	l	1				SVDEALRLVQAFQYAEEHAEV
L						CPAGWKPGTDTIKLNVGDSKE

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26206	56574	A	26353	170	745	ERGSTRVIVRASSLCPRSFOSWF
				1		PVTRASESQPLTSRPQRWSDGA
		1		i		FKEVKLSDYKGKYVVLFFYPL
						DFTFVCPTEIIAFSNRAEDFRKL
		ŀ				GCEVLGVSVDSQFTHLAW\ITT
		F				PRKEG\GLGPL\NIPLLADVT\RR
		j				LSEDYGVLETDEG\IAYRGL\FII
		1				DG\KGVLRQITV\NDLPVGRS\V
						DE\ALRLVQAF\QYT\DEHGEVC
		-				PAGWKPG\SDTIKPN\VDDSKE\
						YFSKHN
26207	56575	A	26354	1	689	MAAEDELLLPRLPMLLETGKQ
20207	30373	Γ.	2035	I.	1007	LLDEVELAAETTGYOIVOEKRA
					i	REHFINYLTQCHYYHIAKFELL
l					1	KTKNNSAENHTANSSMAYPSL
						VAMASQRQAKIERYKQKKELD
ĺ						HRLSAMKSAVESGQADDEHER
l						PPVKSFILTRNTAQAKLFGASYF
1		l			1	SLATMTVSDWYEOHRKYGALP
						DOGIATATPEKFRKAAQQQKY
			ĺ			OEVKEGEDDE/ALYRVREWDN
						WKDTHPGGYGNRQNMG
26208	56576	A	26355	1	810	NYLTQCHCYHVAEFELPKTMN
20200	30370	n	20333	ľ	010	NSAENHTANSSMA YPSLVAMA
						SOROAKIORYKOKKELEHRLSA
						MKSAVESGOADDERVREYYLL
	i			1	i	HLQRWIDISLEEIESIDQEIKILR
						ERDSSREASTSNSSRQERPPVKP
		l				FILTRNMAQAKVFGAGYPSLPT
						MTVSDWYEOHRKYGALPDOGI
						AKAASSSSSSSSSSSSSSSSSSSSS
						SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
ŀ						KAAQQQEEQEEKEEEDDEQTL
		1				HRAREWDDWKDTHPRGYGNR
		Ì				ONMG
26209	56577	A	26356	223	359	RKQQDEPCGHLQSPGKPFLTLS
20207	30377	1	20330	223	337	CRDPWGGLPV*LEKDHRKKKS
26210	56578	A	26357	1	3855	CKDI WOGEI V EEKDIIKKKS
26211	56579	A	26358	1005	1293	SDRRYEWDPCPR*LNGALLCLL
20211	30379	l^	20338	1003	1293	LLEHPEGCPWHSVWSTGHSLEP
		l				MHFRFPSSQDLQLLLPLPGKLG
		l				YRARIRNHGHSCFLORRKTVYO
	l	1				GDGPLREP
26212	56580	A	26359	763	978	ODOFEREP
20212	120200	I <sub>W</sub>	120339	103	7/0	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26213	56581	A	26360	1	1217	MORRLKRRNAGLPCCEVPGYY
20213	3030.		20300	l.	1.2	REDASSPLLPKYKTNFSQCLVH
						FFDELRHHLVKTRHVLFIPLNH
						DIMOAFTLHARVIVGKVPGIFS
						RHPHAVLHLGHSQIGLLMEYPD
						ELLWECKEDALALIRRDAPMLT
ĺ						DFTHNLLNAPLLDKQAEWCEV
						FDRGRTTSLLLFEHVHAESRDR
				l		GQAMVDLLAEYEKVGLQLDCR
						ELPDYLPLYLEYLSVLPDDQAK
						EGLLNVAPILALLGGRLKQREA
						PWDALLDALV\QLGGSSLSSDN
						VKKQVNSEERDDTRQALDAV
						WEEEQVKFIEDNATACDSSPLN
						QYQRRFSQDVAPQYVDISAGE
						GQSSFQLVSYWEKDVQTCLEFL
						PSGGFVVSLASGVKLQTFTETD
						NLVKDITFFGKISTRSLKTYLKD
						VTEKREQSCVNLELK
26214	56582	A	26361	1	783	DOG THE PROPERTY OF THE PARTY O
26215	56583	A	26362	2	1646	PGSTISFRRVTQREKKQPEAELC
						QGSTSNLFQFIHPSLLSAQTVEL
						GLSKFVPKKMIITQTSH\CYMTS
				l		LGILFLINILPGTTGQGESRRQEP GDFVKQDIGGLSPKHAPDIPDD
				ŀ		STDNITIFTRILDRLLDGYDNRL
						RPGLGDAVTEVKTDIYVTSFGP
						VSDTDMEYTIDVFFRQTWHDE
						RLKFDGPMKILPLNNLLASKIW
						TPDTFFHNGKKSVAHNMTTPN
						KLLRLVDNGTLLYTMRLTIHAE
						CPMHLEDFPMDVHACPLKFGS
						YAYTTAEVVYSWTLGKNKSVE
						VAQDGSRLNQYDLLGHVVGTE
						IIRSSTGEYVVMTTHFHLKRKIG
						YFVIQTYLPCIMTVILSQVSFWL
						NRESVPARTVFGVTTVLTMTTL
						SISARNSLPKVAYATAMDWFIA
		1				VCYAFVFSALIEFATVNYFTKR
		l				SWAWEGKKVPEALEMKKKTP
		l				AAPAKKTSTTFNIVGTT\YPINL
		l				AKDTEFSTISKGAAPSASSTPTII
						ASPKATYVQDSPTETKTYNSVS
	1					KVDKISRIIFPVLFAIFNLVYWA
		_				TYVNRESAIKGMIRKQ
26216	56584	A	26363	217	559	MKKALQVAMFSLFTVIGFNAQ
						ANEHPHETMSEAQPQINSATGV
			1			VKGI\DL\ESKKITIHHDP\IAAVN
						WPEMTMRFTITPQTKMSEIKTG
l						DKVAFNFVQQGTLSLLQVIKVR
	L	<u> </u>				KPAQ

SEQ ID	SEQ ID NO	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26217	56585	Α	26364	72	157	ERRKF**SQSS\QKKNKERLQNA
				1		VIYLEL
26218	56586	A	26365	3	620	VSGGGWEPSGTLTAFKTASAIT
						TEMASRS\QGIQQLLQAEKRAA
	1					EKVADARKRKARRLKQAKEEA
	1					QME\VEQYRREREHEFQSKQQA
1						AMGFQGNLYAEVEQATRRQV
		1				QGMQSSQQRNRERVLAQLLGM
		1				VCDVRPQRPSDLQKEEMTTFSP
						SLIIPARACRFLVRAQQSSGHLH
						YRAKDPVGTRSLRHTRSSRIHG
						GVPTEKTCVAKT
26219	56587	A	26366	28	187	TGTESGQYHCKRRKMGPEPIIK
				ľ		SLWARSDEPVFWG/LFGAGGM
						WSAHAPVMIR
26220	56588	A	26367	1	870	MAVWPTGALALTPSPAGDAGA
		1				CSTAGGPCQGARGPRGSGPPA
	1					WGPDAVLEPLRGORKPYVRPM
						TSTWWKKLPFYRFYMLREGTA
		1	1			VPAVWFSIELIFGLFALKNGPEA
1	1					WAGFVDFLONPVIVIINLITLAA
	1	1				ALLHTKTWFELAPKAANIIVKD
		1				EKMGPEPIIKSLWAEPEMINPNP
			1			KRSDEPVFWGLFGAGGMWSAI
		1				IAPVMILLVGILLPLGLFPGDAL
		1				SYERVLAFAQSFI\GRVFLFLMI
		1				VLPLWCGLHRMHHAMHDLKI
						HVPAGKWV\FYGLAAILTVVTL
		1				IGVCTI
26221	56589	Α	26368	741	894	
26222	56590	Α	26369	504	558	
26223	56591	Α	26370	897	1097	RKWSQSTRLPWETGPSSETSPS
						GPIVSPTRSHLASPRRPPPTPP*S
						SPRRLLGAIPPGIGVPPLNE
26224	56592	Α	26371	200	657	GPRRLSFVTGHKAYRGLGIVSG
						PTVPLVCAVCCSYWDPGVPRV
			1			VRLVVRLWPLCRCGGRSGDAS
1						VAAAPLVCGGGI*DWDHCPFV
						CGPSLCALRPSCGCGSGMACRV
						VLLLRCPLAMFAFTSFFSVTEV
		4				GKFSPFPLPEFFFSGFALDLSLP
26225	56593	A	26372	196	404 3162	
26226	56594	A	26373	1		
26227	56595	С	26374	287	349	
26228	56596	В	26375	366	1637	W AVENDEL OF LITTURGES
26229	56597	Α	26376	365	604	VLAVSYPSLCLLL*KPIGPEDAI
						YALSSDFTCGSPTAAGRKQIRG
		1			1	EVCPRERCSVETCLSPNFHSLVS
			L			SFPFSLLQGFK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
26230	56598	Α	26377	1	1404	TLVRCFPPLKLIFSIFKKKAASL
						GSSQSSRTYAGGTASATKVSAS
			i			SGATSKSSSMNPTETKAIPVSQ
					1	QMEGPHLPNKKKHKKQAVKTE
			ŀ			PEKKSQSTKLSVVHEKKSQEGK
					1	PKEHTEPKSLPKQASDTGSNDA
		1			}	HNKKAVSRSAEQQPSEKSTEPK
					1	TKPQDMISAGGESVAGITAISG
1						KPGDKKKEKKSLTPAVPVESKP
ŀ						DKPSGKSGMDAALDDLIDTLG
		ĺ				GPEETEEENTTYTGPEVSDPMS
					i	STYIEELGKREVTIPPKYRELLA
						KKEGITGPPADSSKPIGPDDAID
						ALSSDFTCGSPTAAGKK\TEKEE
						STEVLKAQSAGTVRSAAPPQEK
						KRKVEKDTMSDQALEALSASL
						GTRQAEPELDLRSIKEVDEAKA
1						KEEKLEKCGEDDETIPSEYRLK
Ì						PATDKDGKPLLPEPEEKPKPRS
		1				ESELIDELSEDFDRSECKEKPSK
						PTEKTEESKAAAPGSCVGGCVS
26231	56599	Α	26378	1	688	ITAISGKPGDKKKEKKSLTPAVP
i		1			1	\VES\KPDKPSGKSGMDA\ALDD
				•		LIDTLGGPEETEEENTTYTGPEV
		i		1		SD\PMSSTY\IEELGKR\EVTIPPK
		l				YRELLAKPIGPDDAIDALSSDF
						TCGSPTAAGKKTEKEESTEVLK
				ì		AQSAGTVRSAAPPQEKKRKVE
		İ		1		KDTMSDQALEALSASLGTRQA
	1					EPELDLRSIKEVDEGSLPDFQQQ
		l				SLSLGLPWPKMGQFLSSTFLEG
				1		SPATQRK
26232	56600	A	26379	199	384	VYKECR*GFSHESPPSKPQS/HIE
		l l		-	1	*KFCMCGENGQGLRKKSSSKN
		ŀ				SFFGTSFTWVGRENVKHI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26233	56601	A	26380	166	2172	TYILRNLYKEVMLENYRNLLSL
20233	50001	l^	20300	1.00	1172	GKAVFFPFLH*FSRDLLIT*YVP
	į.	ŀ				OSOOFLSOHVLOIFLGLCAENH
1		1				FHPGNSSPGHWKQOGQQYSHV
	i	l				SCWFENAEGOERGGGSKPWSA
	1			1		RTEERETSRAFPSPLOROSASPR
	1	l				KGNMVVETEPSSAQRPNPVOL
1	1	1				DKGLKELETLRFGAINCREYEP
		1				DHNLESNFITNPRTLLGKKPYIC
}		1				SDCGRSFKDRSTLIRHHRIHSME
		1				KPYVCSECGRGFSQKSNLSRHQ
ŀ		ı		1		RTHSEEKPYLCRECGOSFRSKSI
		1				LNRHOWTHSEEKPYVCSECGR
		1				GFSEKSSFIRHORTHSGEKPYVC
		1				LECGRSFCDKSTLRKHORIHSG
	Į.					EKPYVCRECGRGFSQNSDLIKH
		1		1		ORTHLDEKPYVCRECGRGFCD
						KSTLIIHERTHSGEKPYVCGECG
1						RGFSRKSLLLVHQRTHSGEKHY
		l				VCRECRRGFSQKSNLIRHQRTH
	İ	l			1	SNEKPYICRECGRGFCDKSTLIV
		l				HERTHSGEKPYVCSECGRGFSR
						KSLLLVHQRTHSGEKPQMTFSG
		1				VTPOLLERTVLLLAEMHSRDAL
	1					RSGTHSOPOGAACTTGAMHLC
	1					RGTFWPQPLTQRGQLQKVIPDP
	1					EIPIELKDHWVADTLQVSFFLCP
	1					VLPSLPSESSIFCLVVCSINYAV
ļ	1					APQSGLMREKDVHVWECGPPP
}						FARTAPITPTSDQNWRPLREKY
26234	56602	A	26381	434	946	NTFCLTAMKILCMWFSRWHSR
20234	30002	^	20301	434	940	WVGMQGPSC*PQRTLWMATLS
1						STGRSCVPAACTPAPCGRISAA
	1	l				GRLRCSOLLPHAPAPAACCSCP
1		1			1	SVHISFOPL*QLRTSLWTVOMK
		1			[	SQVTQTQVGSHSSTSQARALQG
		1				HOOVQKPGSRIRTGGVKPQLEG
						PGRWLKIRLEGHSWTCRQ
26226	50000	ļ	2(282		2119	POK WLKIKLEGHSW ICKQ
26235	56603	Α	26382	3	2119	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26006	100004	Ļ	10.0000		2007	NIND V POWER COVEY AND A OWNER
26236	56604	Α	26383	3	2237	NRRKFSVSIGFYTVMDAQYKII
						TKTAHLITKESPQEEGKEMFAT
ļ		l		l		MSKLKEQLTKVRK*FNALLYES
	1	1		l		QQLLIPLEELEKQMTSFYDSLG
						KINEIITVLEREAQSSALFKQKH
	l			ı		QVRTILFKWCNSSQKMTLCLVL
	l				!	GSMISMLSTAKITIAGYKSEVEV
	l	l		ł		SVSHHCI*NCKKTLTLIEKGSQS
	İ	l				VQKFVTLSNVLKHFDQTRLQR
i		l				QIADIHVAFQVICSPC*DWKKH
	l	1				VETNSRLMKKFEESRAELEKVL
		l				RIAQEGLEEKGDPEELLRRHTV
	l					SPPFRDQRVLNAFLKACDELTD
						ILPEQEQQGLQEAVRKLHKQW
		ľ				KVSQDRTAYHLLHLKIDVEKN
		1				RFLASVEECRTELDRETKLMPQ
						EGSEKIIKEHRVRLPHHSPHHLC
1	1					EKRLQLIEELCVKLPVRDPVRD
	į.	1			ŀ	TPGTCHVTLKELRAAIDSTYRK
i	1	1				LMEDPDKWKDYTSR*PQNGLW
						ISTNETQLKGIKGEAIDTANHGE
1						VKRAVEVSSGSLSKRGETLSWL
	1			l		KSRLKVLTEVSSENEAQKQGDE
	1					LAKLSSSFKALVTLLSEVQHLL
l		1				THFGDCVQYKEIVKNSLEELIS
l	İ					GSKEVQEQAEKILDTENLFEAQ
l		ì				QLLLHHQVKMPLSSAKKRDVQ
1						QQIAQAQQGEGGLPDRGHEEL
1						RKLESTLDGLERSRERQERRIQ
1		l		1		VGAGS*ERFETNKETVVRYLFQ
	1	1				TGSSHERFLSFSSLESLSSELEQT
ŀ		1		1		KVYYGSLESIAVQAENLVKEAS
26237	56605	A	26384	T	390	GTSLFDEEGAKIVKDLMSKAEK
	1	Γ΄.		1		NGVKITLPVDFVTADDFDENAK
		1		1		TGQATVASGIPAGWMGLDCG/P
		1				ESSKKYAEAVTRAKOIVWNGP
		1				VGVFEWEAFARGTKALMDEV
1		1				VKATSRGCITIIGKRSYTKLIPI
	1	1	L		l	TRAISIGCITION AST INCIPI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l			sequence		
26238	56606	A	26385	1125	2228	NVMSHLGRPDGVPMPDKYSLE
120230	50000	· `	20505	1		PVAVELKSLLGK*VPGSGAGRL
						CGGGSCQARCYAGSVILLENLR
		ł				FHVEEEGKGKDASGNKVGPVIL
	l					TLLGVRA*VCKRLWLNVNDAF
						GTAHRAHRYQEPCRLPH*EQYS
1						YLLE*PKYFAKALESPERPFLAI
1			i .			LGGYEELFKIML*VLFAW**AIT
1						
1						WIGGGMAFTFLKVLNNMEVGN
1		l				KCQVDVK*LSMIIAGCINEKNG
						VKITLPVDFVTADKFDENAKTG
		ĺ	1			QATVASGIPAGWMVSHLSGLV
						V*VNRNSVVSFIHFVWNGPVG
		l			ŀ	VFEWEAFARGTKALMDEVVK
		1	ľ		i	ATSRGCITIIGKRSYTKLIPI*AG
		l				RILIRGRCTGGGASLELLEGEGL
						LFFGLFGIRVDCAVRGG
26239	56607	A	26386	2	482	TRQAWHEGPRGVPHSASLRSA
						RRQSAPSLTESPTSVPSCISKMA
		1				LSNKLTLDKLD\VKGKRVVMR
		l				VDFNVPMKNNQITNNQRIKAA
		l		1		VPSI\KFCL\DNGAKSVVLM\SHL
		l				G\RPDG\VPMP*QVTPLEPVA/V
		l				VELKSLLGQGMFCS*RDCVSPE
						VEKACANPPG
26240	56608	A	26387	3	378	LOTDOOTH OF SPANCOSENDS
26241	56609	A	26388	311	578	LGIRGQTLGFLSRARCGGSRRS
						LEMQNNAGEFVDL*VPRKCSA
						SNRIIGAKDHASIQMNVAEADK
						VTGRFNGQFKTYAISYFLNLFL
		<u> </u>				HH
26242	56610	A	26389	3	333	DAWDLCRVTSCFLSLSRAVWW
						QQAQPSLEMQNDAGEFVDLYV
1				ł		PRKCSASNRIIGAKDHASIQMN
		1				VAEVDKVTGRFNGQFKTYAIC
						GAI\RRMGESHDSFLRMAKADG
		_				IVSK
26243	56611	A	26390	23	389	LAASFLSRARCGGSRRTQALEM
	1	1			1	QNDAG\EFV\DLY\VPRKN\SAS
	1	l			1	NRIIGAKDHASIQMN\VAEVDK
		1			1	VTGRFNGQFKTYAICG\AI\RRM
		l	1		1	GESDDSIL\RLAKADGIV\SKNFL
						TGEESQDVGIFCHK
26244	56612	Α	26391	206	354	
26245	56613	A	26392	1227	1430	GSSSPRDPQEEDLKLLKFAFSR
1			1		1	GPPLSLVHPPPLLSYPSARR*PQ
						TPPRPPPRHPSLHPLHPPSAQP
26246	56614	С	26393	17	319	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26247	56615	Α	26394	1	645	MIHEQNENIKKNTKTIKKNQTE
						LELKNTVTEWKNLLEVFNNSFR
		1			1	ONEESVNLOTSYLKSLSRGEKR
Ē		1			1	KKKCEEMIRDLGQYQPGPYMH
						DGYSRRESGPNVPRRAQVDGG
1						DARKGTHRRKRVLERGLWLKR
						EDKKAQGYKGR*KGPRV*GTD
		1		1		PQEEDLQRLSAETWLVL*PEPR
						P*KAPAKKGEKVP*GRKGKAD
		1				AGKEGNNPAENGDVKTDQAQ
						KAEGAGDAK
26248	56616	В	26395	1	663	
26249	56617	Α	26396	265	735	VMWLRYDTLSETHMHQLLGL
		1				NLLFLLSQD*VAEFHMELEWLP
	İ	1				ATDTQTNAYIKRPVSLEPYLME
						GGYNKVFLAKGNIPAKSYTFIHI
	1	1			i	LLDTIRDEMAGCIEKAYEKILFT
	İ					KATWILFLNTPKQMMDNTKK*
ļ	1	1			i .	GWVLGPNNYYSFASQQQKLED
		L.,				TTIPS
26250	56618	Α	26397	215	386	
26251	56619	Α	26398	3	515	QLPESAYMHQLLGLNLLFLLSQ
						NRVAEFHTELERLPAKDIQTNV
		ĺ				YIKHPVSLEQYLMEGSYNKVFL
1		ł				AKGNIPAESYTFFIDILLDTIRDE
1		1				IAGCIEKAYEKILFTEATRILFFN
	İ	1				TPKKMTDYAKKRGWVLGPNN
	Į.					YYSFASQQQKPEDTTIPSTELAK
26252	5.000	<b>!</b> -	26399	423	4482	QVIEYARQ\LEMIV KLVWILFDFICLAFL*FFSTYMY
26252	56620	Α	20399	423	4462	SCE*ILVKLTLYFSFHVYLLIYC
		1			1	ECENLTGTLDLVFI*KCKSLLIW
		1	ĺ			IA*TVYKKIHMEGEVKG
26253	56621	A	26400	173	174	AVSLLKHSNNDLCSS/GFPTSRT
20233	30021	l^	20400	173	11/4	ADPTSCGSH\WPWGPOSLKO*P
		1				ELYIGPF*PRLELKQLGCRAPSP
26254	56622	A	26401	135	699	RDLVPCAPAAPAMAKRGQDTV
20254	30022	ľ`	20401	1.55	1000	WAMASEGASPNPCOLPOGVEP
		1				AGOCRRKMWG*SPHTEPPLGT
		1				A*WESLELPROLLNGFDONAD
		1				NDMDNEIQAEVVSDGDEELVG
		1				NOSKGTWCPVPOLLOLWLKGA
		1				KIOFGPWLQRVQAPILASFHKV
		1	1			LSLQGSAEGKCGVEAPTQSPH
		1				WALPSGAVRRGPPSSRPQNGRS
	1	1	1		I	TNCLHCEPGKAADTQCOPVKA
1		1			I	ARREVVPCKAKGAELPKTMGT
		ĺ .			1	DLLHOCDLGVRHGVKGDHFGA
		1			I	LRFDCPTGFWTYMGPVAPLVW
1		1			I	
		1				PIFPIWNSCIYPMPVPPIVSRR

	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /-possible nueleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26255	56623	A	26402	27	264	RLVEWL*PRDLLNGFDQNADN
						DMDNEIQAEVVSDGDEELVGN
		l				QSKGTWCPVPQLLQLWLKGAK
		l				IQFGPWLQRVQAPILASFHKVL
					1	SLO
26256	56624	A	26403	624	955	VPSLGSFHVVLVLSVHRROELR
						FGNLHLDFRRCMEMPGFPGRSL
					ļ	LOR*SPHGEPLLGOCRREMWG
						QSPHTESPLGH*LMEL*HPPSPR
						MIDPPTACAVPLEKLQALNASH
26257	56625	A	26404	851	1387	PKIVELLKYSGDQLERKLKKDK
20257	50025	ľ.	20101	103.	1.507	ALMGHFODGLSYSVFKTITDOV
		1				LMGVDPRGESEVKAQGFKAAL
		1				VIDVTAKLTAIDNHPMNRVLGF
			1			GTKYLKENFSPWIQQHGGWEK
		1				ILGISHEEVD*NIRFVIRNTLCLL
						WSCARWPSDGPTGDYNVOGR
						WSIDVFKTIIPVTGEASGEVSFV
26258	56626	A	26405	1	229	LRRLGITHVLNASHSRWRGTPE
20236	30020	ľ	20403	l'	1227	AYEGLGIRYLGVEAHDSPAFD
						MSIHFQTAADFIHONKRAISAL
		l	ļ	l		HLCRKSGIRQA*MSIHFQTAAD
					l	FIHQNKRAISALHLCRKSGIRQA
26259	56627	A	26406	2	594	SVLGLTLPAPRFKTLRRRWVQG
20239	30027	<u> </u> ^	20400	<b>-</b>	1354	OKVLRKAPFGKKPRGSLTFWR
						ASTRVRDMANNRRELRRLGIT
						HVLNASHSRWRGTPEAYEGLGI
						RYLGVEAHDSPAFDMSIHFOTA
		1				ADFIHRALSQPGGKILVHCAVG
		1				VSRSATLVLA*PHAVPPPLPFVE
		1				
						AIKKVKDHRGIIPNRGFLRQLL
26260	56628	ļ	26407	605	1231	GLGPQLAAGSGSMRGGGEKLR
26260	36628	A	26407	605	1231	NCSNSGVWRISHKKERSIPDSK
		l		l		RRRSRGNTKSSSPRPTTRSLEKL
				l		LTSGSPRIWPVRMS*LHDKARR
				i		ASFSSSSSAIKKAFSSASRSSNES
		l				VSSLSNSSLEGQSKSMSISSSST
						GVGSRLALGLYTSSEMVKGSSF
						ILSSSSLGGSSYSRAAFTGELEIK
				1		GAEMFSSLGNGTPVLRAVTLEP
		1		1		SLSRRTNTLLLQWFPMCNWRL
						RRVWI
26261	56629	A	26408	771	1121	FSPKLLPRREGRKPCEAPARTQ
		1		l		TPRSKSSTPPSQV**SVDSDPQP
		1		1		KGKQDRSRGGPLQERAQRESG
		I		l		PNLLAATVVPRPRAERHPAISTE
		l		1		GPTGPPEGSAPSATSSVAAAGP
		ı	l	I	l	APHSR

SEQ ID	SEQ ID NO:	Met	SEQ 1D NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, ≔possible nucleotide insertion)
				sequence		
26262	56630	Α	26409	3777	4343	DQEEPFSGNSSIIQSLFTIKLNPQ
						SSLQEVCSLDTHNSPVRVFKNS
ļ		1				CSAKFHFKFVWNVILLLQLSSE
				i		ELILSFVIPGVGHCWSSYCYILQ
ļ		1				PRIFPLWSFYIVIYVEDSSICVSS
l	1	l				LFPSWR*RP*IIGSIK*CLSSQMG
	l	l				WNFOSW/NLPR/CVVLVLWSIK
ļ		l		l		KGL/HIWCMPDFPAFRKESLLN
ŀ		l				FRWLGHLLA
26263	56631	Α	26410	473	667	PCSDWGWRSPWNLOLEETWAL
l		ĺ				*CCSHSHKVSOEGTWMKLETII
l	1	l		İ		LSKLLQGQKTKHPMFSLTGGN
26264	56632	A	26411	1416	2108	QRANIQNLQRTQTNLQEKRNPI
						NKWVKDMNRHFSKEDIYAAN
i		l		ł		RHMKKCSSSLAIREMOIKTTMR
		1				YHLTPVRMVIIRKSGNDRCWR
l		ı				GCGEIGTLLHCWWDCKLVOPL
		l				WKTVWRFLRDLQLEIPFDPATP
		1		ŀ	•	LLGIYPKDYKSCCYKDTCTRM
		ı				FIAALFTIAKTWNPTPKCPS\MI
	1	1				DWIKKMWHIYT\MEYYAAIKK
i	1	1				DEFMSFVGTWMNLETIILSKLL
l		l				OROKTKHRMFSLIGGN
26265	56633	A	26412	1	278	FRCSSYYYFKYFFCFFLFSLLLF
		-		ľ		*IFFLFLSLLFASLLFLASPLCVC
	1	1				YFFFIVVAOFLNSLFHFFSLFVL
						CFSGLEVSIDISSSVEILSSAMSIT
	1	1				LMGLSKAFLIT
26266	56634	A	26413	181	742	PLLKSGCISFLLLRLLVKLYRFL
		1				VRRNNSTFNQVVLKRLFMSRT
l		l	Ì	İ		NRPPLSLSWMIQNIKLPDRENR
	1					KAVAVGTITDDVRVQEVPKLK
						VCALRMTSQARSGILGAGGKIL
	l					TFDOLAPDAPKGCGTVLLSGPR
	ĺ	1		1		KG*EVYRHFGKAPGTPYSHTKP
				-		YIRSKGRKFERTRGRLASRGYK
	-	ļ				NYRSYPLIKDCL
26267	56635	la	26414	368	675	SLSTLLSSRDCPLATISKQLRVL
20201	50055		20111			ARGCVVNNCFCKHLLNTCSLA
		l				GTVPG*GASSGRQKFKLLAKFK
ŀ		l				VLARLCSSGGSRGEPFSCLFLFL
ļ						GATGILRLMASSS
26268	56636	A	26415	40	355	LLGNPSPVVKGRPCRHDGSEI/A
20200	55050	<u> </u> ^	120415	l.,		PRVYFRGCS*SSHSWVSHFLSA
		l		l		PSHPRMLPTSRHRPPLRPLT*ER
		1	1			RGKRRDD*PLHHP*P/CWSTCSP
		l		1		STSARATPTPPSGSGW
		Ц_		L		313AKATETEF3U3UW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	i	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence	1	
26269	56637	ĪA.	26416	347	1725	EAKRRPLSTLMEKRCFOPLWT
						RPSRKKPRGRTWRPPALNPTRI
	l	1				AGPPSPPAVSPGFGPIPP*SISCFP
		1				KGPGFSMGFLRLRCFSAVQKVL
		1				APGSPA*PCLSCGPFRTALGDL
		1				ARTPEKLCWLERS
26270	56638	A	26417	525	708	IVAELIOHHOLPCSHPLSGGKIK
						DOOVVFLSLSP*SSHNKTLY*AF
						KTNORPODYPEGCNA
26271	56639	С	26418	1	1050	
26272	56640	Ā	26419	934	1708	PORGVWVLSVILHFPWLGSGPL
						PNSAGD*AARYSWNOILKPDC*
						WKLSSAAGISFORS*VNFHYGE
		1				FCPKIPSGMYESKLGSIITDKTP
		1				HFLPAOKTRSTPSPATAPLPGAT
1						SPRPPRGRRRRRRCPEQQPPPPL
1				ļ.		QAGPTA A ARHRODPLPRFSPLC
		ı				FHSHPRASGAGSRPAPARVSPW
						TRRPAAPVSSGRGRLAPKRSLS
1						PRPPRPGOGGGRVPARRELPLA
		1				PRGLCVRLVYSLCSSLCGSLPSF
		1			1	SLGSLVFSSSDQG
26273	56641	A	26420	630	734	TAARSGYPGRAGTLTGLHPMO
		Ι			1	VCRCRR*PYSRGT
26274	56642	С	26421	4	90	
26275	56643	Α	26422	216	305	ICWKYFCAG*CGKYFTLGPRSH
		i				SYRRSDY
26276	56644	Α	26423	859	1248	CVISVFRASRKSKHNVIAVVFS
	Į.	1				YCSVSVGQRPAVP/QHQVLLQT
		1				QGISGYPGRAGTLTGLHPMQV
		1				CRCRR*PYSRGT**/REPS*LREG
		1				GSAPPKSVCWPVGACIKRLSSM
		L.				SSSFSSFPFIKHAHACCRVLS
26277	56645	A	26424	132	548	SSGFSWGFFSGYQRCRESR/CD
		1				YPPPDMEIRGRVEQRVGYTIEQI
		1				NHMRDVFGTRLRRAEDVFPPVI
						GVAAHKGGVYKTSVSVHLAQ
						DLALKGLRVLLVEVWDHGPTR
						IVGLIISLGPRSHSYRRSDNQTG
						TTVPLVSSV
26278	56646	Α	26425	382	697	YAVKQAKTTFEDMTGRRASLL
	i				1	LHKGYLEFELFLQTAAYQSGSP
	1	1	1		1	APQGTWSGTGSVCHCCSLAE*T
	1	1				PFRTTGACCGLMARTGHARAA
		1	1	1		SICPPDAVAPLSPSPNAWF
26279	56647	Α	26426	167	412	SYVKYFPHQPAQKYFQQIHCAI
			1			GLHNAGYPGRAGTLTGLHPMQ
	1	1			1	VCRCRR*PYTILSLQEQTDVVSL
Į.	1	1	1		[	N
L				<del></del>		

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	delction, \=possible nucleotide insertion)
26280	56648	Α	26427	3794	4021	RGLCAPLPPLTPCFSPPLRRRAA
						SHLAPPTPLPTPQTPTRTRALPS
		1		1		SPGLGRGA*RTVLPSAPPEVPLA
						WGCRRA
26281	56649	Α	26428	65	564	PHPDSGPQ*LQ*PHPDSGPR*LQ
				1	1	*PHPDSGPR*LQ*LQ*PHPDSGP
	l	1				Q*LQ*PHPDSGPQ*LQ*PHPDSG
						PR*LQ*PHPDSGPR*LQ*PHPDS
	1					GPR*LQ*PHPDSGPR*LQ*LQ*P
	1	l				HPDSGPQ*SDSGPRGHR*LQ*L
	ļ.					Q*PHPDSGPQ*LQ*PHPDSGPR*
						LQ*PHPDSGPR*LQ*PHPDSGPQ
				l	1	*LQ*PHPDSGPQ
26282	56650	A	26429	184	438	DPAVDLCDLSSRRLLFS*RYVL
						VMLFSISLVSFVFISVHVICNYPF
		1				ALFFVCASFCGGAGGLVEFVL
						MIVGDASAALLCMPRCEC
26283	56651	Α	26430	524	1995	
26284	56652	Α	26431	601	1058	LPSSGGRCRSPKTR*SACLVSGS
						PRTPAMIRSGAGQPLARSPPTPT
	į.	Į.				PPFCRPLTRAPQASSMTWTGTS
		1				TTTWTLCAMRTDCTGLPSTSPT
						WCFCTRSSSWPAATSGSNSRAP
		-	1			ARSWSTLCLSC*SASTRPGPRGP
						CRRQWWRRATPSRPSAR
26285	56653	Α	26432	1	371	
26286	56654	Α	26433	71	335	
26287	56655	A	26434	2	416	
26288	56656	A	26435	60	370	DOLLEGA DE DITIETA DE LA CONTRA
26289	56657	Α	26436	466	1454	PCVFQIGPRRIHTVRVRGGNKK
		1	i			YRALRLDVGNFSWGSECE*GPL
		1				GVGGKTHLNGFKIHRARPALIF
1	1					LNSAA*EIGAGKDCGLPNITRN
	l					VG*GVVEDELMPHGL*RLRVPF
1		1				ISP*GPHGAEEPGGVCQGHLSSS
			i			LLDAKFLL*AGCTRKTRIIDVV
l		1				YNASNNELVRTKTLVKNCIVLI
		1				DSTPYRQWYESHYALALGRKK
İ					1	GAKLVRVTSL*GLWGGQPDSS
l				İ		LLVMKTLSSSATEGREMRAF*A
		1		i	1	EEGQHWGVQGSRKLPGPAFLP*
	1	1	1	1	1	AHIFVSPFQTPEEEEILNKKRSK
		l		l	1	KIQKKYDERKKNAKISSLLEEQ
l						FQQGKLLGEKADELEVGSRRD

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ļ		sequence		
26290	56658	A	26437	2	787	SQWLKLPSPLPHAGISRY\NWD
						QAP*KTGGPRESPYHKKREVM
l						KLGRPSCPN/NPKIGPPAGIOHSI
						VCRGGYQEIPVPLRLDRGEFLP
l	1					GGSECCTS*NKGSSIVVLQCHL
1		1				NNGAGFVPKTPGWKEFCIVASS
		1				DOOOPYRPVVTSSHLCACPLGF
1						QRKGAQAGLLEERRDF*TKKRS
1						\KKLRKEI*LKRKKNCQNSAVL
		1			0	PGREQFPARGKLSCRA/SRFQGF
						GOLWAEQDGFCA*EGQKSLEF
						LSLGKSKARKGQIKSFVLSSPM
26291	56659	Α	26438	62	872	ANWTEPDDTKTMWRLSVPLDR
					1	SPQTQNCTGEPLMPTGRQELPQ
						RGPEPMEAPAPARPQSRRVPAA
	i i					GPVARQPHMRPPHSKQGEKQK
	į.					MPGSRWPGQRGRGRWGSPLES
	i	1		l		A**TRKIFTGIPILPLLPGTPGRP
						APEEGMQSADKNRVKRRGGTQ
					1	RNSALALEFCELLFVSSKWFCA
				1		LPSTLRLKALSAAVALLAGDPE
	1				1	FGVRNVWVWVAGGVRCKRVA
						HRTTEAGAFFPDWFVWVFAAT
	1			1		KRGDGETSGCEHSEPVSGSSGG
						SPPRGQYLPGM
26292	56660	В	26439	1	606	
26293	56661	В	26440	48	381	
26294	56662	A B	26441	16	209 1275	
26295 26296	56663		26442	2	252	
26296	56664	A	26444	95	266	
26297	56666	A	26444	119	343	CTLRQESKLSRGDLTAPPVSSPR
20298	30000	Ι^	20443	1119	343	GHRSSKKGGNT*LGSMQL*AES
	İ					CRAEPPRPALLCPGRSVSACQW
						GPEGPFF
26299	56667	A	26446	1	383	NTGLGRGKAMTPSMSCRISML
20299	30007	l^	20440	['	363	LORPGGVLVGWDPDAAHPVGT
						*RHSVAQHN*MPW*GAEGMGQ
						PC*WHGMGTSDGPGLSDSERPE
						LS/HADSEGRVSKAKQSELAGP
						GOKR*GOKPPKGYRFOERTOR
26300	56668	В	26447	430	540	OQUE GORTHOTH OERTOR
26301	56669	Ā	26448	1111	591	PGAPSSHSGPRLLAWEPIVLAP
1	15000	1	23770	l	ļ	VASLGLGEAEDCSFLGRKAGV
	1	1		l .		GPRHPR/ARRVHGSGSRETCRG
1		1		I		*OEPRPMLREPVCSAFLRTVKK
1		1		1	1	LSGRVFPPLAVKQVLSAAPAVP
		1		1		ALLRTAPKTPWDGPESAESQPP
		1				SLGPAVVLDISDRRKOETIKAT
		1				GGPGRLRR
	L	1				JOS. G.LEKK

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ	1	sequence		
26302	56670	A	26449	1041	1410	OEERGKVEE*ELEGRRREEKRR
20302	30070	^	20449	1041	1410	GRGRRGSGLEEGRRRRRRGGG
						DETKDKR*RKRGGHRKEKKEE
		1				RRRRRGGGAAKKEEEEDRLP
		1				TRAFSCVEQQSASKSPLVELHP
						GPIPQGPPLAAAGAC
26303	56671	A	26450	288	424	KRPAEGAPNP*GRPGIRPOA*K
20303	30071	<u> </u> ^	20430	200	72-7	RPAEGAPNPRGPRRKEGRSGAK
		l		l		GSLDTGDGGEAWWAGSPHPS
						WP
26304	56672	A	26451	111	540	LPLALSNPKOEVVSGRGGOVDS
		Γ.				<b>QAGLTMTGRAVCCLOLCLNAS</b>
		1				GAGDAEAMSAGPPGPGPARAD
		ı		l		TEQLPSPSLPQVS*HWRGSASTS
		l		1		ATRTWPLRRRCSSMARSTCRAS
		l				ASASAGPWPWPGAPVPWRHSA
		1				EPSCSQLPGPSA
26305	56673	В	26452	57	558	
26306	56674	Α	26453	804	1524	ARETSHGDFLHFPLIWLFSLKG
		1				NVPAARINIMNWNQGLISHVGE
		1		1		GNVNRKHDVIGFNFPWNCLFN
		ŀ		i		VSDLVTMIGSPRQRNHFGLVM
		1				VLTGIHTFHRHVGHCRCGPWS
		1			}	NQASHQKGDDLEHEQNPTNNA
		ŀ				QLLGAHVFYNCPRPFLRPPFFFS
		İ		1	ŀ	P*NKCFRGELFAPSSHHSPSFLA
	1					SFLGAAKLQRCWSAARMGPGR
						KAPARIPPAQPARVPPMPGAVI
				1		VAAPPPVDAPIVRICVHVCLHH
26307	56675	A	26454	2	330	SCSRSGTALGVPVLAGPVRSAL
						TYLPAHSAGQRHQHDAGPTRG
						LGAI*DLPPVVTPGEQPSPCRGQ
	1					DQVPIVAAGE/PRCAPSLGSPPG
		_				LE/PVSLSSMSSPPRPPSCPLSG
26308	56676	В	26455	1	969	
26309	56677	A	26456	43	568	RSRLVFPLYFHASQGPGTASRE
	i	1				VPGGWAWGPVAQRINGICLLH
				l		STGPEAPSTMPPPTRLCGGPCGP
						ALPFSSQLAARGNPRSLPAAQL
	1			ł		RALLSKISPPVVTPREQPSPCRG
			ł	i		QDQGADCGKQVNKMCSQAWG
		1				SPPGLELCPCHQ*AGPPRPPSCP
	l	_				LSG*FVLRTGAPGAAPPSGTV
26310	56678	A	26457	1	456	HEDAASSFQADVSLGNDAAVP
	1	1		l		LSGRGGINTYIPLIIPGFPYPTAA
		1				TTAAAFRGAHLRGRGRTVYGA
1		1	l	l		VRAVPPTAIPAY\PGVDMQPTD
	1	I	ŀ	l		MHSLLLQPQPPLLQPLQPLTVT
1	1	1	ŀ	l		VMAGCTQPTPTMPLPLPLAME
		1_				LALWRVYTEVATADLPPTEVT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26311	56679	Ā	26458	609	1031	I VCKSYPGHQGSSCLPDGQIQLW
20311	30079	^	20430	009	1031	LHGYGOEFCGOETHPFLDG*RG
						AESL*GHNSGHDQWCLGDGCC
	1					WGWLLTYERHEOLPAELEAPG
	1					
	1					GWGKDGDSRGTESTC*EAGAG
						AGPAHPAPPAPAAEGEPDLFQL
		Ļ.	06100	ļ.———	200	PGQGCSRIPCG
26312	56680	A	26459	1	393	
26313	56681	A	26460	357	843	QTEGGAQTDGQQSQTQSSENSE
	ŀ					SKSTPEDNKICG*KPDHK*TFLF
					1	YQEISISI*RCACFPPFSRCMQGF
						GFVTFEKCNFMFPNVVHFFPAL
						FSPCYDMH*SSLSSNSLKCLPSI
	1	1				VVTVHLLLNAS*NFCHILGLPL
		1				VPGFPYPTAATTAAAFRGAHLR
						VFV
26314	56682	A	26461	3	1172	GRAHGEAAADGGGGMQNEPL
						TPGYHGFPARDSQGNQEPTTTP
		1				DAMVQPFTTIPFPPPP*NGIPTEY
	ŀ	l				GVPHTQDYAGQTG\EHNLTLY
		1	1			GSTQAHGEQS\SNSPSTQNGSLT
1						QTEGGAQT\DGQQSQTQSSENS
	İ	l				ESKSYPRNGLHVSYYFLSGFRD
	i	ł				P\DFRQMFG\QFGKILDVGIIFN*
						RGSKVNNATARVMTNKKMVT
1						PYANGWKLSPVVGAVYGPELY
		1				AASS\FQADVSLGNDAAVPLSG
		1				RGGINTYIPLIIPGFPYPTAATTA
		1				AAFRGAHLRGRGRTVYGAVRA
i		1				VPPTAIPAYPGV/DLPGTDFTVL
i		1				TSMVDMQPTDMHSLLLQPQPP
i		1				LLOPLOPLTVTVMAGCTOPTPT
1		1	1	1		MPLPLPLAMELALWRVYTEVA
i		1				TADLPPTEVTVKPLQMGQPPSS
26315	56683	A	26462	1196	1459	KOCORRCLETEVWKLSKLOIST
20313	50005	l^	20402	11120	1439	KASNRODRSTFSAPPRKSOLM
ŀ		1				W*TSLLSYFOKLPOSPOPSATT
		1				ALISQQPSTLNPQPWPGSCPGG
26216	66604	١.	26463	2234	2702	MLFIAAMAPPSLSSDAAMTTGI
26316	56684	Α	26463	2234	2702	
		1				SSCLPSTACRRAFGTKSIG*GPTI
1		1				PESSRWQQKGGVSGDGRSSCR
		1				RAVAPLEPVPRAPEAA\ARPRPP
1						SHGRDPPPGPDPPPLRTPASAM
		1			1	DKSAGTSCRLSPLKALGSARAE
l		1			1 .	QTMGRPAAERSYPLLRAQYSSR
25215		١.	25151	70	200	MARTIN AND PROPERTY OF THE PRO
26317	56685	Α	26464	70	398	MLFIAAMAPPSLSSDAAMTTGI
		1			1	SSCLPSTACRRAFGTKSIG*GPTI
		1	1		1	PESSRWQQKGGVSGDGRSSCR
		1	1		1	RAVAPLEPVPRAPEAA\ARPRPP
		_			I	SHGRDPPPGPDPPPLRTPAS

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26318	56686	В	26465	18	123	
26319	56687	Α	26466	19	347	
26320	56688	A	26467	3	746	SRKLLSKSVP*LNP*SR
26321	56689	A	26468	1705	2031	CDAPGDPQPGLRDISWLGTTDR SASPQRLAAAALTAGNGRRCSS GPRRRPPP*PLARPRQRRQPPER QPVVWPPAFPARWAEHTCPLA PWQPRSPTTPSQPAAVTARAS
26322	56690	Α	26469	1	420	
26323	56691	A	26470	65	330	RDCEARCARGPFWSWLSPRRK GKRQKSQLISQRLERHFLSGKN RQKRPSKMAGPDGAAPLEPGA VAAPMGPKSSRGSPGRAGKAA ETS*SPGRAGKAAETS
26324	56692	A	26471	327	981	ASYOKFFOLLPOCNLAPSPHPO VPATPSTSWOHLSKPPGAFKKR HSSSRCPKAGHQWGGGQRNTP TAAHFRRLSAGSLQLCPQLEVS PLTTOSLPPRSKEPPRTPAPPSPY PNCRPLPKSTRTTSVGWSOPPSC GTELQSHPGAPAG*GSVRRFF LGP*RMPS*ALL*KHTGGL*GPP HPPMPTMCQPKQASKLQLLNC PQPSFSQGAGATMGNVG
26325	56693	Α	26472	336	923	LKNIFLSLPRSINIRFATLLDTPG VENLVIACLQKHS*PYF*GS*NI CLSFQDGTLYHKMHAVCLKCL *KPSLLSLL*DIEYIRSHYNIEDFI YFSHHQREEHGHMHHFALNPIF RHYTKFFLKYYL*SCTQTSVLS LSDILSPKI*IAVFQFQNPYAHSL TSALHYLVPVRPRLLPGLDDQC PGHNTFPVVSIN
26326	56694	Α	26473	97	298	DNLTLLPRLECGGMIMAHCSLN LTFSSDPAASAS*VAGTTGT*H HAWIFVFLCNWLRNRGVTVKK RS

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
26327	56695	Α	26474	1958	3269	KFTMSILKIHARELFDSRGNPTV
20327	30093	^	20474	1938	3207	EVDLFTSEGLFRAAVPSGASTGI
						YEVLELQDNDKTRYMGKGVSK
						PVEPINKTIAPVLVSKKLNVTEO
		1				EKIDKLMIEMDGTENKSKFGAN
						AILGVSLAACKASAVEKGVPLY
						HHIADLSGNSKVILPVPVFNVIN
						GSSHAVTKLAMQEFMVLPVGA
						ANFREAMPIGAEVYHSLKNVIK
						EKYGKDATGVGDGGAFAPNIL
						ENKEGLELLKTAIGKAGYTDK
						VIVSMDVEASEFFRSGKYDLEF
						KFLDDPTRYISPDCLADLYKSFI
		ĺ				KNYPVVSTEDPFDODDWGAW
						OKFTASAGIQVVEDDLRVTNPK
						RTASAVNEKKCNCLLLKVNQIR
		l				SVTESLQACKLAQANGWCVM
		ì				VPHHSGETENTFITDLVVGL*PG
				i		OLKTGAPC*SERLAKYNOLLRI
						EEELGSKAKFAGRNFRNPPAK
26328	56696	Α	26475	2	684	HSGSSLLHFPILLINRKGFSPTG
20020	30070		20112	ľ		MISLMCNRIVLSTHAKLQSCTP
						SNLPSQLPIGLSMSTPTKYRKLS
1		ļ				FPGKTSONITVPDSIVSPIFKETL
						EFISKGGSSTCIVSPGPA*SLSNA
	l		1			VSSSSMSSSLSNATNTPQSSSH*
		l				KSCFPWYTPSVKP*PRPSSSNST
						PKNIPETVLSANRGPLKRTTPG
		Ι΄.		1		NFSSPDLSCTFTGQPPSIWRPLL
						KLVSGFKQAEPLLTIGNCQK
26329	56697	Α	26476	1284	2339	APPSARGACAASRRAAVPALPT
					\	PPSVCSGSHMSTYWPAAPR**T
				1		PGSSTAASPSPAASRAPRAASPV
		1		1		LTASPPLPAASPSPAASHAPPAA
1						SPVLTASPPLPAASPSPAASPAP
1				1		PAASPVLTASPPLPAASPALAAS
1		1				PVHTASPPVHVASPPVHTASPP
		l				VHVASPPVHTASPHVHVASPPV
		1				HTASPHVHVASPPVHTASPPVH
					1	VASPPVHVASPPVHIASPPVHT
		1				ASPHVHVASPPVHTASPPVHVA
1					1	SPPVHTASPHVHVASPPVHTAS
		l				PPVHTASPPVHVASPPVHVAYP
1		1				PVHVASPPVHVASPPVHVASPP
1		ĺ				VSCSGDSTSDCFPPQPGAVFPHS
		1				LAPSLGGWSHLVAALP
		-				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nueleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nuelcotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26330	56698	A	26477	131	544	TGRPLPRPLKTQEIPSGCGVMG
				İ		RATPGTSGLGDSVRRVRGAIPA
						PRSSLGRGFTCV*LTTGAOLAPS
						LVPAAPRLPAALMDIQPEPLAS
	1	1		İ		AAPAATGPAQVTAATPLTTASA
	1	1				TPLTTETACSLGSSAASPLAPRA
		1				HCV
2633I	56699	Α	26478	1440	1877	PFQNLFQRNERTSCLCCLCMGA
						TWASLRALCCSPSP*HGWISW
l						WWSTPTPFANGSVTSCSALTRS
i		ŀ				RWRPTWSEASGLWHAPAALL
		1			]	WKLRPLTPCFRSPISLSDLDLTS
		l				HHQQGAPTMHTCLGVGSSSWE
						LQAIFVLSYWFSPLHC
26332	56700	Α	26479	56	345	ITWHLGLMMLSRSLGL*SGISFI
l		1				NFPM\K*EMIPY*KLS*IQNLFQF
						PKVRPKGSQFGQVKH
26333	56701	Α	26480	392	634	
26334	56702	Α	26481	416	601	FLITDPRIWKASSDPSAKLFTFP
	1	1				SGFLM*AGTWMKLETIVLSKLT
						QEQKTKHCMFSLISGS
26335	56703	С	26482	34	279	
26336	56704	A	26483	173	307	
26337	56705	Α	26484	196	527	SAVAAACSRPEEDAMELVLVF
						LCSLLAPMVLASAAEKEKEMD
l	1					PFHYDYQTLRIGGLVFAVVLFS
						VGILLILSRRCKCSFNQKPSGPR
						R*GSPGGRTSSPPMQQKPQKAE
26338	56706	Α	26485	597	797	PSENELKALGYTSSAWKRFSEQ
		1			\	QWGLSLGSSAPSWRLPW*GDW
						ELPGEPGGDSSHRPFPGPIPRAP
26339	56707	A	26486	3	184	
26340	56708	Α	26487	256	635	GCVAPQIREQHAQSTENAAKPT
	1			1		RRIHSROSEKPGRWRHGWRAG
				1		GWRRSKRAPARHRPRCPAVCP
l	1		1			RDGEDCSREAAGA*GLSGSSAC
	1		1			PTSSTGASCCFCVPGOLNSVGF
						AVLGSKVLWTPGESPFCQ
26341	56709	A	26488	1	378	
26342	56710	Α	26489	1	571	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		_				
26343	56711	Α	26490	105	849	RRQDSGQSPAWPAGALLLTLLT
						HCAVPGSWAQSVLTQAPSASG
	l	ŀ				TPGQRVTISCSGSSSNIGNNPVN
	1		į.			WYQQLPGTAPKLLIYRNNQRPS
						GVPDRFSGSKSGTSASLAISGLQ
						SEDEAQYYCAAWDDSLNGSYV
						FGTGTKVTVLGQPKANPTVTLF
		1				PPSSEELQANKATLVCLISDFYP
						GAVTVAWKADGSPVKAG\VET
		1				NKPSKOSNNKYAASSYLSLTPE
		1				QWKSHRSYSCQVTHEGSTVEK
		1				TVAPTECS
26344	56712	A	26491	129	1191	RSRPOCLGPOGRRVTISCTGSSS
	l -	1				DIGAGYDVHWYQQLPGTAPKL
						LIFRNSNRPSGVPDRFSGSKSGT
		l				SASLGHHWGSRVEDEADYYLP
						VPIDSSLSGSTVLQARGELRQEP
1		1				TSSSARRSMKKGRDLGEAQLQ
1	1					LRVEKTGLRTISSMAWSPLFLT
			1			LITHCAGSWAQSVLTQPPSVSE
						APRQRVTISCSGSSSNIGNNAVN
				1		WYQQLPGKAPKLLIYYDDLLPS
			1			GVSDRFSGSKSGTSASLAISGLO
	1		1			SEDEADYYCAAWDDSLNGYVF
i		İ				GAGTKVTVLGQPKAAPSATLF
	1					WPSFEDASDDEAEL*CAIRDYY
1						PKAVMVA*KTNITPLKQGKDTP
	1					SPSLLTPSSDEVKSYKNLLPGFP
26345	56713	A	26492	283	840	TLPAGFTDVISIHKTGENFCLIC
20343	130713	l^	20492	203	340	GINGRFAVHCITLEEAKYKLCK
İ	1					VRKIWFHDAHTIHYLDSFVKVN
1						DTV*TGKITDFIKFDTGNLGRIG
		İ				VITNRKKHRGSFDVVHVKDAN
			İ			GNRFAPWLSNIFVTGKCNKPWI
						SLPRGKGIRLTIAFHSDKWFCSD
i	1				ľ	
1	i				ŀ	ISVQNLCKRFSQGDTGIKNSEA
26246	56714	١.	26402	1	0.40	RRCSNLQV
26346	56714	Α	26493	['	843	MARGPKKHLKRVAAPKHWML
1		1				DKLTGVFAPRPSTGPHKWRECL
1						PFIIF\LRNRLKYALTGDEVKKIC
		1		I		MQRFIKIDGQVR\TDITYPAGFM
		1		1		DVISIDKTGENFRLI*LTPKGSAF
		1		1		AV\HRITPEEGQVQSCAK**RYI
		1	l			VGTKRNPFI*VTHDAR\TIR\YPR
		1		I		NPLIQGEMDTPFQIEFKKTWPR
	1	1				LT*FPSKVPNTG*PCVMVTWRC
		1	l			LTLGRI\GVIT\NRERHP\GSFNV
	1	1	l			VHVKD\ANVNRFA\TRLSNIFVI
	1	1	l			GKGN\KPWISLPRGKGIRLTIAE
		1		I		ERDKRLAAKQSSG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26347	56715	IA	26494	375	11327	QPYFPMETVMTLEGGQKPVME
		1				SYTLHYLPCLLCLPWRNPESSE
		1				WQRQLLDFPLASAPGSGLTQH
						MAAPKSGQNLEAKPKGQASLV
	ı	1				LSSRKICGVLSGACAACPGGPA
	i					R*VDPAIPFPLAGEAGLEGRPRP
						ORCAAKWOSRDLIPGLPGSTGL
						PFPPY/PPCSPGALLSOSPPOAAC
		1				SLLARTPHAOGCPPPRLRPARIL
	1					PWPASSARRYTPOPSRKGTORT
						PLFSLNLLETTTASYSLDFLLTA
						PEGFSPLFTASOEHDONOOEHD
i				į.		FLLQDEGLRSPVKTRARLPLGL
	l	1				HGDKVEKAGPWSLGARESNLC
		1				SATSQRSAVAAGVPRAQPLPPK
l	l	ı				GKGWLDPPTWOGRRDTORTLR
	i			l		SIHHRFYGYSARGWPGPLALLO
		ł				GFVRSLELPCAGSDONRGORLK
		1				GNPGAAFAIPKTLDFSKAGKED
		l				KGGNGVCTTPSOAFDPLPRSSO
1						SPLGNMAVSGSSSSGSWKSSGT
1	l	1				OEKKSLNOKRKVDEAEKKEEK
						EKKKEPEPNFQLLDNPARVMP
1	l	1				AQLKVLTMPETCRYQPFKPLSI
1		1		1		GGIIILKDTSEDIEELVEPVAAH
1	ì					GPKIEEEEQEPEPPEPFEYIDD
26348	56716	В	26495	1919	2074	
26349	56717	Ā	26496	179	431	PPTSLIRVSCTSTSTSLCTSWLCS
						SLSWLYSWAGPFFSGKMTASC
1						RGSGQINREIVLMLLLRS*VFVV
1	i			i		ISPLEGGSETSPFMDL
26350	56718	A	26497	37	199	DGLPGLALGLDAQASWSASVV
		1				TGHRPPAPPGLALGGCHGPAAP
						P*SGPAGSPCH
26351	56719	A	26498	3	224	TGHRPPAPPGLALGGCHGPAAP
						P*SGPAGSPCH*TAPRGAGTPLP
		l				GSRRTGTSPWPHPPGLPHIPDVT
		1				GGHRH
26352	56720	A	26499	151	403	MPRHRRSASVVTGHRPPAPPGL
20352	30,20	ľ.	20.00	1	[	ALGGCHGPAAPP*SGPAGSPCH
				1	1	*TAPRGAGTPLPGSRRTGTSPW
			1	1		PHPPGLPHIPDVTGGHRH
	1	_	l		I	I III I GEI IIII DY I GORKH

SEO ID	ISEO ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		<u> </u>		<u> </u>	1.00	
26353	56721	A	26500	1	465	VSPKLLPSYASRPYLVPNALSSP
		1				SVPPALSASSAPPRPATRRRPPP
		1	l .			RGLSASWPLRRRSRQDAGAGS
1			ĺ			RRLRERQNRGRRRSDLAPTLGA
						GLRRDRPGRQPRPGKALAPFAV
		1	İ		l	PRPRTNFRGRS*KSGSQRTRTPP
	ĺ		l	İ		RREICRTHSRDRPRKLVRGRGT
						ANGARALPGRGWRPGRSRRSP
			l			APSVGARSERRRPRFWRSLRRR
						EPAPASCRLRLLSGHEADRPRG
		1				GGLRRVAGRGGAEEAESAGGT
		1				LGDERALGTR
26354	56722	A	26501	1	1344	
26355	56723	A	26502	548	689	LGKFAPGLTASKAEATAAELCL
						KYPLEICTFL*GCVCVCVCVCV
		1				CVL
26356	56724	A	26503	154	476	TLA*AAAASTSCSPRPPPPSPAS
20330	30,24	Ι.	20505	1.5.	1	TTTRWRAPWRTR*EPPESLCTG
		1				MRSWPSGMTACTQTPSTAPPSP
į.	1	1				HPPSLSDSSALCSSASVRRMWI
	i	1				MKRLKPSMMHVLCMTVDL
26357	56725	A	26504	920	1420	TLA*AAAASTSCSPRPPPPSPAS
20337	30/23	l <sup>A</sup>	20304	920	1420	TTTRWRAPWRTR*EPPESLCTG
İ		1		l		MRSWPSGMTACTOTPSTAPPSP
	t	1				HPPSLSDSSALCSSASVRRMWI
		1				
		1		l .		MKRLKPSMMHVLCMTVDL*LI
		1				PTSTPTT*PSELLAPSPNSPIDTT
		1				QMSGLTATSVPKKLAFSWQQL
		ļ.,				CYISLIQPLSL
26358	56726	Α	26505	1118	1403	AGWDPSFLISFSGLSNAISSSSSS
l		1				LSSQ*ESNASA*YSSATSGSSGIS
1						WYPRSDVASSTIDSSSWRSMEG
	ŀ			i		IG*DSGRFSKVGSSDSSSLPCHL
		_				SS
26359	56727	С	26506	29	379	
26360	56728	Α	26507	3	948	GVSLCCPGWSAVVGSWLTAAS
1		1				TFRAQAILSSSWAYREPPVRVG
		1				RRPQPPLLLTRAQGRVISSSFRH
		1				LHDFVWRTAGKESTSGANETG
l		1				PLPERGRRPGGRGPGSRSPRSH
		1				AVQREGAAGSVPAAGRDGGRA
	l	1				GHDVPHEGORAEAAAGEAGGE
		1				FPLLLSDRRGRARRSPAAGALO
	1	1	1		1	SRPGRARHLLHOLH*GP*EEVS
		1	1		1	L*VQQRGAVSGVDGGSASGQL
	1	1			1	RVHAEKAHLLQERNPEG*RAK
	1	1	1		1	DPLGTVSALSEEARFOLRWLAG
	1	1				VSAGHGGORAAGRDWPCPAM
	1	1	1		1	NRLAMPGSVLFWFLVFGSGFH
	1	1				
		_	<u> </u>	L		CVAQARVQWCHSSL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
26361	56729	A	26508	31	202	ILITYIIKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQFL
26362	56730	A	26509	471	1716	EREGGYGQLLEPRETHIGQILYA RRQGADAAGDSDFCTEWPAAL DSDEKCEKHFPIEIDSTDYVHH GPSVRNPRARVVVLRWLRITLH GPSVRNPRARVVVLRWLRITLH GSAVFGLAVFPARRHEFEY SIPSPSQAFTPAVLATRVTCQLG GHTQIQNFTVAPTILGNTTFIFLI TCFRIFISLPRHLFPKDKWRTLG APPLKTLLLVGTESSVHLSGIPP DLLVFEQSPTYLNTRSSNRWD RLILKAMNLDKQTTTITGMLP STEAPSSTTHQDLVVNTNSTSY SKELTIDF WARFTSLNESIITKI NKVSPSTDFISNPDNKTISPFFEP IDTKLSHMPVPPGLNSSKQLLN KTKGYNSRNHTSANEDEVSVT SKTWLVSVALCTSVIFLGCCIVI LASGCCGROGGYKPCGRKSG SLQIKNRNHIMKENSS
26363	56731	A	26510	410	867	LLTLSRTTFLMSLGFFGIPKMIN RPRQSSPIKLQNSSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRYWTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISRFVFAA GQGLLGGYSNPRYSFSF
26364	56732	A	26511	135	756	VITILTPMLADRTREIERPPKK GTTSLIGORKULTGDWPSVYP VA\HPFKPSAVPLPVPNGLSSK KRACPWQ*EGRVLELKINPNFS GF*LPVGN*KSTCEALKDF/CAL SGFAALGGWTRKC*GR/PFSI*I* GH*LWFHQDHPVRNFRARX LKSKAFSV*I*HDHAKKTLITLV GERYCKTPDVLTIKQNRWPLRS QTTIMPYVIL

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2 (2 (4	A C#00	<u> </u>	0.0510	161	2150	har by the transport of the ball
26365	56733	A	26512	161	2150	YLDAEKMGQKASQQLALKDSK
		1				EVPVVCEVVSEAIVHAAQKLKI
	ł	1				YLGFEYPPSKLCPAANTLNEIFL
			l			IHFITFCQEKGVDEWLTTTKMT
		1			i	KHQAFLFGADWIWTFWGSNKQ
						IKLQLAVQTLQMSSPPPVESKP
1		1	i		i	CDLSNPESRVEESSWKKSRFDK
						LEEFCNLIGEDCLGLFIIFGMPG
						KPKDIRGVVLDSVKSQMVRSH
1		i				LPGGKAVAQFVLETEDCVFIKE
						LLRNCLSKKDGLREGGASPGSL
						RLAAPGPPLTLNAACPLRLAVL
						AAMAAAALPAWLSLQSRARTL
		1				RAFSTAVYSATPVPTPSLRVDD
				İ		LHLTEIVGMLDSVLTPEDSSGK
		1				YRFISGEVLCRITGCFTGVRVEA
		ı				KDLFGGCCSNPNEVMVTWIKV
l		i i				VEKEVWLYLRYILKALPPRTEK
ļ				1	1	MAVDQDWPSVYPVAAPFKPSA
						VPLPVRMGYPVKKGVPMAKEC
						NLELLKIPNFLHLTPVAIKKHCE
İ						ALKDFCTEWPAALDSDEKCEK
			İ		<u> </u>	HFPIEIDSTDYVSSGPSVRNPRA
i		1				RVVVLRVKLSSLNLDDHAKKK
		1				LIKLVGERYCKTTDVLTIKTDR
	ļ	1				CPLRRQNYDYAVYLLTVLYHE
		1				SWEYWKEWGKK*D*SRHGKSI
1		1			ŀ	YGENSSSERKYPGKRFSR*KLL
		1				RKNMGN*LKKSSLGTKEIEEYK
		1				KSVVSLKNEEENENSISQYKES
26366	56734	A	26513	3	1186	PASTMSIRVTQKSYKVSTSGPW
20300	30734	ľ`	20313	ľ	1	FFSSCSYLSGPSAHISSLSFSRAG
		1				SSSFOGGLGRGYGGASGMEVIT
		1			l	AVMVNQSLLSPFIDKVQFLEQQ
		1				NKMLENKWSLLQQOKMAQSN
		1				LDNMFESYINNLRWOLETLGR
		ı				KKLKLEAELGNMQGLVEDFKN
		1				KYEDEINKYTEMENEFVLIKKD
		1				VDEAYMNKVELEYRLEGPTDE
1		1				
		1				NFLRKLYEQEIRELQSQILDMS
						VVLSMDNSHSLDMDSIIAEVKV
		1			i i	QYEEIANRSWAEAERMYQN*Y
	1	1				AKLSQLEAALQRAKQDMALQL
		İ				HEYQELMNFKLAQDIVITTYRK
	1	1				LLESEGSWLESGMQSMSIHMK
		1				TTSGYAGSLSSAYGGLTSPSLS
1	1	1	1			YSLGSSFGSGAGSSSFSHTSSTR
		L				AAVVKKIEAQNGKLVSKSSDV
26367	56735	В	26514	361	1215	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	tocation of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
İ				sequence		
26368	56736	A	26515	230	561	VRTRHLFCEAAAEETPVFTMA
20300	150750	l^	20313	-30	150.	NEKPTEEVKTENNNHINLKVAG
		1				ODGSVVOFKIKROTPLSKLMK
						AYCEPRGLSVKQIRFRFGGQPIS
2 (2 (2	56737	ļ.,	0.000	1242	1415	GTQRNLS*KKESVDAASFIVVL
26369	36/3/	Α	26516	1242	1415	NSPSDSSLVWAWRRPQSRSWS
	1					ERGGGANNRGGGRLLGNSVFG
26370	56738	В	26517	1	585	RK*LPHRRVSRVPNTK
26371	56739	B	26518	258	1081	
26372	56740	A	26519	42	275	TFAWSEEGTSPPSIQSSWDPRCP
20372	36740	A	26319	42	2/3	HRNTPAOTGKPPKRAWPRHPV
		1				HH*EPHGDQQDDGPAVSPP*SY
						SQYPWPEGLDV
26373	56741	A	26520	646	1905	SQ11 H12G221
26374	56742	A	26521	6510	7361	
26375	56743	Α	26522	1	879	DCQDKVPRRKEPSMCSGLLRV
		1			1	KSWVSLQTYWKPRATQGVYV
		1				LPLTEERMVVLGASRVGKSSIV
		1	i			SRFLNGRFEDQYTPTIEDFHRK
		1		İ		VYNIRGDMYQLDILDTSGNHPF
1		1	1			PAMRRLSILTGEAHWCLGWGG
1		1				RARAWVRSVLGT*OILEVKSCL
1		1				KNKTKEAAELPMVICGNKNDH
		1				GELCROVPTTEAELLVSGDENC
i .		1				AYFEVSAKKNTNVDEMFYVLF
						SMAKLPHEMSPALHRKISVOY
		1	1	ľ		GDAFHPRPFCMRRVKEMDAYG
	1	1				MVSPFARRPSVNSDLKYIKAKV
ł		1				LREGOARERDKCTIQ
26376	56744	Α	26523	2	478	
26377	56745	A	26524	120	1167	GHVGHMCTGQHMASAYVGRV
				i		NVLRKEVDRACFGEKAKQ*VG
1						S*EELWAIWGQGREVCLGIEEA
i				i		GAIISTRHCNSQNGVRVWAPYL
1						WALEAAPV*VQDRSSPGSQACS
						LPSPCALTMGTGIMPLYQEAK
						WKPRQRPGTSGGTVSSEPHC*D
						AGSGCWLCQPGLREVAHVSAE
						ITYTSKHSVEVOVNVMSENILT
		1				GTSGSDSVDWSSKGRGYTAAS
1						LLRAEDAPGPGPKVLEVPPVVV
1		1				RCPFYFSLGGRWQRSGHLT*LE
1		1	l			TKWRNGDIVQPVLNPGKSRGH
1		1				QQQVPLLTGDA*EAGALHGFV
1		1				HGGKKEAPWPLHSCPLAHCCFS
1		1				GRYNRPGAVAHACNPSTLGDG
26378	56746	A	26525	225	438	SITTING ON THINGING STEUDO
26379	56747	A	26526	216	364	
	1-0.11	1				L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nuelectide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequenee		
26380	56748	A	26527	2	397	SCCSDWSAMA*SQLTAISASWV
20300	307.10		2002	Ĩ		OAMLLPRRPE*LGGSNPEGTG*
1	ŀ	1				SERRLCHYA/HSLGDRARIHLH
	ļ.	ĺ				KKGROEGSKEMSRAOTRRVW
						HATMETEQKQNYGRL*CCSPST
						NTRRRTSMRKNKAIAREIERYS
		1				KGI
26381	56749	A	26528	312	1061	QQTLYSFGVSFYFSSYCLIFSHG
20301	30743	^	20320	312	100,	CSSSSICRRARLYHWAAPFRPP
İ		l				GRKRRDCTGQRKTSAGEPEIPP
	1	l				PLHHHHHHYSHHHHRHRHHH
		1	ł			HHHHGLORSSKNFLLWPE*ILF
		į .				CGSRRLGRAALFLLRSFSHPAK
1	ŀ	ı				QGAESLLGKQS*KHLASTQCGP
						RGRGS*EKWPRAQLGRKQPSES
						AAGAAGLAHGPODSLVLERAG
		1				EK*SGLRGEGNRPFGGSSSLGG
1		1				HPLLQRSPAESSPAGTGVRTSH
1	Į.	į.				LEGRPASFR
26382	56750	A	26529	161	453	SSSLPCSPSSCPHTSFFLDAROEP
20302	150750	ľ.	2002)	101	1,33	RTCRVVGLKEL*QKQGLPHCR*
		ĺ				OEREKSCSPSGSPDLGAPOPRA
		ı				VTPSLGLCSSWHLQASRRHCTP
1						RCPOWKR
26383	56751	A	26530	301	630	RWKPKIRGSEGSAS*POGR*LLP
2000	100,01	1				SGRRG\ATGSAESTLPKAESSAG
		1				DGPVPYSQGSSSLIMPRPNSVA
						ATSSTKLEDLSYLDGORNAPLR
		ĺ				TSIRLPWHNTAGGRAQEVKA
26384	56752	A	26531	h	1394	
26385	56753	A	26532	240	1150	LLLHVPSPSPASTGPPSCGPCWP
						PRSAPAAGRGSSSGCLAGEDPA
		1				TTHKSAGTGECHRGPVGHCGO
		1				AHTGPSYPSGPPASCGPAASAV
		1		İ		TRGOSCRSLTFRPGRHOIPGAE*
1		1				QLPRGQGETGRTGLGHYLTLLS
		1				CSSRWPLPKSGDGSPSRWEYRD
1		1				S*ERPGRRTAPRCCSRSTGLGD
1						GLKKFPSSY*GP*KCAPSGCGG
		1				QAPWSAGGSTCPPDART*MPR
		1				ARARSWAHTGRPCFPRLLSIOA
		1	1		1	TP*RTGGRTCGFCLAS**GSRRG
		1				RPSSAESLPIPAPPGCGOH**PER
		1	1			SARLSWGGGMRGPR
26386	56754	A	26533	1463	1627	
20500	100104	10	1-3333	1	1	l

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26387	56755	Α	26534	I	1758	MHKYVRYSTVHNSEDMESTQ
		1				MSINDRLDKENIIHIHRGILCSH
					i	KKKODHVLCKNIGEAGNHYPQ
		1				QRNTGTEKQIQCVLTYKWKLN
		1				NKNTWTQSEEQYAVGPVGGRI
		1				GRLTNNRHTQDSESWVRGVTA
					1	FWSRGANNALDIPAFIIKFSEGR
					j .	GSLHTHDGPPGPTSSLKLSFSHS
				I	1	FDSTGLCRPHDLVLGLIIPTMVN
				1		ITSOLDWLEDAOMAGEALFLE
						GKLTTRKDIYTENPSLHHHHOR
						PKVDKTTKMGKKQNRKTGNS
				1		KTQSASPPPKERSSSPATEQSW
		1				MENDFDELREEGFRRSNYSELR
		1				EDIQTKGKEVENFEKNLEECITE
		i				ITNTEKCLKELMELKTKARELR
						EECRSLRSRCDQLEERVSAMED
		1				EMNEMKREGKFRDKRIKRNEO
						SLQEIWDYVKRPNLRLIGVPES
			Į.			DVENGTKLENTLODIIQENFPN
		İ	İ			LARQANVQIQEIQRTPQRYSSR
	ľ	1				RATPRHIIVRFTKVEMKEKMLR
	ŀ	1				AAREKGRVTLKGKPIRLTADLS
		1				AETLOARR/DVGANIQHS*RKE
		1				FSTQNFISSQTKLHK*RRNKILY
		1				RQANAERFCHHQACPKRAPEG
		1	1			SAKHGKEQPVPAAAKSCONV
26388	56756	A	26535	620	886	INGVILSKPPLPPISTTPIAGALLI
		1				PLTKEQRGDF*KPSRNMRTSCW
						KTPESRANFLKFRPRSHCLTRM
		1	İ			GSSCLLPSKTCLSSSSTFHH
26389	56757	Α	26536	237	415	RCLORPSAGTAGHPPSAGRPPL
			I			AAGLAG*RARHRSDLPGSAASS
						QESWCLRAALPEAPA
26390	56758	Α	26537	373	691	
26391	56759	Α	26538	2	233	
26392	56760	A	26539	5	68	ALQWEEKHEL*EQSLHRKPGG
26393	56761	Α	26540	184	434	GGRRGCTVGEAAVTQSLSLCS
						HEGRAIRHQRDSASIVLLDQ*Y
		1				TRHPVLDKLLAWI*ALAEDKAT
			i			LGSAIAAEWKITPAFSFP
26394	56762	A	26541	466	683	GRPHSLPHPHADSSELTTDCS*
						WRWIFKHKTDHIRHQRVHTGQ
		1	1			KPFKC*Q*GKAFRHSFDVTKHQ
		1	1			RTDAVGLHQTCCLGGVLLWGA
	1	1	1			HWRGHPSYSLWSAHCCQHGGE
1		1	1			GASGGGLSLHLDRLSLDAAGRI
		1	1			QPVLPPTGQNILVGPLPQISLCS
1		1	1			RSLCVLRLDGLSQLSPGEEGSH
l	1	1	1			SQKWTSQEVKLFRSRHQSTSDV

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26395	56763	Α	26542	194	558	GCDRPSRPRPGAPRPPAATASC
			l			PPRSCWPLVPSPHCP*PCRKRRY
1						PGERRTSPAPPVPPGPGRPAG*T
i			l			PPCELRPSSTHVALLGLALPGSE
						GTGLRTSVRARDRLHRRTRERA
		1				AAGTAPGP
26396	56764	Α	26543	ī	248	MVAIHNADDAKCWGDVEOLE
				ľ		LSFTAALPVLPHPSLPGERPLQE
		l				AVAFLCWLLVDVLLKATVSKV
			İ			GGGSALASVARVMKAQAFSPL
		l				LRILHKASTSSFRARKDSAHTPS
		1			1	CLLTPSGPERAGPLTQDSCQPSP
ĺ		1	ŀ			HDSFRAPALLEPSSALSTAVASL
1		1				RRREERLEPEORVGELGSLGER
l		l				QHEPSDNHDFQPKSKQEQLQK
l		1				TLOPSGGPHCSSLLLMVFWWK
		l				OWRKTEPLKAERTGYKEKEIST
						KCSSSPSGQLSQSSAAGPAWPE
						DARPEATWSATLLSFDPRCKND
						SIEEPCSVHISCTAYSDPLKIHNS
					ì	YRECGLCPEVNLEVADPSSSSR
						ELWFRAGAQGAGAMQGVTEL
l		l				RPPEFVKSRKPQVGSGHMGNC
				i		LSKGKRFLGHCQYKQGLPQRH
						OLOAEERESGMRHTTGGAYAV
1		1		1		LTTGVSPWWIWIWERRWPCAF
						PGKNEEPAGKVPFPSELVLTLQ
1		1				RC**COMLGGCGAIGALIHCCS
ļ						ACAASPFSPWRKAPPRGCCFSL
1		l				LASGRCAPEGNCLKGGRRORT
l		1				CQCGSGYESTGF
26397	56765	À	26544	423	621	LPSRGAGLGTCSPPCLSLPSPPW
20397	30703	l^	20344	423	021	APVRPEPPR*SPPPAPORPVPSTT
						QGLNCAGAGHGTGRQLHR
26398	56766	A	26545	1162	2027	MTPEPEWSLS*VGNYKRTVKRI
20390	30 /00	^	20343	1102	2027	DDGHRLCSDLMNCLHERARGV
1		1	1		1	SRADPTMAGAE*PAASLPCTGP
ĺ		1	1			OYGTVEKAWMAFMSEAERVS
l		1	1			
		1				ELHLEVKASLMNDDFEKIKNW
1					1	QKEAFHKQMMGGFKETKEAE
0.000		ļ. —	0/0//		504	DGFRKAQKPWAKKLKE
26399	56767	A_	26546	1	504	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
				sequence		
26400	56768	Α	26547	3	1215	QTMYFLTPILVAILCILVVWIFK
	İ					NADRSMEKKKGEPRTRAEARP
						WVDEDLKDSSDLHQAGAGGN
						AVEGVDQSKVNGRATGFASKL
						DIGKRRREGELETGSYPPKTHA
		ŀ		1		YALKKSGPWNPGTWQHRKIVR
		1				GLQFYTVFFPHSSVLAFLAPVID
ĺ		1		ŀ		PSVASSSSLRSSTTDNELAELSE
		1				FADADEWQESEENVEHIPFSHN
				ļ.		HYPEKEMVKRSQEFYELLNKR
		ŀ				RSVRFISNEQVPMEVIDNVIRVT
		ŀ				GTAPSGAHTEPWTFVVVKDPD
		l	ŀ			VKHKIRKIIEEEEEINYMKRMG
						HRWVTDLKLHRTNWIKEYLDT
		l				APILILIFKQVHGFAANGKKKV
				1		HYYNEISVSIACGILLAVF*NAG
1						LVTVTTTPLNCGPRLRVLLGRP
				1		AHEKLLMLLPVGYPSKEATVP
						DLKRKPLDQIMV
26401	56769	Α	26548	3	263	RPGEMACKYPLRCSGARVERL
			l			AKKKAHACLLWTATIKVITNSV
						KLRRSS*GNRLKPSILC*DMKA
						LRQYPMPLRAWLLPMVVWVM
26402	56770	A	26549	82	318	SGEAGKEEGTRMVRIRPEPKRS
						LLWTATIKVITNSVKLRRSS*GN
ļ		1				RLKPSILC*DMKALRQYPMPLR
						AWLLPMVVRVMV
26403	56771	Α	26550	91	714	SESLVLVWCGRVSCVLFCVCD
			l	1		VCVLVGGSGVAVRCFGGRGCG
						PRRVGRRWSCWCGWCGAVLIR
		ĺ		1		RVCLAVMFGLALCVHPLLYPR
						TLLLRGQKVDRFKTNLSSGESL
						VTLVIFPAHGLARSRFLNLDVL
						FGVHFIAVEFWHAVGLIVNKQ
						VKGKILAKRINALIEHIKHSKSQ
						DSFLHCANEQRQT*QCAGPCM
L		L_				GPEPRQACLNTCIRS
26404	56772	A	26551	29	363	FAKMTNTKGKRRGTRYMFSRP
		1	l	1		FRKHGVVPLATYMRIYKKGDI
		1	l	1		VDIKGMGTVQKGMPHKCYHG
						KTGRVYNVTQHAVGIVVNKQV
						KGKILAKRINVRIEHI\KHSKSR
					l	DSFLKR

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon fur last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26405	56773	A	26552	186	512	FHLSKHRAPPYPVTAPPRTSWG
20403	30773	n	20332	100	312	SLVKOVNESNGSRLLRTSLVHE
						DLEGVSVVSGMNCDSALARYII
						ILETLIIYLISPRCWIIDSSGACSG
						LAMYLPLLGDDGVLLCTPNFM
					ł	AWRSNRTQFMMRSSSHMVDAS
		l				PRGRHMSPREEAFGYSSRASHM
						LLSLLAPPWPQLMGRGLGCQQ
				l	1	OERPOECVPLGMTRSPYSEIHF
						GSSRALGSSPGSCAHEVLGPSIL
	1	1				TVNPFIPGSSVHVWPSNGNETN
						KLPHTRAGSCGSATCSVKRWG
		1				POKPRPLPKPPLVPOALLLVRG
		l				PAAAREEAVQPPKEEVTQRPGG
		l				HSSPGVFAHLKGPRSVVEIRME
		l				YGEE*PPGRCVTSSFGGWTASS
	ļ	1			i	LAAAGPLTSRRAWGTSGGFGR
		l				GRGFWGPORLTEOVAEPODPA
		1				LVCGSLLVSLPLLGQTCTEDPGI
		l		l		KGFTVRMLGPKTSWAQDPGED
l	1	1				PRAREEPKWISL
26406	56774	A	26553	1	382	FRTSCROLSAAPPPARSPLRPPG
		1		[		GG/EPAPGRTSRGHRPQM*SGT
		l		1		PAPRPPARSTVSPASPLPKPRAG
		1				RCGSRPRSACSTFRPC*SLASVS
		1				SAKTOGWKMWOPATERLOHF
1		l				QTMLKSKLNVLTLKKEPLPAVI
		1		ł		FHEPEAIELCTTTPLMKTRTHSG
l	i	1				CKV
26407	56775	Α	26554	797	1213	AWLKFLLGTRRFLRFSKYSFSID
1	l	l	İ			SARSLVPGRWPAPGRTSRGHRP
		l		l		QM*SGTPAPRPPARSTVSPASPL
	1	l				PKPRAGRCGSRPRSACR*GAPG
		l	İ	i		SRGPAFPRRTPSVTRWALGLPW
1		l				LQGLRTAFCWQILSRVTAATLP
		l				DKIH
26408	56776	Α	26555	1002	1655	KEFCIYNRNPNACSYGVAVGV
1	1	I	l	l		LAFLTCLLYLALDVYFPQISSVK
1	1	I	l	l		DRKKAVLSDIGVSGEPHPAGTP
Ī	1	l	l			CTESTEGCPGHRRRKDNPLNEG
l	l	1				TDAARAAIAFSFFSIFTWVSTAT
		1	l			AHQPTLVPFPH*APGWVVFPAS
l		l				AQP*ASPACRGRQPCITPGSEVA
		1				GAPSTLGGQGRHYMDPSQDSS
						MPYAPYVEPTGPDPAGMGGTY
		l	l			QQPANTFDTEPQGYQSQGY

SEQ ID NO:	of peptide sequence	hod	SEQ 1D NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion. \=possible nucleotide insertion)
26409	56777	A	26556	262	628	QHFQTPWPWPLCAAAGTSAGT SHSGSSSGAFSSWPCWTAAEPA ARKRGRPAGSWSSPATGAPGR CRHRILSRGAGGSAGFVCSGLR GIGPLGI*LSGTFPGLTAGPETPA TERAPGASQHFR
26410	56778	A	26557	1098	1599	RIRKSHHCINTVTLGRGNSLGK DFVRESPGGDRLNVQGTHKH GLGRFAOPHGTSAGTSHCGSSS GAFSSWPCWTAAEPAARKRGR PAGSWSSPATGAPGRCHRILS RGAGGSAGFVCSGLAESGL*ES SSPGRSQG*PQGQRHPQPNGLP APPSTSVSVLVRISR
26411	56779	A	26558	440	698	IKLWAATFIKVCRLSFSCGMSIL *RCTGSKSCCCCCRRPLWAGPT SCAGGCGCCWGPGPPAELGPD TPAAEEAAEACCWDAAIFLA
26412	56780	A	26559	448	576	
26413	56781	А	26560	513	782	EIWWWAWTKWCGCWVVSCF HLCGRHC*GTCWSSETWR*MC GTSGTAPPCECWREGKDDCGR DRPMETHGCCSSFSISSPRAGKD ATTGT
26414	56782	A	26561	798	1505	FLRATSPSGHHFSYHLWIWSLR. SFLCNECSESCCLLNSSMWQAP GLSHYSLLLIWLWLVFQTLNFR HLLHLLFSFLNVVDRLCSCQHH HHQ*CHILHHNLH*NISHRH HHQ*CHLHHNLH*NISHRHH HHHQ*RPLHYHLHQIIHHHQ NHCQQHHIRYHQHHVQHIDH YRHHIPWLAGARALCDSN AGCPGSTGDGWRPYSADSDSL DALSFPRLFFPDCQSLRGLASA UQGYNWLVLTENHILFHLF

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26415	56783	A	26562	li .	1073	MHATNSSSVPOEIQVEALCPLL
						TOPOKSPSITSAMLCOLKKPOPS
						RSKEREADPISCGPECOGNWDL
						CVEAATGLYGDGHLRDSSRTR
						VLMTTGTYRDLQGLEGRAGHV
			i			AELHVLPVWAIQDRGYVLWC
		İ				WTASLHPRDVAREQGFPNDCT
					ł	WALGCTLTAESTHTHSAALAR
		1				QAYSQLSKKPTLLNEPEHITEK
1		1				KFINLARFEALNSRTWLGVLY
1				ŀ		WIAQIQDVPVTVESTTGQRAAR
		1				ISPREADRTLVKGQVQGIRQTVI
1		l				MSVPGRKEGDKLKEVSDGREA
		l		l		ANQAGMKWGKECKSSSGTEN
		1				AMSGKEVGILQEEKGDWSHGV
		1				VRGWQEKWMTYNFWACGRG
		1		l		KNATCRLEMTRTSENDLKHNQ
		1				EGLWHGRERAMLGDTHTLAW
ł						REEEMEQKQALRIHSLYGKTSG
		1				QRALGSWWVERFMGMRSGSSS
l		l		1		DCNGLVTEG*TLQSACIPEPTCS
		l				H*GSPAP*LHP*GAEKQSSTTEH
		l				SPCPGLPRQAERGAQPRVPPCP
		<u> </u>				QDPADPCKFQWS
26416	56784	Α	26563	1	387	MESTEIGPHIYEQFTLTKMTRKF
						NKEQLVLISLALLDSGHTSNSL
						AWPSCLIVSGVGSCRWVCGLT
		1				D/CQE*SLRPSQSAGVCRRSTPD
		l				PVCLGVTRGGCRTEKIAACSFL
	4/504	١.	2000	47	472	WKLRPRGAPARCQPELSCM
26417	56785	Α	26564	47	472	LLRLHFWQEERLKPSRKKITKK HTKKRTASLILHAMICCRSLNSS
		1				
		1				KTKNTKCLNSINQRLKILSLQK GDPLESTCRH*CCHVHRRTKAP
		ı				GORRVGROHVVSAGNHRHPHK
						GDPLESTCRHATVTGQGLLEFA
						GGPLQTLFA
26418	56786	Ā	26565	329	615	TKTEIGTRSINELRQQLFATTNT
20418	30780	l^	20303	343	013	FFFPSIFGESNTTSTSLTLKNSAI
	1	1		I	1	WCPTGTKLPEGRTGSNLCCSAA
						SAGDTQANRVWSGPSAN/C*QT
		1		ĺ	1	CRRRSC
		Ь.	L	L	I	oranoc

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26419	56787	A	26566	525	716	PTCLLTPPSKGRQTPYATGELR
	1	i				LASDGCPSGTKLPEEGAGSNTQ
		1				ANRVWSGPSANSSRPAEEGPDC
						CRTTCCRTTCWKPTTVTTCSST
		1				PCCQPACCVSSCCQPCCRPTCC
		1	ļ			VTSCCQPSCCSTPCCQPTCCGSS
l	1					CCGQTSCGSSCGQSSSCAPVYC
						VSSCCQPSCC*SGPSSAGLLEFA
1						EGPLQTLFAWVLLPAPSSGSFV
		1				PDGHPSDASRSSPVA
26420	56788	Α	26567	3	390	EGPCCKGWCC/RSPDTML/CPT
		ĺ				VFITCRPGDSLRCLHHQGPRFQ
1		i				AQN\CQPFGQTSS*LQEFFPIPQ
1		1				WCLECRRALAGIWQVPLWDEA
l		1				SLPEEGAGSNLCCSAASTGDTQ
		1				ANRVWNGPPANSSRPAGEEAD
26421	56789	Α	26568	658	1005	NSKYWTPSGPPPRLASGAIYGN
						SLSV*AAGAPYRNAGPLQPGCF
1				1		PPS*SLPNGGIHPGPGPGSGPHL
		1		i		GPDG*MVGSQVQHDNELYFC/
	1					APAGSYPLWVKALPQPPSQPFL
		1				KPVASM
26422	56790	Α	26569	1149	1715	VLQLNLPGPVASWCSRDVGPPL
		1				ARPIPPPAPHTPLSSAGPSAAAP
		1			,	GPARQLPHPRGDSRTARLLPGQ
		1				GSS*SWR*GAWQSGCQSYRKP
		1				GLSV*AAGAPYRNAGPLQPGCF
		1		ŀ		PPS*SLPNGGIHPGPGPGSGPHL
		1				GPDG*MVGVGPSGAGAAPEPA
1						PGLWDPPGHCSQASTPPGACKE
		<u> </u>				RETLPTALPRLS
26423	56791	Α	26570	32	335	LWSLFDHHVQRAVCDSRAKYR
				ŀ		EGRRPRAVKVYTINLESQYLLI
		1				QGVPAVGVMKELVERFALYGA
		1				IEQYNALDEYPARRLY*SLSY*I
						YELTKCKDSQEKNG
26424	56792	Α	26571	407	842	TEPLITINRLQRRRRSAPVAAAG
						PAGTLARRAPAVTAERAAGPG
						PASVHRRPGWRRAQSGPAAAQ
						ALRPPPPR*PRDSASPLSRKELL
		1		1		KLLGTKHYGRLTATEAQAPQG
	1	1		1		QHKLLCRETGELVPHWAGSHY
L		L				RGISNPINNIQDHIL
26425	56793	Α	26572	409	614	GLPPPAVGDRQRCLPVRH*RPS
		1		1	1	QTIRAEQEPRSAAPRKRRPKEG
						CRRSRGSSPLADNLGDLGSGGQ
						GG
	1	_		L		122

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26426	56794	Α	26573	3	266	GNHCRRQYRDAQ*WP*EAGRY
		1				SSCAGSARLGKAKG\RGPQGV
	İ	l				MGNE/MRSRRAQEFKKYLHSK
		1				TSR*KSHTGPEAELTSPGAKKE
					ĺ	gcso
26427	56795	A	26574	36	384	GWYCSSRSDVCSGGNSSAHSO
						LPHQPLPRLRPGGSCHPRESSSP
	İ					SKORGGPVGDRORCLPVRH*RF
						SQTIRAEQEPRSAAPRKRRAKE
	ĺ					GTRRSRGSSPHPEKLGDLGSGG
		1				OEVRP
26428	56796	A	26575	101	334	CSTSKEKWQCGLRAECSPVFPA
20420	130770	^	20373	101	334	TEVPEYSC*GRKPSHLSCHRAP
		1			\	TLEEAANRKWPCTQYDAIQNA
						CYYNDSLVLRLS
26429	56797	A	26576	435	761	OGTNTWVPHWVLRLGLLHTSP
26429	30/9/	A	20376	433	761	PEGIAELPRSLPSLTEHQACQLD
1				İ		CVLVAIGTAILVAOTATTSPPIC
						GEADAHPASTPLPPSWPPQGRQ
						LSC*NPPLGPWPSGRVOTP
26430	56798	١.	26577	38	236	RLLPLENCCLSSASGTCAHQAP
26430	56/98	Α	265 / /	38	236	LLLCSCPNC*SCCCCHHCCCPC
06401	6 6 7 7 7 7	١.	24670	1316	1548	GCCCWHCHRPSTKGNSATFTA FFSITGLSSVAGGOFVNLYLKR
26431	56799	A	26578	1316	1348	
						LNSNFIYLSGYVIVYINIYVFIYC I*KFVLHVTLRTDCCKTIVKKH
			i			
26122		١	0.4400		272	VFRLFLKAM
26432	56800	A	26579	1	272	RPVNSRLDDFVAACAAMAKIK
		1				ARDLRGKKKEELLKQLDDLKV
		1			1	ELSQLRVAKVTGGAASKLSKM
		1			I	*VRRPDHSPRGWGARVHRDRR
		L_		<u> </u>		RISKLA
26433	56801	Α	26580	1	363	
26434	56802	A	26581	286	867	IYALSLGAGGAAASAGLCSNEP
						RFKARDLRGK\KKEELL\KQLD\
						DLKGGSCPQLTRSPKVTERCGP
1		1			l	PKLSKIR\VVRKSIC/RVFSPVIYP
					l	DFRKENLQGNSYKG\KKYKPLG
		I			1	PCGP*GRTRAMRPPGSNKARRE
		1			1	NLEGPKEAGSGKGAAFTRCGK
		1			I	*RGSRALRGRLCQLKHKENLKT
						KKQQRKERLYPLRKYAVKA
26435	56803	Α	26582	164	346	LHPGRRPGLTHLGVPSPGPGPT
						EKLAPGKPSSAACAPSPPALD*
		l				HIAFGVDALCPTFGLN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26436	56804	Α	26583	316	723	LVGGWGGLWGGLHGPLYGQA
						OGASPLLPPPPPAHRPPPHRHST
		1				EHGVEHPLVT*TAPLSPCPLGFR
	İ	1				LGQLALHRGASTKGLLTGGVW
		ı				GLHSWPIGDGRATIHEAVVRAS
		1				PWPSRLGTIHGVRGGRDVQEG
		1		j		AELPAV
26437	56805	Α	26584	177	418	RNPVVAQGLLCACRMFKVGNR
		1				TPSSSAEWPSSFAPPKKGPLPKA
		İ				TSEPLFPHPKRR/PLASVPSHREC
		1	İ			RPPLGASKTAPRD
26438	56806	C	26585	149	277	
26439	56807	A	26586	1037	1455	EESYGLLSVPSVTGSLLLQDLH
	i					KLGCHQFGHSKKRRVSGIWMA
						VLPFPFRCQPHLLLLLENPRAN
ĺ		1				GPARQPTNHQPP*KAGTQLPNS
		1				VAPVQSQTGFPPTPARKARAPT
İ						WPGAARPPGTASNKSPARSPCS
		┖	<u> </u>			SPSFSILP
26440	56808	Α	26587	175	450	
26441	56809	Α	26588	77	337	RDHEPTRRKKVRTHPNVRRNK
						LRTRRL*EL*HSLRGSAASFLKE
	İ	1				GRPWRSGGGAQRR*KYWRKG
		_				KYSGKMQSWSRVYCSLAKVRA
26442	56810	Α	26589	1043	1555	ALRQGPEGARAPNMDSSVSRC
		1				QVPGPQVCRAVPTEILASPAVE
						RAPAAALSSTTIWMPMSLCPW
l						RPVLAACTSMTVRGRSTMYLP
l		1	i i			TTTGNAGCTWPKASLATRWLS
l		1		1		SPMGRQARSLMLGAQVTLSWD
	1	1		Į.		RSMPWRRRGRSSGRNLSTI*WR
		4.	0.000	1	462	LDWSLRRTWRSGRAWMSGIST
26443	56811	Α	26591	313	462	VCFTPEPARPRIRQTRPDRRNSE
		1		1		HIRT/RRRKKLRTHLNIRRNKL WTRHL
26444	56812	A	26592	630	777	KERRGREKKKEEEKRRRGRRG
20444	30812	I <sup>A</sup>	20392	030	/ <i>'''</i>	GRRRKRRRRRGRGRGRGRGR*
			ľ	1		KERRGREKKKEEEKRRRGRRG
		1	İ			GRRRKRRRRRGRGRGRGRGRR
		1	ŀ			RGSRRFL
26445	56813	A	26593	284	461	HSPGGSAASFLKSVRRRTHQFR
20443	30813	^	20393	204	401	TH*FHIHKNRTFTSR*SH*RMRO
1	İ	1		1		WDOREVKVLFL
26446	56814	A	26594	573	968	AQRFCHSQWRCSSSRAVLEENP
20440	20014	l^	20394	J'''	/00	APLDTTPLSGRSKSSGRGCLVS
	1	1	1			LGL**PPSTRRSSHL*OPSSP*AS
	1	1		1		TFLQVRMTAPSGL*PQRPA*KL
l		1		1		RSSPLLLTKNPFPEAAAF*SRGP
l	1	1	1	1		PVSLKDTASLQAAFLGWP
L		1	L		L	1 TODICOTAGO WI

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26447	56815	A	26595	3	699	RGRSKANSPQLLEGGADPTVG DIGHLSVGVGPVHANVGACQP DQTTPKHLADNPGPWTLDALT YQPHAANSCHKRGIAAS'SLMII WUIFLVLLEWENEWNDEAVMS TLEHLHVDYPQNDVPVPARYC NHMIJQRVIREPDHTCKEHVFI HEPPRKINGIGSPKKVACQNLS AIFCPGSETKFKMTVCQLIEGTR YPACRYHYSPTEGFVLVTCDDL RPDSFLGYVK
26448	56816	Α	26596	2	483	
26449	56817	A	26597	2	1041	WPODOSCTWLAVAMGCWLAT OGOSLTRVPVATSGIOGCOAAP SPMWAAWTHGWASCYFRAAL QLPLPPOSTGNOSMSTSTAYSA SSPOFMYTKAGGERSDHKENV FYVQHOKYYGGATQAFAKEN FYVQHOKYYGGATQAFAKEN ONGAYKETYGVSHITHENDL IPKQQQNEKYQVPQFDQSTIKNI ESAKGLDVWDSWPLQNADGT VAEYNGYHVVFALAGSFKDAD DTSIYMFYQKVGDNSIDSWKN AGEVFKOBSKPANDPILKDOT QEWSGSATTTSDGKIRLFYTDY SCKHYGKQSLTTAQHLQQVLT YKRSFSIVVDAILALPPLKRAAW PKSRIPPQVGLMEVQHLFPIPN NFEEHV
26450	56818	Α	26598	116	338	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26451	56819	A	26599	971	2485	FISSCFVRACGTLNPGVTMFYV
						LGKFCDFAEPWFPHVMQEQLR
						VVGKGLWGFVRVSLSGFRIHGE
					ŀ	HQKTASLAQVHKAVLHDGRTV
						AVKVOHPKVRAOSSKDILLME
1						VRALPFSFLCPQSTFMWLVDEA
1						KKNLPLELDFLNEGRNAEKVSC
1						MLRHFDFLKVGGTMQCRVWW
		i				SGGLMEFVDGGQVNDRDYME
						RNKIDVNEVRSRAOGCCAGER
						GVNGFVHCDPHPGNVLVRKHP
						GTGKAEIVLLDHGLYOVEEAFV
		1				TOPWGLWGQSLIWTDMKRVK
						EYSORLGAGDLYPLFACMLTA
		1				RSWDSVNRGISQAPVTATEVG
		1				GPSRPCLFLNAEISHLLNHVPRO
		1			1	MLLILKTNDLLRGIEAALGTRA
	1	1				SASSFLNMSRCCIRALAE*VWA
		Į.				PPSPPLLAP*ISFSEAFNLWQINL
						HELILRVKGLKLADRVLALICW
					1	LFPAPLCTVHVTILLLLWNPLRT
		1				LWPLSQGPQAELWHSSLFFSKK
		l				TOOPTFPFLVCAIGLDVPTTSVK
26452	56820	Α	26600	831	1205	RKEGQGPSVHPLGSGCFPPGHA
		l				FWEALEANTWVPCVRL*RTPV
		l				SAELLGLAPGGRWRAVNRDRG
		l			1	RVAAASSLGEPCYSSPADASFP
		l				RSDSGGLDRQGGSCRYPKELFG
		l				SHPQRARCTEGSLQVL
26453	56821	Α	26601	377	962	LFSIFITQDPKLRELLDVGNIGR
		1				LEQRMITVVLKACV**LCSI*AN
1		l	İ			ASVIYIFQEWTNDHLLVL*SMC
		l				HLNLSPLLCSLHSIYRNREGGS
		l				WGRKKTIC*LRCFISQNDSIPQE
		l				DFTPEMQILE*NLV*KILIAWFFI
		l				VFSGAKSKPYLTVDQMMDFIN
		l				LKQRDPRLNEILYPPLKQEQVQ
		$l_{-}$				VLIEKYEPNNSLARK
26454	56822	A	26602	I	810	MDAKKRKLYKYASTDSPAFAI
1		1				TFIIMPYMENQAAKLAFERLSL
		ı				NELVFSSEALTHSETFLPQPDNR
1		1	1			HQNMSSTIHTAPIDTALGGNPA
1		1	l			FLYLFLQDFQPTQDNSLASVTP
1		ĺ	l			SAGVSARLAPPPTPGPFTDVVV
1		1	l			LDVLDEVGQGGEVESAAPESA
1			l			GIGEEGGGGDACHGATSRAP*Q
		l				ASPPPPSSPIPADSGAADSTSPP
1			1		1	WPTSSSTSRTTTSVNGPGVGGG
		L				ARRAETPAEGVTDASELSCVG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26455	56823	Α	26603	28	457	GGIPDSTARLSILTPRHHLQRSC
	ŀ					SCNGTATRFSGQSYVRYRAPAA
1						RNWHIHFYLKTLQPQAILLFTN
	l					ETASVSLKGFEGCLDAVVVNEE
1						ALDLLAPG/NDGGRLAGDTSPH
		1				PVLPPQ*LLQPEHMPQWWEVL
						MDPRGRLCLQMS
26456	56824	В	26604	205	1722	
26457	56825	A	26605	11	374	VSPSRSGIPGSTHASGQL*TGDR
	i	1			l	S/GPMGPPITAT\Q*DGDSDAYH
	1	1				GLATLHALLPALPGAAGF/PSGT
1		ı				SEPCPSSPC\GQHHHAGQLGHD
		1				LPVHCSEDPRPQPPPLGGPLEDL
		_				PSLLWHSDFFI
26458	56826	Α	26606	69	551	QSGRSPQHVFPSVRGSGARSRG
i		1				WILVHPSQYHHNPQRIYSACGR
		1				SGEHISPGYPCS\DGHDAYDQQ
		1				ADGTHHDACIFH\PRGSPRSP\G
		1				QCCLLTGGSRSGT\SGASATPG
1		1	į			GRRGG\PAQGGE\PASRNSSVEE
1	I	1				LTARVLAPAPAPALASAQPTLP
		_				GFSISPSTK
26459	56827	A	26607	476	1016	CLWLLSCLYCSLGDCCLWWAV
	į.	1			1	SVLCQVSAPRQALCFAPGENGD
	1	1				GGQQGLRGAPPGPGPRGPAPQP
		1			1	GPGYPGARQRGSPQQP*LSSEP
		1				GPYLRLSRSGGR*GPGRCCSRSP
		1			4	PGR*PVQAGDEDGQDAGSHI*T
		1				QPRVSEEGGTDEDQWSLPQEVP
						SASVPYQPLSHCQTVPASLQPH
						CLFS
26460	56828	Α	26609	247	342	RSIMPWLPKGSGWEVSSIPP*RC
		1				LHQLWSTSRNMAL/HVRVLQT
		1			l '	EQAVKEYNALVAQGVRVGGV
		1				FHSTC*WSLKRRINH
26461	56829	A	26610	129	272	NDTVSGLGRLESPTLMRQRNV
		1				CSHCYPGSAK*GYMIYKDALPR
		L.				RTSL
26462	56830	A	26611	133	453	QVDPNTVLRNAVHTNTYLQGL
	1	1			I	THPSANHKSLYTLLNNFLHICR
	1	1			I	LHTRRMHGKTGRVYGITQRAV
		1			l .	GIVVNK*VTGQILAKRIVPIEHI
	<u> </u>	L			L	KHTKSQ*SFL*ELRPSPVAS
26463	56831	Α	26612	352	543	VPSINCGVPQGNMALMCRVLQ
						TEQAVKEYNALVAQGVRVGG
L	L	L		1		VFHST\SDGSLKRRINH*VPKKK
		_				

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26464	56832	A	26613	1576	927	FAERTRTHH*PKPRWKGALGC
		ľ.				RARTAVTSRGCLAPSRRRRRLP
	1					GRRAASQPGPNADPKACRPWN
	i					PRGSOVHAKRNALCFSRASDAF
	1					PRPDASPGQIFPGRRRKECQTC
						KTRVRLGCL
26465	56833	A	26614	67	415	ALARKLPTNFOWVKKIDASPGS
20403	30033	ľ	20014	0,	113	PIPLNAP*PSPSVOTTPTTGHPG
	l					RALSTVSEVPGAGARLTYRVPF
		l				TRCKRSLILPSPVWVSRIPSTAK
					1	SPILISSPGGAHAASVSALTLVS
						GYE
26466	56834	Α	26615	87	347	GIRY*LCHGFYHAYLGFRRRTS
20400	30634	l^	20013	l°′	1347	SPLQVSRPPPPRGTQSEP*AQSP
	1				i	RSPELELGLHTASHSRAANAAS
	1	l				SFHLRFGFPGFHPRPSPLF
26467	56835	A	26616	3	175	GFVTSSFFLGCLSFPDAYDLVFL
20407	30833	l <sup>A</sup>	20010	ľ	175	
						LARE*HWKH*TQSILTLIAQCVF
06160	55025	١.	0.6610	530	mon .	PEQPKRLCWVS
26468	56836	A	26617	539	788	EKEVPTLLDCCAALGQ*KCKMI
			l			QLLWKMV*SFSTKLNILLPNNP
		ľ				AVVLLGIHLKELKTYVLTETCT
		_				LMFIAGSQRNLRDYFRP
26469	56837	A	26618	843	1136	VKEQVYRRIAASRSVRRCSYQS
	1					RPGLLPTAGHHPQFHLYSDCHG
	1	1		1	į.	NDIYSVYYQCEHGHAASSSETG
	1					VPRFPCPWWSETAQ*TGCASHP
		1				GPSAQRSAL
26470	56838	Α	26619	2073	2329	LVQTSRPPDPSWA*SATVTRPE
				!		QASWARNLSRFPLLGMATVSG
		1				RGLPSGPGPRAMSPAGEPAPGA
		_				AEPAPPGSAAIPHRRPLLGQ
26471	56839	Α	26620	723	1023	ITLLGLSLIPLISRLPWTQSWGPL
				Ì		SFLSTPTSLLISSTPLILNTINSLM
				1		TLRFLPPGGAFP*TPEPCIPPTQH
						PHLDVSLTGISNLPRPQSCFHCL
		L				HLS
26472	56840	Α	26621	99	288	CLCQNKLGEGRDDNFTSWQSS
						AC*TFCFLLAVDSAETTAAES*C
						CCCCCCSAAGGWRRLVH
26473	56841	Α	26622	130	450	RQLKLTAGCAKSPWLFWLKSY
			l	1		HSLYLAAACLLGLTYTRLGRSQ
						SSPPIHSHEFPPATSL*QQLHGQ
		1				PA*WLYDGPATP/SIAPPAHLLP
		1		l		PPWRGGTPSPWLPPSPLQE
26474	56842	С	26623	1	672	` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` `
26475	56843	Α	26624	408	581	LIKDESAPRTPQTVLASAQFCLL
	1	1	1	l		CR*ARCCRGGSCCCCCCCCCC
		1				WWWCCCCYFGND
26476	56844	С	26625	66	264	
		-				

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	nf peptide sequence	deletion, \=possible nuclentide insertion)
	İ			sequence		
26477	56845	A	26626	70	551	AAEDVWVYPSELYWPGPHGHO
						ETPRAGVFVVTSHEEGPGAGTA
						SSSSKGPSWARWGLEVSPLRWI
		1				SGQVGGAGSAESGQPLGSGFTF
					ł	KAMGNLGESRAROAOLIHDRN
	l.					TASHTAAAARTQAPPTPDKVQ
		1				MTWTREKLIAEKYRSRDTSLSG
	1	1				FKDLFSMKP*VSPLRWPSGQVG
		1				GAGSAESGOPLGSGFTFKAMG
		1				NLGESRARQAQLIHDRNTASHT
						AAAARTQAPPTPDKVQMTWTR
		ı				EKLIAEKYRSRDTSLSGFKDLFS
		1				MKP
26478	56846	A	26627	479	961	POSSLOGNLOMPWGSCLDSST
20478	30840	r	20027	177	201	HYRPSLVGVDFQLPSFWLVICG
		1			1	TCKHCHRMLHSVALFWVPLHC
		1				GWSIPRPRCPHPHHPPPLRGPSC
		1				HPPSPPWACPPRTGVQSATCPF
1		i i		ŀ		A*RPTWSFTCDPTTKRSMRGLT
1		ı				HILRSGEKRPLPALCARSTSGSA
						TTSPGT
26479	56847	A	26628	1	223	MGAVQKAYNLOKKRRRRRGR
		1		1		RGRIRGRRGRGRRRRGRRRRK
		1		l		KKKKEEEEEEEEEEEEEEE
		1		1		EEEEEEEE*EVEEEEEEEEE
	1	1		i		<b>EEERRRRKKKKKKKKKKK</b>
						KKRKKKKKKKKKKKE
26480	56848	A	26629	1	341	
26481	56849	A	26630	78	354	ENDSFYNDL*ATQRRRRRRKK
		1		l		KKKGEERRRKEKKGEERRRRR
1		1		Ì		RRRRRRRRRRRRRRRRGRG
		1		ł		RGRGRGRGRRRRRRRRRRRRR
		_				RRRRRRRRRR
26482	56850	Α	26631	1	327	
26483	56851	Α	26632	41	246	
26484	56852	A	26633	1	170	RKRRKRKKRKKKKKKKKE
1		1				KEKEKEK\RRRRRRRRRRRRRRRR
1						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
		<u> </u>				RRRRRRRRNTNNETGE
26485	56853	A	26634	1	282	MCIESEREEEEEEEEEEE
1		1		1	1	EEEERRRGRGRRRRKKKRKKK
		1			1	KKEEEEEERRRKKKRKKEEEE
		1				EEEEERR/MRKKKKKKKKKKK
26486	56854	A	26635	1	396	KKKKRQSL
26487	56855	A	26636	1	255	MLWLPQPALGTRAAETLACSR
20707	155655	1	23030	Ι.	1	RRRROLYNCCLYLRRRKKEEE
	1	1				KEKEEEKGKEKEKEKKEE\KRR
l	1	1				RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
1		1	1		]	RRRRN
		_		<del></del>	1	ladou.

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
26488	56856	A	26637	1	290	MKKKKEGRRRKKEEEGEEEGE
		1				E/DRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
l		1				RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
l		ı				RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
		1				RRRRRRRRRRRRRRRRRTTT
						TTTTTT
26489	56857	Α	26638	2	423	
26490	56858	Α	26639	3	167	QQKEDEEKEKEEEKEEEDEEEE
		1				/ERRRRERRRRRRRRRRRRR
						RRRRETQEAETI
26491	56859	Α	26640	1	325	MEKNEKEQEEEEKKEKNSKKK
		1				EEEEEEGGGEE/ERRRRRRR
		1				RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
		_				RRGRRRRKKKKKK
26492	56860	Α	26641	1	618	
26493	56861	Α	26642	1	291	
26494	56862	Α	26643	3	155	YRHLPKKKEEKEEEEKEEEEE
ļ						EEEEEEE/ERRRRRRRRRRRR
		$oldsymbol{ol}}}}}}}}}}}}}}}}}$				KYEKKCL
26495	56863	A	26644	1	1410	
26496	56864	A	26645	578	842	TQEAELAVSRDHATALQPGQQ
		1				SKTPSEEEERRKKEKEEERRRR
		1				KKKKEEEEG/MKKEEEGRRRRR
ł		1		ľ		RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
		1			l	KKKEEEEE
26497	56865	A	26646	215	471	
26498	56866	A	26647	432	761	
26499	56867	Α	26648	2	357	
26500	56868	A	26649	533	281 758	FORMANGENERAL VALUE OF THE STATE
26501	36869	Α	26650	233	/38	EQKKKKKEKKKKEKEKEEE
1						EEEEE\ERRRRRKRRTRRRRRR
		l				RRSRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
26502	56870	A	26651	264	429	RRRRNTEK HRAAPATSDTQE*HRSNAFGEE
26502	30870	A	20031	264	429	EFEEEEEEEEEEEEEEEE
		1		l .		EEEEEEEEEEEEEETLFSNM
26503	56871	A	26652	1	279	EEEEEEEEEEEEEEEEEEEEEEEE
26504	56872	A	26653	li -	795	
26505	56873	A	26654	i	642	MKKCKTSVIGIATFYLSIPHIYT
20505	50875	^	20054	1	042	PPNOTSSFMACAIAIEVOLTSAE
		1				PASIGFPVQKSPCGHLQLNGYK
		1				SSSKOGFPTPLLKOESWNSSVKI
-		1				TTCNVGDKKNINDRRSANMMH
		1				VNNFPFRRHSWICLDRVQSETL
		1				POEKKEEEEERRRRRKKKEEE
		1				ERRRRKKKKKEEEEEEEEE/
		1			[	RRGRRRRRRRRRRRRRRRRRR
		1				RRRRRRRRRRKKERISSL
				L		MANAKKKKKKKKA

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop cudon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26506	56874	A	26655		1167	MAPRPQAARLPSCGTRSQGAA RPPPLGTAAAY RPLSSRLTGPP PASSSWLAIHFRIRVGSSGQGN QRIKYLGIQLTRDVKDLFKENY KRLLBEIKEDTNIKWNIFCSWV GRISIVKMALLEKVQAILMLVLE LHLFCKYNIVGMENAGNGHD WSLDRIHLMQASANQQATQLAI SRPSNQSKAQDFLRLLRKEKQT LDTTAPLKEQAQKWNEDGIR SSVIPGIQHQSLLLAVLTFNSK TSLGDRARPVSKKKESRKK KKKKKKKKKKKKKKKKKK KRRNNKKKNKKNKKNKKNKKN KRNKKKKKKKK
26507	56875	A	26656	342	616	RILHKSFRKLLCKGSFCSTRSPT REIRSKKKEEEEEEEEEEEE/ERR RRRRRRRRRRRRRRRKKKKKK KKKKKTKTKTKKKKKKKK
26508	56876	Α	26657	1	705	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26509	56877	A	26658	1	2267	I MKVELMGFAEGLAVRVREOEE
20309	50877	l^	20038	l'	2207	VRLNWKVELLWTDLRDVPKG
		l				ANSFRVSGSSGVEVFMVYNRT
						RVKEPIGKARWPLDTDADMVV
		l				SVGTASKELKDFKVRVSYFGEQ
		1				EDQALGRSVLYLTGVDISLEVD
		ĺ				TGRTGKVKRSQGDKKTWRWG
		l				PEGYGAILLVNCDRDNHRSAEP
	l	1				DLTHSWLMSLADLQDMSPMLL
		1		l		SCNGPDKLFDSHKLVLNVPFSD
		l				SKRVRVFCARGPEDVCEAYRH
		1				VLGQNKVSYEVPRLHGDEERFF
		1				VEGLSFPDAGFTGLISFHVTLLD
		l			1	DSNEDFSASPIFTDTVVFRVAP
1		i				WIMTPSTLPPLEVYVCRVRNNT
	1	1				CFVDAVAELARKAGCKLTICPO
		1				AENRNDR WIQDEMELGYVQAP
		1		l		HKTLPVVFDSPRNGELODFPYK
						RILGPDFGYVTREPRDRSVSGL
		l			1	DSFGNLEVSPPVVANGKEYPLG
		1			l	RILIGGNLPGSSGRRVTQVVRD
				i		FLHAOKVOPPVELFVDWLAVG
	l					HVDEFLSFVPAPDGKGFRMLLA
1	1					SPGACFKLFQEKQKCGHGRAL
						LFQGVVDDEQVKTISINQVLSN
						KDLINYNKFVQSCIDWNREVLK
İ				I		RELGLAECDIIDIPOLFKTERKK
	1	1			1	ATAFFPDLVNMLVLGKHLGIPK
		l	0.00		1	PFGPIINGCCCLEEKVRSLLEPL
			l			GLHCTFIDDFTPYHMLHGEAYS
1		1				LECRQHWGKNLYFRVGLKKK
						KKKKKKEKEEGQEEEEEEEE
26510	56878	Α	26659	1	990	
26511	56879	Α	26660	1	235.	MTAKCVCGWGVGEREREKER
		1		1		EEEEEEEEEEE/ERRRRRRR
		1				RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
	1					RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRRRRRRRRRKI
26512	56880	Α	26661	1	1101	
26513	56881	A	26662	348	806	
26514	56882	Α	26663	39	684	LRCENPISSHVGHVGVSLAHTR
	1	1		I		GLFSRLILADREDISENWCSLVC
		1		1	1	CVCVCVCVCVWWLCISLFPGD
		1		1		MMTLLMKKDTLTEEET\QFYIS
	1			l		ETVLAIDSIHQLGFIHRDIKPDN
	1	1		1		LLLDSKGHVKLSDFGLCTGLKK
	1	1		1		AHRTEFYRNLNHSLPSDFTFON
	[	1		Į.		MNSKRKAETWKRNRRQLAFST
	1	1		1		VGTPDYIAPEVFMQTGYNKLC
1		1				DWWSLGVIMYEMLIGKLHG
		1	i		I	DW W3LG VINITENILIGALING

SEQ ID	SEO ID NO:	Mot	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26515	56883	A	26664	3	276	IKSIDDTSNFDEFPESDILKPTVL SSAP*AVHWRQGSESTLTSISFP VATSNHPETDYKNKDWVFINY TYKRFEGLTARGAIPSYMKAA K
26516	56884	Α	26665	95	405	
26517	56885	A	26666	3	349	GPGGWLSLSPLVL*ALES*KEEE EEEEEEEEEEEEEEEEEEEEE ERRRRRRRRRRR
26518	56886	A	26667	1	370	MHVAWSCPTAQSSQATVDSGK TLAETESPIGLSSKVGGKNIRAG EWDELKYDRFPGQKPKKKKRK RKEEEEEEEEEEEEKKKKKK KKKKKKRRRRRRGRRRMQ QSHPNPTSAILAPWA
26519	56887	Α.	26668		430	MTFFPDKRETDILLINFSMEH CTRGOPPLGYOTTKGFKEDTE TPEKESLESKAECLGRRRKKN KEEKEEKEKEKEKEKEK KKKKKKKKKKKKKKK
26520	56888	Α	26669	1	708	
26521	56889	Α	26670	1	1233	
26522	56890	A	26671	1	366	MSYVAAVMFFCSVLGKFQMNL EEEVEKRRRKKDKKEKEEE EEK/DERRRRRRRRRRRR RRRRRRRRRREEEEEEGEE EEEEEEEKKKRRRTLYCM*IA CKLKYLWTVSGHILCPNTN
26523	56891	A	26672	1	667	MSKEGNNRIWDRLEGGWRR VRVEKRLFRDYPSSHPRGAEAF SPDSIGRCTLRFPGLQMGLHQ PALIAILRSGADLSHLEGFMLEG GASACAPAVSGDQALQHEG GGRKVPGKRRRKEEEEEEEEEE KRKKKKKEEEEEEEEEEEEE KKKRRRRRRRR
26524	56892	Α	26673	365	670	
26525	56893	A	26674	29	370	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amine acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26526	56894	IA	26675	1	1364	I MEMIWPSKGMPFTSTSYSNKES
20320	30874	^	20073	ľ	1504	SLLSVVQTSSYSHTHTRGSSEE
		l			i	VESLNRPITGSEIVAIINSLPTKK
						SPGPDGFTAEFYORYKEELRIK
						YLGIQLTRDVKDLFKENYKPPL
		1				NEIKEDTKKWKNIPCSWVGRIN
					ł	IVKMAILPKIIVEDALOIYYDMV
						,
						LVCVGVGVSCRIVISSLEVLESR
						RGQRIFFLVQAEQVLWAFKEVS
						SNCNDKSTLRGSVVKLQCTSGT
						SAFDIFQVGSRVLGEHRLPSVH
l						SATYMSLTYFELAGLLEKSSQL
1		1				VGSTGVEDIVAIMIPEPKGKEIV
						SLLERNITVTMYITIGTRNLQKY
						ERWKKKRTKGLEYQEFGFDDV
						KFRSLLDIEAEMPDLHRLPRNM
					1	HASSPSKRTARGRNKNKSSRLT
		1				MFGVEIQEEEEEEEEEKKKR
						RKEEEEEEEEE/ERRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRRRRRRRRRRRGGRRRRRKH
26527	56895	В	26676	1	499	
26528	56896	A	26677	I	1684	
26529	56897	Α	26678	2	297	
26530	56898	A	26679	68	319	IQHITS*TKKKRKRKKEEEEEEE
l		1				EEEERRRRRRRRRRRRRRRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRSHTSIPKESTLLQSQSVGLG
26531	56899	Α	26680	1	1617	
26532	56900	Α	26681	92	338	LEKEEEEEEEEEEEE
						EEEEEEEEEEEEEEEE
						EEEEEEEEEEEEEN*NVERY
						KKEGQW*KQRRQEKGLILPDG
26533	56901	A	26682	1	548	MVDQRHLVLTSSTKKNQNNNF
						QVFVIENVGREPQTDKIASPGA
						GQSCTASVTADLLSRDLHFTKV
			1			PSWSSDGPPYYPPACHLMSEPY
			1			FWGSCCYDTPIKTKTTNEEEEG
			}			EGEEEEEEEEEDEEEEEKEE
						EEEEEEGEGEE/ERRRRRRRR
		1				RRRRRRRRRRRRRGRRGRRR
		1	-			RKPRGGR
26534	56902	Α	26683	1	1215	
26535	56903	A	26684	1	571	
26536	56904	A	26685	1022	1365	TSLLPPSSSIPSRLPSVVLSVRILS
		1	1		I	LWILACLAPWRWDLLRKASCL
					1	PAFSLLLSGANGSFSLGFQALL
			1			GRKEEEKEEEE*EKEKEKKK
						KKKKKKKKKKKKKKKKK
		L				KKKKKKKNF
26537	56905	A	26686	24	355	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown. *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
26538	56906	Α	26687	120	594	
26539	56907	Α	26688	117	487	
26540	56908	Α	26689	2	2482	
26541	56909	Α	26690	2	654	KGDVGEWLSAGKGESSAMFAS
		1				EQEISKDEQGTPVLGSFYWEVD
	1	l				SPRKESSQAWAPGQEWIKLERD
		l			i .	TTEEKMFEQLKPIEPVQKTLPW
	1	l		1		VGEVAATLQEAMKRDCWREA
		l				RVKKKPVTFEDVAVNFTQEEW
		1				DCLDASQRVLYQDVMSETFKN
		1				LTSVAWVRKKEEEEEEEEEE
	1	1			l	EEEEEEEEEEEEEE
						EEEEEEEEEKKRKRKRKRERK
						KKKKKKKERTTWLWGNPLT
26542	56910	Α	26691	789	1072	
26543	56911	Α	26692	1246	2367	-
26544	56912	A	26693	579	1214	
26545	56913	Α	26694	119	1870	SCSRNRLLPPVSESLTRPLPSLA
						RWLPPPGLRQPSSRDYWPKGRL
	1	l				RLSAVPSPASPWALVSCLLPPSS
	1	l			l	SQEKAGKILKKRVEKQQPEEKV
		1				GKGLEESLCPCSSMSNHTKERV
				•		TMTKVTLENFYSNLIAQHEERE
ŀ						MR*RILFEKIEEEGLKDEEVINIG
	1	1			i	NVFLRKETEFLRLKRTRLGLED
	1	ł				FESLKVIGRGAFGEVKITATCQ
	1			ł		VGHVYAMKILRKADMLEKEQ
	1			İ		VKHSCSSAFILVEADSLWVVK
	1	1				MFYSFQDKLNLYLIMEFLPGGN
	İ	l		ł		YLTMKGHKDTLTEEETQFYIAE
	1				i	TVLAIDSIHQLGFIHRDIKPDNL
	ŀ					LLDSKVLGGHWHELPFQEPRLR
	ł	1			l	GFLSQCCDTPFRALRFLASPSFQ
	ı					VPLHSPRPDLCTGLKKAHRTEF
	1	l				YRNLNHSLPSDFSKW*QLR*PK
	i	l				AETWKRNRRQLVSNICGF*KN
		l				AENVSLGQVRWLTPVIPYIAPE
		1				VFMQTGYNKLCDWWSLGVIM
1		l				YEMLIGKLHGFRGLPQETYKK
	ŀ	l				VMNWKETLTFPPEVPISEKAKD
İ	İ	l				LILRY*RTSLHLQIKSIDDTSNFD
1					ŀ	EFPESDILKPTGNTTSIVSCDYK
						NKDWVFINYTYKRFEGLTARG
26546	56914	Α	26695	271	446	YLVHILDALPRDPTALRRRQRC
		1		1	1	LGS*RKHQTRLRSGRPSSGPGG
		L				TDISVTAVSAPAQK
26547	56915	Α	26696	1	171	WGVIWRENGRCFSGLLRAGLG
	1			1	1	AAWEPRVGEIKILVS*LGTC*IK
I	1	1		1	1	LICQSWVGANPRA

SEQ ID	ISEO ID NO:	Mat	ISEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
26548	56916	IA	26697	1	179	MWKGPKGLDMYGKSSVSPKTS
		1				DILGRD/NSPAGLEGANSGVAN
i		1				CLWRGPCGRKLWEASRN
26549	56917	A	26698	2	140	DN*KGVHKRILSKLAPELGSFK
		1				GFRSLAVNTHNSYGGKGNRPL
		1				KIR
26550	56918	Α	26699	3	601	
26551	56919	Α	26700	232	1809	
26552	56920	Α	26701	1	851	MQQEDPEESTKSPNPTTNKKQE
		1				KKLSLFGGLFTWTRVKFGAVT
						QIGGPPLGDQSPVLLLLQRLFSK
						GYRVSPSKAQISSPSVTYLNSVS
						LIKTLLKTTLLPKEAGVIHCKG
		1				HQKASDPIALGNTSADKGLFRP
						PPFPSHQARGFAPAQDWQIDFT
			-			QH/RP/GVRKQKYLLV*VDTFT
		1				G*VKAFPTRSEKATAVISSLLSD
						IIPRFGLPTSIQSNSRLAFISQISQ
						AFFQALSIQ*NLYIPYSPQSSGK
						VEQTNGLLKTHLTKLSLQLKK
						DWTVLLPLALLRIRACP
26553	56921	A	26702	434	867	RLILPNRLGSPLLVWVDTFTG*
	İ					VEVFPTGSEKVTAVISSLLSDIIL
Ì		1				RFGLPTSI*SDSRPATKSSFSLISP
		1				TLGSHDAPNPTRSSPEKHRPLSL
	İ	1				HTIPQNFRCPDTLPLFRFIFFAFF
į.		1				SNTLHIMGKMAAEGPKSTLYC
		١.				QFTEK
26554	56922	A	26703	96	415	
26555	56923	В	26704	1422	933	DODDEDIA PROCEDIA INICIALI
26556	56924	A	26705	1422	1774	DCPPSPIAFPQCTHQHHHHQYH YHHRHHHRHHHYQR*K*NPGL
		1				PLFVYCYFQNH*ACHCSWGNS
		1				EHMTIASESQAVPLOPPODSQG
ŀ		1				FFEDLELHYFFGDPSETRPGKQP
	1					KVSVQQIL
26557	56925	A	26706	355	1014	RHLRPQERAPAPSGSVPSRPGCS
20337	30923	l^	20700	333	1014	QAPGGLLRVGRGGMLLPGCAA
i						VADLOEEVPGFSWDAWAVKG
						EQRQGGGGVVKH*DAIPGQRV
	i					SDPGPPEPLASAPGQLSPSTPEY
1		1			1	RRPPGESRRHRRPDLAQDQRGA
		1				AVLLLAGARGLSPLPRIPALGA
		1	1			ASFPPTLQFFLQLPSSGASTTSA
		1				GFFLLVLHQPLWLLLLDFLFDN
		1				LLLLRHSLFIPHGFLKCVSIPAF
26558	56926	A	26708	95	298	GSTQVLWAAWGGAGWTPRWP
20336	50920	\^	20708	73	270	VFATWPWVQDMWPQQAWPLP
		1		1		QGVDIP*ACPPPPLRT*WL*ENR
		1		1		KAGS
26559	56927	A	26709	110	195	KAGO
20339	30721	1^	20/07	1110	172	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26560	56928	A	26710	241	957	KSPOIGLOGSWGAVGVGMRDP
						KERATEASKPDLLAOROGEGHI
						FILFFSDYIPIFSSYLSLORSSRGP
						SFFGPFSSPHNIPCEGRQNSETPP
						WPSLGKRSKKSSLYPLPKAPOP
						KSRAPSPISNNLKNFPOPSEKKD
						GPQPLWPQKWPLAPLFSRSPS*
						DDSGPCTEYCRRARRFKSFEDM
						AHIGPPKKVLYKIALGKFWELA
						DAKKKRKKGTSETETCLLSRAT
						ELLPKGKRHCRGIL
26561	56929	A	26711	496	708	GMLFRGSGACRRGGRTGGSGH
						A*PEPPVLPPLLHAPEPLNSMPH
		1				GLPAPPASPCHFPNLDSCVHSHS
		1	i			DTPLSVLPLPHLKSPLSSSDFCS
		1				YEVKKDAILSPMLSWWAGHRS
		1				AAGED
26562	56930	IA	26712	302	561	TFLLQLAAVWSADRVREALRP
				ļ		ALWDWRSAVPHPSPQGPTG*R
		1				GVGVHPAAASRGGESSHPTAF
						DRSPPPPKPLRI*PEPSARSGLP
26563	56931	A	26713	1	411	LLVFOVHOCLHCKLL*/PSYVPL
		i	-			GYTEAFLATONIGRVSLWAKH
						GHPDPFPLARADFRAQESPSPN
						DPSWLL*YFER*WSQATTKG*N
						RCC*RCD*LQAPSRRPEAVHTN
						DPR*REVREEHMVLQVLTR
26564	56932	С	26714	361	642	
26565	56933	Α	26715	1805	2260	
26566	56934	Α	26716	472	1667	AIHLLSLQTEFLVAERSSAAGRT
						TPATRAAFLAASCGPLHSCPTL
						LCSQLCCFSRSRSRVSGPKASLG
						IKEIASVDRVNTRRPACSTSSWL
						HNSGFTLSLANRDGGKRIRSET
						AKKGMSGDRSMKSWEVRRGY
		1			1	RWSSRAVRRPRACSSDGGTHF
						ALPMAARGSSGPSPGSPANSVR
	1					QSLKSESSISAIWVAEQAAGNV
		1				PRTSAQFGTGSESANTAARLIE
	1	1				KLLRAELDKPEIRDERIVGWWT
1		1				TFGRPQLGSRVGFCACSLAARM
		1			l	SSTSQNLEAAFGGKFCFLWALL
	1	1		1	1	LGLDDTFESRISDTGSAGLMLV
1		1			1	EFFAPW*VHSESANTAARLIEK
l		1				LLTAELDKPEIRDERIVGWWTT
		İ				FGRPQLGSRVGFCACSLAARMS
l	1	1				STSQNLEAAFGGKFCFLWALLL
1						GL
				<del></del>		

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide logation of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	Sequence		03/240,817	sequence		, , ,
26567	56935	A	26717	2	237	SVRQTTATSPAHKNSKRLIRSC
						QGF/HPEPPPTGACYKCPQPRIP
		1				HEPCPI/S/SQDPTENWTVQLTW
		1			1	QPLPEPLELWPKAV
26568	56936	A	26718	I	313	MESAQKEAVEIFGQPHAASSSG
						DVKPLLFIDFYKCSGEKVVCME
						HALRACYMCRKSGHWAKECP
1						QPGIPPKLCPIC\GDPTGNQTVQ
						LTWQPLPEPLELWPKAL
26569	56937	Α	26719	377	583	
26570	56938	Α	26720	1221	1394	VASFYSLLQPPYPSTSFSFQSWR
	1	1		1		HTSISPFS*FQFLSFSGIFWQPLP
26571	56939	A	26721	160	234	EPLELWPKAL
26572	56940	A	26722	163	414	
26573	56941	A	26723	212	399	YSLKDCWPLSLSLNHFLLSILAS
20373	30941	l^	20123	212	377	PFNLSLLLISVPFLFW*RTETRFI
						WOPLSEPLELWPKAL
26574	56942	A	26724	809	874	WQI ESEI EEE WI IE IE
26575	56943	A	26725	49	220	
26576	56944	A	26726	71	375	LRSGDLPWEI/NPLSSCSLLREK
1		1		i		DPPTTSGPQT\TSPRNISPILNPEL
				1		ATSARNLATRPRNACSPGFLLS
				1		RVPSVRDPTGNRTFQLT\WQPL
						PEPLELWPKAL
26577	56945	Α	26727	1	I01 I	CSEYEDSSPAPVPATDLSSTLSS
			1			SVPQPQDTGTSQQLHPLDPWHE
		1				LLRAQELQGATNHKGYSHAEH
		1	1			EHAGLGVQGGNGALAFSNSGH
1		1	l			RHAVPTISSGTGRRRTPSSSAFG
		1	ł			LLNLHQWFVSGFQAFSDRLKA
		1				ALSASLLLRFGDSDWLPSSSAC
						KCLMLGLHFVIVGNICATLKEK
		1				YSSMLHLDVTMKKNGEKRTRL
						QKRKKGMPPHPAYEDLNIAAIT
						LPANVVLHQPSGFRTSGQLDPV
			ì			WWSLDTDAHEIWCQDPGLGSG
		1		1		DFPWEITPLSSYSLLHEKDPPTT
						SGPQT\TSPRNISPISNPRQRRQV
		1				LSMDPKLRHRSRTGKAAFPWC
		$\perp$				LIIAGTPL
26578	56946	Α	26728	150	211	
26579	56947	A	26729	445	549	
26580	56948	A	26730	193	249	LRSADLPWEINPLSSCSLLHEKD
26581	56949	A	26731	372	564	PPTSSGPOT\TSPRNISPILN/PEK
		1		1	1	KETRFIRGPKTPAPVMD
26582	56950	c	26732	185	640	RETIGIROTRITAT VIID
26583	56951	Ā	26733	1662	1774	
26584	56952	A	26734	233	527	
2004	1		177.7		1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26585	56953	A	26735	380	731	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTVTSPRNISPILNQEL ATSTRNLATRPRNACSPGFLLS CVPSVRDPTGNQTVQLTWQPL PEPLELWPKALCLTDSFPDLLG LTAED
26586	56954	A	26736	2	182	
26587	56955	Α	26737	2	89	
26588	56956	Α	26738	2	89	
26589	56957	A	26739	161	460	KMKEFMKKSSRTKDTRQQEQV LEPLFTIAKTWNQPKCPSTID*I KKMWYIYTMEYYAAIKRNKIV FFAGTWMQLEAIILSKLIQEQKT KHHMFSLIRGR
26590	56958	Α	26740	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDVFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTMEYYAVTRRNKIVSFA ET*MELEVIIVSKLTQEQKTKHC MFSLTSGS
26591	56959	Α	26741	902	1065	
26592	56960	A	26742	326	484	WYSWDCQLVTPWRPRIIPGPLG TWMELEAIILSKLTQEQKTKHH MFSL*SGS
26593	56961	Λ	26743	527	825	QPLWGQLH*EVPSCWRFSA*IC YSSGLTVMLSSWLDLIRPPWTL R*PREWRQCMGENHIGRGLGF* RPWTWMELEAIILSKPTREQKT KHYMFSLISGS
26594	56962	A	26744	398	557	HYWLGTVVHTCNPSTLGS*GR QIT*AQELETSLGNKNVGCSELI LLSTLGNRV
26595	56963	Α	26745	3	359	HRPGIPGTTISSWMDAWGRLEA RYMSYLHSRRGDHA*DKLQRD NRFASQTHSHWAKSSCHCRFES RFFFLPSPSWSYNRSWGGESAE RTWMKQRGTCLSHSPLDLLHP GLCQHKVGAR
26596	56964	С	26746	127	216	
26597	56965	A	26747	135	197	
26598	56966	Α	26748	84	202	VLIHIRRDIMIPETVD*WEY**P* RLVPGQVQWVKPAIP
26599	56967	Α	26749	483	669	
26600	56968	Α	26750	1	274	EIRNKIHVSENSQIKTVKEKPSIS SSVSRLKGVNKVRASFPEDRKD YTGSKAPKGS*GYTIN*LK*NN KRKKKQNKKLMPKTEQGQKN SIR

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
26601	56969	Α	26751	63	398	TPLRQPCSIRNVQQEPVGRFSGT
		1		ŀ		GLPLSVARSSPWEAWPQCKWR
						FONAGD*DIROPDRGQGPRPAE
						PEKREPYLRSQQGAFLGSHSSGI
						QSQLLGLGESCSYGATGKPVHP
26602	56970	Α	26752	3	231	SVHEEEKMALPLGQSHCGLLY
						LYY**RCFKCYSFYCILFIKNAFI
					l	Y*NI*IYINTHTHTHTHTHIYIYI
			Ì		ł	YNCLYI
26603	56971	A	26753	4266	4944	TDEIGASRLSRVESLAPEVKON
						TTASGCELMHTEMQALRADW
						KQWEDSVFQTQSCLENLVSQM
	1				1	ALSEQEFSGQVAQLEQALEQFS
						ALLKTWAQQLTLLEGKNTDEE
						VECWHKGQVSWLPV*KAEPRT
						EDLKSQLNELCRFSRDLSTYSG
		i			ł	KVSGLIKEYNW*A*TLLKGCON
					1	KEQILQQRFRKAFRDFQQWLV
			ļ		1	NAKITTAKCFDIPONISEVSTSL
		1			1	QKIQVRVLSI
26604	56972	A	26754	3	556	,,
26605	56973	A	26755	143	724	GWIPSDNSICVQEDCRIPQIEDA
						EIHNKTYRHGEKLIITCHEGFKI
	l	1			ŀ	RYPDLHNMVSLCRDDGTWNN
	1	1			l	LPICQGCLRPLASSNGYVNIYEL
	1				ŀ	QTSFPVGTVISYRCFPGFKLDGS
					l	AYLECLQNLIW/RPAHPGALLW
	İ				1	KEEDLNIFSLSFISHTSGWOLLC
		1			1	FIFALC*SPLPPQHLPVPQLAPPH
						LCSKCCSPAIKDV
26606	56974	Α	26756	3	1393	CLRPLASSNGYVNISELQTSFPV
		1				GTVISYRCFPGFKLDGSAYLEC
		1				LONLIWSSSPPRCLALEVKIPVS
						GAVRVTITLPVTLGHPNVVTQR
		1				WKAGASDKGELVVLKLLFSPT
		1				AOVCPLPPMVSHGDFVCHPRPC
						ERYNHGTVVEFYCDPGYSLTSD
		1				YKYITCQYGEWFPSYQVYCIKS
						EQTWPSTHETLLTTWKIVAFTA
				ŀ		TSVLLVLLLVILARMFQTKFKA
						HFPPRGPPRSSSSDPDFVVVDG
						VPVMLPSYDEAVSGGLSALGP
		ļ				GYMASVGQGCPLPVDDHSPPA
	1				1	YPGSGDTDTGPGES*TCDSVSG
						SSELLQRLYSPPRCQESTHPASD
	1					NPDIIASTAEEVASTNPGIDIAD
						VDSSNIKLPDWQTKYRVASPAR
				I		STCEDRSGAPVGTHESLFFSIPS
	1			l		SARODWAPLDSQLESPOCRLPT
	1	1	1	1	1	
	1		1			LORDFLVDPOAERPVPLDPELT

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon,/=possible nucleotide deletion, \=possible nucleotide insertion)
26607	56975	Α	26758	1	500	
26608	56976	В	26759	19	148	
26609 26610	56978	A	26761	184	441	LPAKEEEGHSKKSGPLLGPRRA LPGTALGARGAEQGDPEADH* GADTTKRCPGLGPAPVPRKGIP AEGPRRGSRAGLGMWGPGLGA HRTAAPSPAEAPSPCQHPSSHSC PVACFEPVF DENRELLGELDGIDVLLQQLSV
						FKRHNPSTAEEQEMMENLFDSL CSCLMLSSNRERFLKGEGLQLM NLMLREKKISRSSAL/KVL/DHA MIGPEGTDNCH*VCLTFLALR:T IFPLFMKSPRKIKKVGTTEKEHE EQCCSILASLLRN
26611	56979	Α	26762	1	2403	
26612	56980	A	26763	17	751	AKMPFDANKLYCSEVLAILFFS PLENRELLGELOGIDVLYFA*Q VFKRHNPSTAEEQEMMENLFD SLCSCLMLSSNKERFLKGEGLQ LTLL*LSHSSDSCEMPTWRGGS MEGOGENGLGLVSVGLEHALL LTYGLYQRLPPQPQNAQPSFVH REKKISRSSALKVLDHAMIOPE GTDNCHKFVDILGLERIFPLFM KSPRKIKKVGTTLPPLPAAATPT NRPSAMNGRVRMEAEQSSAHC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26613	56981	A	26764	1	1914	MAEGERGADVPH/GPRGLAGR
					1	RGVGGAARGRAG/PGGT/EGGG
						GPESLSGGSGVGDSGGGCAPGP
						SAPPARRRVPLAMGPRNLLIDW
						IWIMDTTLGLGTEGGGHSPPVL
						PLCASVSLLGGLTFGYELAVISG
						ALLPLOLDFGLSCLEQEFLVGS
		l				LLLGALLASLVGGFLIDCYGRK
						QAILGSNLVLLAGSLTLGLAGS
i						LAWLVLGRAVVGFAISLSSMA
		1				CCIYVSELVGPRQRGVLVSLYE
				ĺ		AGITVGILLSYALNYALAGTPW
						GWRHMFGWATAPAVLOSLSLL
						FLPAGTDETATHKDLIPLOGGE
		ŀ				APKLGPGRPRYSFLDLFRARDN
						MRGRTTVGLGLVLFQQLTGQP
						NVLCYASTIFSSVGFHGGSSAV
		Į	1			LASVGLGAVKVAATLTAMGLV
		1				DRAGRRALLLAGCALMALSVS
						GIGLVSFAVPMDSGPSCLAVPN
						ATGOTGLPGDSGLLQDSSLPPIP
	l					RTNEDOREPILSTAKKTKPHPRS
			1			GDPSAPPRLALSSALPGPPLPAR
ł		ļ				GHALLRWTALLCLMVFVSAFS
l		1		i		FGFGPVTWLVLSEIYPVEIRGRA
l		i				FAFCNSFNWAANLFISLSFLDLI
				ĺ		GTIGLSWTFLLYGLTAVLGLGF
		1	1			YLFVPETKGOSLAEIDOOFOKR
		1				RFTLSFGHRQNSTGIPYSRIEISA
26614	56982	A	26765	201	632	NLLLCPLSAESRPEEGVRLFCSO
20014	30902	ľ	20703	201	032	FRSRORPOAHKSAWGTTALSES
		ı		1		MNCFASFGASISSSADOEOLHL
		l		ı		PGAVGSGRPGECLGPSGRCSK*
		1	1			GATFPGOKGRWKEARPSPVPAF
		1				AAGLOSRAGHPRGGIRPGRPHG
1		1				ERDSAACWGR
26615	56983	Ā	26766	197	777	LPSRGAGLRTCSPPCLSLPPTPW
20015	30983	l <sup>A</sup>	20/00	197	l'''	TPVRPEPPORAPPPTPRRPVPST
		ı		1		TOGLRNASARRGTGR/PAPP/VS
		ı		i		PGAGSTR\EASWAPESAARAGL
1				1		WGPSNSVQRAAESASRPHGFG
1		1		1		
1		1	1	1		QPPKAPARPGWLTGKFPASVPS
1		1		1		ASRRAPPAAVTSARHYYLRQPP
1		1	1	1		PRPSSCPECNKIRLWPAFQLTPL
		Ц.	<u> </u>	<u> </u>	L	CQGPAASERDRRKPQKRR

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26616	56984	A	26767	178	697	ATLFIQKHQSGVKSTNP*IGRRS LTPEITAELGLERLNPRRCSSCL LGLKFEYHNSNLPLQLHGQAC GDPTNSVQRAAESASRPHGFGQ PPKAPARPGWLTGKFPASVPSA SRRAPPAAVTSARHYYLRQPPP RPSSCPECNTIRLWPAFQLTPLC QGPAASERDRRKPQKRR
26617	56985	Α	26768	1	858	
26618	56986	Α	26769	10	1332	
26619	56987	Α	26770	1	1086	
26620	56988	Α	26771	1	1392	
26621	56989	Α	26772	i i	987	
26622	56990	Α	26773	1	336	
26623	56991	A	26774	46	302	APGAVKKTWFGKKGREREKQE RR*RQLGKENENIVALQLIRTD QEYWRHHSWHFFLSAAACQPE LFLLKHTAKNNRRIRVSQKWK
26624	56992	A	26775	1	1839	
26625	56993	A	26776	284	816	APGAVKKTWFGKKGRERGETR EKNNOPTVRTNSQTRDTFFKT* DLF*RMPSWELPSPASS*ASKTI KYLGIQLTRDVKDLFKEKYKTL LNKIKEDTNE WKNIPESRIGIINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPEBAAEQQILPN SQSCYLLIPLEASSQRGSWLY

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide inscrtion)
				sequence		
26626	56994	A	26777	1	2547	MVKGSIQQEELTILNIYAPNTG
					1	APRFIKQVLSDLQRDLDSHTLI
					1	MGDFNTPLSTLDRSTROKVNK
						DTQELNSALHQADLIDIYRTLH
						PKSKEYTFFSAPHHTYSKIDHIV
						GSKALLSKCKRTEIITNYLSDHS
		İ				AIKLELRIKNLTQSRSTTWKLN
						NLLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYONLWDAFKAVC
				ľ		RGKFIALNAYKRKOERSKIDTL
						TSQLKELEKQEQTHSKASRRQE
						ITKIREELKEIETQKTLQKINESR
						SWFFERINKIDRPLARLIKKKRE
		1				KNOIDTIKNDKGDITTDPTEIQT
		1				TIREYYKHLYANKLENLEEMD
		İ				TFLDTYTLPRLNQEEVESLNRPI
	1					TGSEIVAIINSLPTKKSPGPDGLT
						AEFYQRYKEELVPFLLKLFQSIE
	1					KEGILPNSFYEASIILIPKPGRDT
		1		ŀ		TKKENFRPISLMNIDTKILNKIL
		1				ANRIQQHIKKLIHHDQVGFIPG
		1				MOGWFNIRKSINVIQHINRAKD
		1				KNHMIISIDAEKAFDNIOOPFML
	į .	1		1		KTLNKLGIDGTYFKIIRAIYDKP
		1		l		TANIILNGQKLEAFPLKTGTRQ
	1	1				GCPLSPLLFNIVLEVLARAIROE
		1				KEIKGIQLGKEEVKLSLFADDM
	1	1	İ		ŀ	IVYLENPIVSAQNLLKLISNFSK
		1				VSGYKINVQKSQAFLYTNNRQ
		1				TESQIMSELP\FTIASKRIKYLGI
	1	1		,		QLTRDVKDLFKENYKPLLKEIK
		1				EDTNKWKNIPCSWVGRINIMK
		┞		ļ		
26627	56995	A	26778	1	489	SISWKLWFTEFTLFRFFQPSVSA
		1				VPVSTLAVVLGLKTLSLLFSHSF
			i			PGRHSWALRAISLLPSFLYTSSL
						MNSFSYTVHLYLGGLLRLCGSR
		1				DPHACGFPEGSPLPSGSAA*PFI
		1				WGMRKPSCVLAPSCSRRDSFG
	i	1				CLSFSGHQCLHKSHVGSPSGPQ
		<u> </u>				ERLYNG
26628	56996	Α	26779	354	685	YRGYLRGECFP*KALCCEPAAY
		1				LQTCPNPFSGPACSGHALHSLN
	1	1				VGDCVYLICPRYPPLRRAGKPR
	1	1				DTGIEGRTLSSGGPSVHSSFHSA
						VLFPYTSKLLWIERRRPAGQS
26629	56997	С	26780	1	867	
26630	56998	A	2678I	139	513	
26631	56999	С	26782	1	948	m. incovince i am mar
26632	57000	Α	26783	630	734	TAARSGYPGRAGTLTGLHPMQ
			1			VCRCRR*PYSRGT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, v=possible nucleotide insertion)
26633	57001	A	26784	1	224	SRAGYDHVVEPVERGTSGVRW
						YACCGLMVCPANPQHFAHGY/
				1		VGKIPGYPARAGTLTGLHPMQ
						VCRCRRCPVYEI
26634	57002	Α	26785	112	254	
26635	57003	С	26786	1	567	
26636	57004	С	26787	1	543	
26637	57005	Α	26788	165	633	RIPGLLLCPAYPQHFAHGYVDK
						IPGYPGR\GTLTGLHPMQVCRC
						RRQAPCMKSNNALIVILGTVTL
						DAVGIGLVMPVLPGLLRDIVHS
						DSIASHYGVLLALYALMQFLCA
		1				PVLGALSDRFGRRPVLLASLLG
						ATIDYAIMATTPVLWIYPLVNS
26638	57006	A	26789	264	800	ISNFELCSRSIHLLCSSTGYPGR
		1				AGTLTGLHPMQVCRCRR*PAV
26639	57007	A	26790	1	738	
26640	57008	A	26791	84	162	AVLDLGPPTGRDPPQGSPDPYS
		1		Ī- ·		GAFLLASCGAPLGORSORKEO
						AAIFAVLOLLLVIPPGVGGTOT
					l	NRVWSGFPANHGNPGYPGRAG
						TLTGLHPMQVCRCRR*PPYRVI
		į.		ŀ	i	PQCGTPLGQGQPEVFVKQFWIL
	1					GLRLGETPHRGHQILIQGHSC
26641	57009	c	26792	1	531	obverbilling in direction of the control
26642	57010	Ā	26793	216	519	ORESTIPSRPVERSNLGVRLYAC
200.2	15.010	ľ.	20175			CGLLLCPAYROHFARGYVDKIP
						GYPGRAGTLTGLHPMOVCRCR
						R*PDRRGTERVSARKHVCFVVV
						SLFVAACRPPLRA
26643	57011	c	26794	1	606	ODI YIMONI LIGI
26644	57012	С	26795	1	1059	
26645	57013	Α	26796	1	3285	
26646	57014	С	26797	1	1390	
26647	57015	Α	26798	211	679	RIFKCKADLLLYDMLVYVTLWI
						HRAVTYTHRVPNHSYRRSNIKS
	1		ŀ			ETTVPTRIVGPVERSNLGVRLY
	1	1	l			ACCGLLLCPAYPQHFAHGYVD
		l				KIPGYPGRAGTLTGLHPMQVCR
	-	İ		1		CRR*PKPAPLPGSPOHLCSHOPH
		l	İ	1		LAORKTGOCFLOGHCFPEKNW
		1	1			GTV
26648	57016	С	26799	1	774	

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26649	57017	A	26800	542	1269	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVRKKTILAPNTQTASPRALA DSLMQLARQVSRLESGQRKYP GCRLYASCELLCPVNPQHFA GYVDKNPGYPAGAGTLTGLHP MQVCRCRRQAPCMKSNNALIV LIGTYTLDAVGIGLVMPYLPGL LRDIVHSDSIASHYGVILALYA LLMQFLCAPVLGALSDRFGRRPV LLASILGATIDYAIMATTPVLW
26650	57018	В	26801	I	1531	
26651	57019	Α	26802	1889	2154	
26652	57020	A	26803	147	162	APSLHLKDTVDRSNLGVRLYA CCGLLLCPAYPQHFAHGYVDKI PGYPGRAGTLTGLHPMQVCRC RR*PGAHTVVDIRPREDHLGSA GQPNCPENGCLQGFHTGLAYPE HHPCI
26653	57021	Α	26804	2381	3641	
26654	57022	Α	26805	1	2367	
26655	57023	A	26806		488	MDLLYMAAAVMMGLAAIGAA IGIGILGGKFLEGAARQPDLIPLL RTQFFIVMGLVDAIPMIAAIAFV LFVLFCMKYVWPPLMAAIEKR QKEIADGLSSAERAHKDLVLAK ASATDQLKKAKAEAQVIIEQAN KRRSQILDBAKA*GRQEPLVQV FLESARKR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
26656	57024	A	26807	2125	2435	VSPROKSARPDLT*IRTLLCKVL
						GVLFSVAGGKKGPTCILQILKG
		1				QRRQEA*CISVMAERVWASGQ
		1			1	A*WEVWLHWAKSIDWFLFWK
		1				QHVHALRVRLDTCLFSLEEGSS
		1				FWNQGLTWKVVRRTFSESINH
		1		İ		TPRITLGVPYSVHGIQLPGLLNF
		l				GEFKVCFVLSPRIFNLTHENFLS
		1				SEGPERRGLLGATFNCLNKRLA
	1					KYRMRNVHPKPKLVRYLHSRL
						PPEPAAAP*AWCGPRHLSRRQN
	l	l			ł	SSSSQIGNDSFQLQVTPVHLLPL
						SHTTRKNPEMYDLPLLIFNPOES
						AILQLFHQDGECLHCSPIVGDW
		1				CHLGHSQACPSFHVPSGLFVPS
		1				LLCGAAFGRLVANVLKRYSVC
		1				VRVCAHVHVCARVRVYACVC
		1		İ		VRMTISLTVILIESTNEITYGLPI
		1	l			MVTLMVSTLPPGPCQAQGHVR
	ł	l		1		PTGPIFRSLLEWETEVEMDK*G
						HDFAHVLVSECISSEA*GMLLL
					1	GGGPDRSLFSTFRAVWSLSRLL
						DSVIAAGKQ*A*RT*SVGYSLL
}						CPDLKGDPSAVFILRTTVHHAF
						PVVTENRGNEKEFMKGNQLISN
						NIKFKVKKTA*EERQVRDKRSR
						LTRLSALPIRNMCDEHIASEEPA
						EKEDLLQOMLERR*EPGGAPTA
						RRATORWGEPLAOML*LTFHG
		l				LILRSQLVTLLVRGVCYSESQS
		1			İ	VSLSEAEISQARPDEARGVGRC
		1				RRADLTLLNPRMIVVRRAAPAG
26657	57025	A	26808	24	369	ING IDET DET TO THE TAIL AC
26658	57026	A	26809	4	371	
26659	57027	A	26810	82	703	
26660	57028	A	26812	1	1692	
26661	57029	A	26813	293	563	NVWPSSSVRGRNE*GREGGRR
		İ				RTQQAAGLGPAPSDLWWLWLS
		1				WCLQKNMSQGGENLPAGPGSC
		ŀ				CGREAQEGAGTSLEDAPFFEAQ
		ŀ				LLOLH
26662	57030	A	26814	1	488	VARLYWKRPSLHACHFRDPRA
2000		Γ.		ľ		GLSENPRLLQCSPSSSSGNVWG
		1	1			PHLYAVPCL*NGRIIPSPWNYRS
		1				LNSTTSSTCSSFAVVSSPSCPWV
		1	l		l	QLPGSCLLSRSLLQRVAWSQAP
		1	l			VPMRSEQDQLQKPPPPSAGLPA
		1	l			SVHANL*PGDRKGSVWTPAGV
		I		1		AOIPSPWP
26663	57031	В	26815	51	90	AQIFSFWI
20003	15/031	I <sub>R</sub>	ZU813	131	90	

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26664	57032	A	26816	299	707	RPPCRISCHPHTRCEGGRLRSRS
20004	37032	l <sup>A</sup>	20810	299	1,01	PLLS*MPLSHPOGPSOPPAGSMS
		1		1		
	1	1			l .	SSPPATTSTCSCSPPAAGCTRGR
1		1		1		TTGRPFWTASGPAELDWASGSS
		1		ł		VGL*SQGSQLGACGASYAGLG
ŀ				1		VPPRLLGPMTSCCMSLPFPSPAR
26665	57033	A	26817	146	330	IP TVARRMELTPALLRALLNGILPI
20003	37033	^	20817	140	330	SEPPSNRIFACWGKPAWTACCN
				1		SLRARR*RAISCCPSH
26666	57034	Ā	26818	1326	1694	IFGWFGACCSLGSCCVVFTAST
20000	37034	1	200.0	1.520	1071	CTTVCGGCAIKVGSCLSLATMG
		1				CCVCCTSGLGCACSCWRGVSF*
	1					CLMESWGICGSLCWSWSACRW
1	1	1		1		
1						MVCFCLVWKHCRVFTCS*VCS
26667	57035	A	26819	1	1407	SGGWLSFCCLADCD
26668	57036	A	26820	175	1397	SRGSGREKFPAQLSYQTLLGKG
20008	37030	^	20820	1/3	1397	PIEGTSLSNLAQQRCKEHHCHF
		1				LREQGPNCLIIERFMDRYTGKYI
					1	HMASHTTRCRPHVSRRPKARLL
	1	1		1		APATRSRSARARLRETRVRRGS
1		1		1		
	1	1		i		PSCLWLNRRSRLPAEHSVRSPP
		1				RDMVFESLGLPSTKSSEFRSAA
		1				PEAAERAQPGDPCGLQTPAPLR
		1				PGFRRNQDPASAAAAAEEVRS
		1		1		GGGRGRILATTLWGCNTLCITQ
		1	i			YTRIRKLTLVYCGVESKQEWG
	1	1	1		l	EYHEGVQAGLTRPGRSPKLISK
	1	1		1	I	FLEKELTDRNWDQEDEAEEVK
	İ	1				SSFPKND*VLKNRAIKKAKRRN
1			1		i	VGFEVSAPLQLLLFKGLVVPSG
	1	1			l	GGRFSGFGSGAGGKPLEGLSNG
		1	1			NNITSAPPFASAKAAADPKVAF
1	1					GK*LPSPSRLLVDKVSNPKTNG
l	1	1				DSQQPSSSGLASSKACVGNAYH
						KQLAALNCSVRDWIVKHVNTN
26669	57037	A	26821	3	89	AASGRSFRGYSRRHCYHRR*QL
						HACHCP
26670	57038	Α	26822	150	383	LCLGEVWKGSFFLTGTKRPGVF
						LSLHKKACYHHNHHRYHHHH
İ				1		HHQTKP*QQELNSLLLHFPPHQI
		L				QGDQFHHHLYYL
26671	57039	A	26823	105	417	LCLGEVWKGSFFLTGTKRPGVF
		1		1		LSLHKKACYHHNHHRYHHHH
1		1	1	1	i	HHQTKP*QQELNCENMPQYNF
1				1		QNGSQSYQTLLL/SLSTKFM*YS
			1	1	I	KFFVVISVMFIASSPETDF
		_			<del></del>	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26672	57040	IA	26824	189	554	AMNSCVTGDRYSPCGGFGFAF
		1				LYSSVSVSSSSEYQLSPLPPAKE
		1		1		PLAAQQSCSIPIASVFQQTIHSLI
		1				AKDKKEFSSNLLDSKVNMCHE
						AHQLISHS*ANFRSICHIPORW*
		1				NLIFEKFSDVSMGSGTFG**AE
		1				WS*TLSIAASLVYSLLHKIQ
26673	57041	la	26825	84	239	ACTKKACYHINHHRYHHHHH
20075	37041	^	20025	04	237	HQTKP*QQELNSFRFSLSQPSLL
	1	1				AVFLFLRP
26674	57042	A	26826	2	245	AVILLERF
26675	57042	A	26827	154	546	LIVTVHVNHLGVLINHRFRISG
200/3	37043	l <sup>A</sup>	20827	154	346	GVCGTDCISHKFPGAADATGPS
		1				
		1				WTTHCAVITFSLTTGSATKKTE
		1				DNNTFVFNVDVKAN*HQITRA
						VKKLCDIDVPEVNTLPNVSISFF
		<u> </u>				FLLCSTVFCTLTVFFLRENG
26676	57044	Α	26828	331	612	NHRGLPFPDYIPGTYFLFFFFLF
		1				FSFSSFSSSSFSFPASGNHNSTLY
			l			FYGINFFSFHIGMRMGGIFLCLT
			l			CFT*HDVLQAHPHREGRQDLLI
						HD
26677	57045	В	26829	928	1617	
26678 26679	57046	A	26830	3	1128	LYNRRRRRRCSHCRHRCRRLSS
20079	57047	I <sup>A</sup>	20831	3	1128	
		i				GLRKEEVISLGASLGRVFVPCSI
		İ				PTVSAARGPTGAPGGPNSKPLS
	1					GCCDDGFNLGRQQWGNPLPFC
	1	i				SKTISSSLHWTWSQVNLVEILP
		1				AIFSSFLNLQHVNLWFLAAAM
				1		KAVTEQGHELSNEERNLLSVA
						YKNVVGARRSSWRVISSIEQKT
						ERNEKKQQMGKEYREKIEAEL
		1				QDICNDVLVRGQCFCFEQWFL
		1				NSINLMYKCRLSNYFRYLSEVA
		1	ŀ			SGDNKQSK*YL*KEIRPVMEPV
		1	ì	l		FFHRDFLTILIRLGLALNFSVFY
		1		l .		YEILNSPEKACSLAKTVRKTLC
		1	i	İ		DI*P*ONSACVINFILFLNILRDN
		1				LTVSTTSTGFIVSFLFTYLIIHCY
		1				LOEVCSVSLCTLNIYPLCDKKK
26680	57048	1	26832	139	601	EGRGHLAQELLSERVFVPCSPP
20000		1.	20002	1.00		TGMTMDKSELVQKAKLAEQAI
	1	1	l			RYDDMACSSERHVTEOGHELS
		1	l			NEEKKSCSLVAYKECW*APRR
		1	1			SSW/RVISSIEQ/KTERNVEGSSR
		1			1	WGKEYREKI\EAELQDIC\NDVL
						ELLDKYLIPNATQPESKVFYLK
26601	57040	١.	0.6022	70	100	MK
26681	57049	A	26833	70	122	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26682	57050	A	26834	179	876	CIVILFFFSOFNFVGRILGPRGLT
						ANVNRYLELHTLYGYMNLFIV
					l	SIMKDVLSL*RE*F*SCTL*IF*E
1						EONRGKPNWEHLNEDLHVLIT
	14.					VEGV*I*LLYLWTVSNAFISCVF
						HV*AEGEDRYCCLYTSF*ISLLT
		1				VAALAFSLAATAQAAPRIITGP
ļ		1		l		APVLPPAALRTPTPAGPTIMPLI
		ŀ				RQIQTAVMPNGTPHPTAAIVPP
1				i		GPEAGLIYTPYIYIISKYLWLLSS
İ		1		i		CSPEP
26683	57051	A	26835	3	915	AEAHPRLPDAADERQEAHDSLP
20005			20000	1		NFCGIFNHLERLLDEEISRVRKD
		1			1	MYNDTLNGSTEKRSAELPDAV
1						GPIVQLQEKLYVPVKEYPDFNF
						VGRILGPRGLTAKQLEAETGCK
		l				IMVRGKGSMRDKKKEEONRG\
		ı	i			KPNW\EHL\NEDLHVLITV/EKV
1		1				LQEQGQEIKLKRAVEEVKKLLV
		1				PAAEGEDSLKKMHLMELAILN
						GTYRDANIKSPSLAFFLAGTAQ
		1				AAPRIITGPAPGLPPAALGTPTP
						AGPTIMALIRQIQTGGMPNGTP
		l				HPTAAIVPAGPEAGLRYTPYEY
						PYTL\APATSILEYPI\EPSGCI
26684	57052	Α	26836	1182	1360	KLSICVYIYICMFIYTHVSV*FYI
		l				YIYTHRHTENHYFCNSVQFVLY
i						LFTFFCYYFIWPA
26685	57053	Α	26837	3	348	RNSKHVCRAEP*GHFCYK*HF
			1			WNHTEHTAVLEI/EQINARDET
		1				DF\YLGNRCTYVCKEQHSGPGS
		1				KSNTTIVIWGKVTCAQGKNSV
		i				VCAKFQSHPPAKAIGHRIHVML
						YHWRIQIH
26686	57054	Α	26838	264	527	NSKHVCRAVP*GHFC*K*HFW
	1					NQREHTTVLEIEGVYARDETEF
		1				YLGNRCTYVCKEQHSGPGSKS
		l				NKTRVIWGKERGSGWCRLSGR
26687	57055	В	26839	26	515	
26688	57056	Α	26840	92	341	
26689	57057	Α	26841	224	1111	
26690	57058	A	26842	2	592	HSLTGRCIFFLITGTSPGSPEMST
		1				TLKIMSSKEPSISPEIRSTVRNSP
		l	1			WKTPETTVPMETTVEPVTFSPQ
						LVFARLMTGVGLGAALPNLIAL
		1	1	1		TSEAAGPRFRGTAVSLMYCGV
		1	1			PIGAALAATLGFAGANLAWQT
						VFWVGGVVPLILVPLLMRWLP
						ESAVFAWRSISNKRA*FRDCRC
		L				CSAAIIW*RRFPFKSKPVM
26691	57059	Α	26843	2	141	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn nf first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26692	57060	_	26844	11	978	
26693	57061	Α	26845	144	647	
	57062	A	26845	1642	2652	FGILVLLALIVIWYNNFFGAETE
26694	57062	A	26846	1642	2032	l
		1				AILPYDQYMHRFAAYFQQGNM ESNGKYVDRNGNVVDYQTGPII
		l			1	WGEPGTNGQHAFYQLIHQGTK
		1				MVPCDFIAPAITHNPLSDHHQK
	i e	l		l		LLSNFFAQTEALAFGKSREVVE
		l				QEYRDQGKDPATLDYVVPFKV
		1				FEGNRPTK*ILLREITPFSKLNEV
	1				}	KAISDTICVIRDGOHIGTRDGIE
					l	HLTAWHPVNRHIKRVNDVSFS
		l			l	
						LKRGEILGIAGLVGAGRTETIQC
						LFGVWPGQWEGKIYIDGKQVD
		1				IRNCQQAIAQGIAMVPEDRKRD
		1				GIVPVMAVGKNITLAALNKFTG
	1	1				GISQLDDAAEQKCILSHPRCSW
		ļ.,				QGRHLLH
26695	57063	A	26847	52	137	MOLICUPDIALITY CALIFORNI TOO
26696	57064	A	26848	1	1858	MGLKVDDKVPLFAVVSRLTSQ
		1	l			KGLDLVLEALPGLLEQGGQLA
		ı				LLGAGDPVLQEGFLAAAAEYP
		l				GQVGVQIGYHEAFSHRIMGGA
	İ	1				DVILVPSRFEPCGLTQLYGLKY
l						GTLPLVRRTGGLADTVSDCSLE
ĺ						NLADGVASGFVFEDSNAWSLL
	İ					RAIRRAFVLCQGQFHHRTTDVE
			Į.			YKGDPKAVKIEESEINYLLNVY
			ł			NTHFKKQLSRDDIVWTYSGVR
						PLCDDESDSPQAITRDYTLDIHD
		1	ł			ENGKAPLLSVFGGKLTTYRKLA
1		l	1			EHALEKLTPYYQGIGPAWTKES
		l				VLPGGAIEGDRDDYAARLRRR
		l				YPFLTESLARHYARTYGSNQRA
l	i	l				ACSAMREREARTLPQKLAGTL
1		l				GMLSKVMRIPRQQEVTALRTY
		l				LQIRIGLHAAFNACEEMCQRVA
		1				LERQLDSEERALLIERSQTVIRQ
						GRDLLHAWDATWNSAQALDN
					1	ALQPDRAGQFADALEKYAADE
	1		1			SFFAQLDKYDIPVVVIGKVEGQ
	1		1	1		YAHVYSVDTDNFGDSIALTDAL
	1		1			IESGHQNIACLHAPLDVHVSVD
				1		RVNGYKQSLAAHNIAVRDEWI
	1	1	1			VDGGYTHETALKAARQLLSQS
	1	1	1			PLPEAVFATDSLKLMSIYRAAA
	1	1	1			EKNI\AIPQQLAVRILFGLHL*IV
1	1	1	1			LSTRAGFGNLAHY

SEQ ID	lego in vo	Date:	SEQ ID NO:	INueleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
110.	sequence	11100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26697	57065	A	26849	136	3261	PMSPTIYDIARVAGVSKSTVSR
20077	37003	^	20047	130	520.	VLNKQTNISPEAREKVLRAIEEL
						QYQPNKLARALTSSGFDAIMVI
						STRSTKTTAGNPFLLEVAQAFP
İ		l				AKAE*KGFQVLVRTSHNPAEDL
						QKCESKIKQKMIKGIIMLSSPAD
						ESFFAQLDKYDIPVVVIGKVEG
	1					OYAHVYSVDTDNFGDSIALTD
						ALIESGHQNIACLHAPLDVHVS
				ŀ		VDRVNGYKQSLGAHNIAVRDE
i						WIVDGGYTHETALKAARQLLS
	ĺ					OSVSLSVAVSWSAC
26698	57066	<del> </del>	26850	73	174	QSVSLSVAVSWSAC
26699	57067	A	26851	252	575	PGFPRGPPPPPGFAPFHVSIWDT
20055	37007	^	20031	232	1575	DLSDPAARAGLGVRWTPDPPR
		ı				RAARSPVLPRGLSAGQRPAARL
	1					LGGMEEGRFRQVAVFSES*SAV
	1					CPPPSPPPLSPLAPWTETA
26700	57068	A	26852	1	462	AOSVNSQTFSELRATQTFYKTT
20700	37000	<u>۱</u> ^	20032	1'	402	SHNSPGVFHTSTKR\FIDGNPPGI
	1					FSAITA*RLMMP*RSSIFSASASI
		l				LSVSFSGSTCNNDQRPARFGVL
1		1				*DTRGETGCA*TGRPRRAR*LR
		1				RVEVRAV*LLRVRARNGAQMA
		1				LVKTPCQTSAHNAPCRGRE
26701	57069	A	26853	692	918	LVKITEQISAIINAFERGRE
26702	57070	A	26854	1	2427	
26703	57071	A	26855	1347	1978	LPHCVANHGCALR*OKWVHD
20,03		ľ.,	20000	1.5.7		KEQTTQTLKMVAENGRWVIDD
1	1	1				IVSNHGSVLQAVNSENEKTLAA
i		1		l		LASLQKEQPEAFVAELFEHIAD
ł	l	1		1		YSWPWTWVVSDSYRQAVNAF
	1	1		i		YKTTFKTANNPDEDMOIEROFI
l		1				YDNPICFGEESLFSRVDEIRVLE
	1	1				KTADSARIHVRFTLTNGNNEEQ
		1		l		ELVLQRREGKWEIADFIRPNSG
	1	1				SLLKQIEAKTAARLKQ
26704	57072	A	26856	1	733	LSEVDVDVRQSIHSAHAKTLDT
I-0.07	[ · · · ·	1.	1	ľ	I	QGLRNEFLVEKVFVADEYTMV
	1	1		ŀ		YSHIDRIIVGGIMPITKTVSVGG
	1	1		1	1	EVGKQLGVSYFLTSNRRTINKY
		İ				LVPDVLETCOSSMGLTELAPGN
	į .	1	l	1	1	*WNTMPCHTHERRMEVYFYFN
	I	1			1	MDDDACVFHMMGOPOETRHI
		1			1	VMHNEQAVISPSWSIHSGVGTK
		İ				AYTFIWGMVGENQVFDDMDH
		1	1		1	VAVKDLRANHHQRFIISQRSDI
		1			1	HLTTQWIKRAAQTIHPPVSIIQQ
					1	IVAFFE
26705	57073	A	26857	2	255	ITIMIE
26706	57074	A	26858	1	597	
20700	15/0/4	1^	1~2020	1	1277	

NO:	SEOID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	North and tour disconfine	[A       X
26707   37075   A   26859   2   640   EARGRQPQLIHILPHPPRA: LALQPLGRSRRCPPPPGA A PRPPDMGDLPGLYRLSIALR DOPPYRYVDGRGQNRT TGSSYKVEVKIKPSTLQVE GGVLGPLELKSKEPDGR TGTYDTEGVTPTK SGERK TMPFTDIGTETTWQVKF HKRDHCQWGSPSVIEFVE ETRSLMWYNKESFL							
26707   57075   A   26859   2   640   EARGROPQLIHLPHPPRA:   LALQPLGRSRRCPPPGAA PRPDMGDLPGLVRLSIALR DGPVFYKYDQGRGQNRT TGSSYKUPVKINFSTLQVE GGVLGPLELKSKEPDGDR TGTYDTEGVTPTKSGERK TMPFTDIGTFETTWQVKF HKRDHCQWGSPFSVIEVE ETRSLMWVNRESFIL   26708   57076   A   26860   218   426   TOPRVWSQAQ/RALQPDT PPQTPKSDTDQMLSVKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			, ou				deletion, \=possible nucleotide insertion)
LALQPLGRSRRCPPPPGAA   PRPPMGDLPGLVRLSIALR   DCPVPYKVDQRFGQNRT   TGSSYKVEVKIKPSTLQVE   GGVLQPLELKSKEPDGDR   TGTYDTEGVITPTKSGERG   TGTYDTEGVITPTKSGERG   TGTYDTEGVITPTKSGERG   TGTYDTEGVITPTKSGERG   TGTYDTGTYGALQPDT   TPQTFKSDTDQMLSVKKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK							,
LALQPLGRSRRCPPPPGAA   PRPPMGDLPGLVRLSIALR   DCPVPYKVDQRFGQNRT   TGSSYKVEVKIKPSTLQVE   GGVLQPLELKSKEPDGDR   TGTYDTEGVITPTKSGERG   TGTYDTEGVITPTKSGERG   TGTYDTEGVITPTKSGERG   TGTYDTEGVITPTKSGERG   TGTYDTGTYGALQPDT   TPQTFKSDTDQMLSVKKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK							
PRPDMGDLPGLVRLSIALR   DGPVFYKVDGQRFGQNRT   TGSSYKVEVKIKPSTLQVE   GGVLGPLELKSKEPDGDR   TGTYDYDEGVIPPINSGERK   TMPFTDIGTFETVWQVKF   HKRDHCQWGSPFSVIEYEE   ETRSLMWVNKESFL   TGPRVWSQAQ;RALQPDTI   PPQPRSDTDQMLSVKKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	26707	57075	Α	26859	2	640	EARGRQPQLHHLPHPPRASSPP
DOPMYRY NDGQREGONER   TGSSYKVEVENDERSLQVE   GGVLGPLELKSKEPDGDR   TGTYDTEGVTPTKSGERK   TMPFTDIGTETTWQVKF   HRRDHCQWGSPSVIEVE   ETRSLMWVNKESFI   ETRSLMWVNKESFI   TQPRVWSQAQ;RALQPDTI   PPQTPKSDTDQMLSVKKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			l				LALQPLGRSRRCPPPPGAAAPD
TGSSYKVEVKIRPSTLQVE	i I		l				PRPDMGDLPGLVRLSIALRIQPN
GGVLCPLELKSKEPDODR   TGTYDTEGVYTPTK SGERK   TMPFTDIGTFETTWQVKF   HKRDHCQWGSPFSVIEPE   ETRSLMWVNKESFI.							DGPVFYKVDGQRFGQNRTIKLL
TGTYDTEGUTPTKSGERK			1				TGSSYKVEVKIKPSTLQVENISI
TMPFTDIGTFETVWQVKF  HKRDHCQWGSPFSVIEYEE ETRSLMWVNKESFL   TOPPRVSDTQMLSVKKK   FRESHMWVNKESFL   TOPPRVSDTQMLSVKKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			l			l	GGVLGPLELKSKEPDGDRAVY
HKRDHCQWGSPFSVIEYE   ETRSLMWVNKESFL			1				TGTYDTEGV\TPTKSGER\QPIQI
ETRSLMWYNKESPL			l l				TMPFTDIGTFETVWQVKFYNY
26708   \$7076			1		i		HKRDHCOWGSPFSVIEYECKPN
PPQTPKSDTDQMLSVKKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			l				ETRSLMWVNKESFL
	26708	57076	A	26860	218	426	TOPRVWSQAO/RALOPDTELPO
			1				PPOTPKSDTDOMLSVKKKKKR
KKKKKKKKKKKYPQT			1				KKKKKKKKKKKKKKKKK
26700   57077   A   26861   I   423			1				
26710   57078   B   26862   I   252	26709	57077	A	26861	1	423	
26711   57079   A   26863   1   171							
26712   \$7080   A   26864   S   254							
26713   37081   A   26865   16   220   ILDTSPMRWTQKNFSMLL   QCCKTLSQNKNKDRIKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			-			254	
QQCKTLSQNKNRDRRIKK   KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK							ILDTSPMRWTQKNFSMILAQPE
	20.15	2,001	ľ.		1		OOCKTLSONKNKDRRIKKKEE
KKKKK * EEKKKKKKKKKKKK	1		1				
EEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			l				
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK			l				
C			i				KKKKKKKKKKKKKKKKK
26714   \$7082   A   26866   32   286							
26715 37083 A 26867 I 847 EVKDLYDKTFKSLKERIK RWKDLPCSWIGRINIVKM KAIYRFNAPIKIPTOFFNEI ICKFIWNNKFRAIATILK TSGGITMPDLKLYVRAIVI WYWYRDRQVDQWNRIEL NPHTYGHLIFDKGAKTIQU DSIFNNWCWFINWLLSCR DPYLSPCTKVKSKWIKELL ETLKLIEEKVGKSLEDMG FLNRTAMACSKKKEKKEE EEEKEKEEKEKEEKEKEEE KKKKKKKKKK	26714	57082	A	26866	32	286	
RWKDLPCSWIGRINIVKM KAIYRFNAPIRIEITOFINE  RAIYRFNAPIRIEITOFINE  GERIWINNKERPIAKTILK TSGGITMPDLKLYYRAIVII WYWYRDRQVDQWNRIEI NPHTYGHLIFDKGAKTIQU DSIFNNWCWHNWLLSCR DPYLSPCTKVKSKWIKELI ETLKLIEEKVGKSLEDMG FLNRTAMACSKKKEKKE EEEKEKEKEEKEKEEKEKEE KKKKKKKKKK							EVKDI VDKTEKSI KKEIKEDI B
KAINRENAIPIKIPTOFFNEI ICKFIWNNKRPIAKTLIK TSGGITMPDIKLYVRAIVII WYWYRDRQVDQWNRIEL NPHTYGHLIFDKGAKTIQW DSIFNNWCWHNWLISCRF DPYLSPCTKVKSKWIKELL ETIKLIEEKVOKSLEDMG FI.NRTAMACSKKEKKEE EEKEKEKEKEKEKEKEKEKEE KKKKKKKKK	20/15	37003	l^	20007	ľ	047	
ICKFIWNNKEPRIATILLE   TSGGITMPDLKLYYRAIVI   WYWYRDRQVDQWNRIEE   NPHTYGHLIFDKGAKTIQU   DSIFINWCWPHIWLLSCRE   DPYLSPCTKVKSKWIKELLE   ETLKLIEEKVGKSLEDMGT   FLINRTAMACSKKKEKKE   EEEKEKEKEKEEKEKEEEE   KKKKKKKKKK							
TSGGITMPDLKLYYRAIVII WWWYRROQUOWNITE NPHTYGHLIEDKGAKTIQU DSISINNWCWHNWLLSCR DPYLSPCTKVKSKWIKELI ETILKLIEEKVGKSLEDMGI FI.NRTAMACSKKKEKKEE EEEKEKEKEEEE KEKEEEI KKKKKKKKKK							
WYWYRRQVDQWNRIEL NPHTYGHLIFDKGAKTIQU DSIFNNWCWHNWLLSCRE DPYLSPCTRVKSKWIKELL ETILKLIEERVGKSLEDMGI FLNRTAMACSKKKEKKEKE EEEREKEKEEKEEKEEKEEEEE KKKKKKKK			1				
NPHTYGHLIFDKĞAKTIQU DSIFNNWCWHNWLLSCR DPYLSPCTKVKSKWIKELI ETLKLIEEKVĞKSLEDMĞI FILNKTAMACSKKKEKKE EEEKEKEKEKEKEKEKEE KKKKKKKKKKK			1				
DSIFNNWCWINWLLSCER DPYLSPCTKVKSKWIRELI ETLKLIEEKVGKSLEDMGT FLNRTAMACSKKEKKEE EEEKEEKEEKEEKEEKEEEE KKKKKKKKKK			l				
DPYLSPCTKVRSKWIKELL ETLKLIEEKVGKSLEDMG FILNRTAMACSKKEEKEE EEEKEKEKEKEEKEKEE EKKKKKKKKKKK			1				
ETLKLIEEK VĞKSLEDMĞT FLNRTAMACSKKEKKEE EEEKEKEKEEEE EKE KEEEL KKKKKKKKKK							
FINRTAMACSKKEKKEE EEEKEKEEKEEEEEE KKKKKKKKKKKKKK			l				
EEEKEKEKEKEKEKEKEKEKEEI KKKKKKKKKKKKKKK							
26716 S7084 A 26868 I 376 MIMINDPQWINSSIFISTHLØ  RRQAEVGAQEPSRRIVG GAQVDEGEEEEEEEEEEEKE KKEKKKKKKKKKKKK KKKKKKKK			1				
KKKKKKKKKKKKKKKK 26716 57084 A 26868 1 376 MI.MKDPQWNSSIFISTHLA KRRQAEVGAQEPSRRIVG GAQVDEEEEEEEEEEEE KKKEKKKKKKKKKK KKKKKKKKKK			l				
26716 57084 A 26868 I 376 MLMKDPQWNSSIFISTHLA KRRQAEVGAQEPSRRIVIG GAQVDEEEEEEEEEEEEEEKE KKKEKKKKKKKKKKKKKKKKK			1				
KRRQAEYGAQEPSRRIVG( GAQVDEEEEEEEEEEEEEEE KKKEKKKKKKKKKKK KKKKKKKK			<b>!</b> —		ļ		
GAQVDEEEEEEEEEEEEEKEE KKKEKKKKKKKKKKKKKK KKKKKK	26716	5/084	l <sup>A</sup>	26868	Į¹	3/6	
KKKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK						1	
KKKKKKKKKKKKK LSLPMIRPILPHPRWASSP: AKP						1	
LSLPMIRPRLPHPR WASSPS AKP			1			1	KKKEKKRKKKKKKKKKK
АКР						1	KKKKKKKKKKKKKKKLL
						1	LSLPMIRPRLPHPRWASSPSSMV
26717 57085 A 26860 I 2031			L			L	AKP
20/1/  5/000  A  20007  1  2001	26717	57085	Α	26869	I	2031	
26718 57086 A 26870 1 957	26718	57086	Α	26870	1	957	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26719	57087	IA	26871	171	495	SOLLDMRKPFOKPGLROLKTLP
		1		\		QYLNTR/CILDYLDNISPQQIRK
		]				LFYVLSTLAFSKQNEASSHIOD
		1				DMHLVIRKQLSSTVFKYKLIGII
		1			1	GAVTMAGIMAADRSESPSL
26720	57088	Α	26872	1	3114	
26721	57089	Α	26873	173	397	
26722	57090	Α	26875	823	1194	
26723	57091	A	26876	I	1263	MESNAVQLTRMEYAMKSLSLL
		1				YPKSLSRHVSVRTSVVTQQLLS
						EPSPKAPRARPCRVSTADRSVR
	1	1				KGIMAYSLEDLLLKVRDTLML
	1	1				ADKPFFLVLEEDGTTVETEEYF
		l			i	QALAGDTVFMVLQKGQKWQP
	1					PSEQGT*WRRTQRKDSPVSRPC
ŀ		1			-	STHGLQEIQL
26724	57092	Α	26877	128	317	
26725	57093	Α	26878	431	574	
26726	57094	Α	26879	112	482	EGPEAKPKRSNCAPEKRSSPIPD
l	1	l				WEPAFSEDGRARTVARLQHPPL
	i	l				GGPTHRYHHFLRRHDPPLRVHP
ĺ		l				AAERQEAHPGTSI*QSSPNSKQS
	1	l				PQGKWKITFPNSLSLTRKYYFQ
						QPRGWDFFKKT
26727	57095	Α	26880	3	179	
26728	57096	Α	26881	977	1127	
26729	57097	Α	26882	121	708	
26730	57098	A	26883	38	828	GSRLRRLQAAAARPALPLPLPP
		l				WEWKHLPHVPEAKWWLTTAR
	i i	l				HSAAYRADPLRVSSRDKLTEM
l		l				AASSQGNFEGNFESLDLAEFAK
	i i	l				KQPWWRKLFGQESGPSAEKYS
	į.	l				VATQLFIGGVTGWCTGFIFQKV
ľ	l l	l				GKLAATACGEVDF/LLLQLANH
	1	l				TWVHQSLTGNEWEKDIEESPKS
ŀ		l				SLKIRKSQSDYLLRSGAKAAGR
		l				WCHFVKKNVLVTWGIFPEAFC
		1	1	I		LAWHPKEDDLHVPLFPGFFPSQ
				1		QPFTLHHRDIESLLLFFPWPSFP
		_				GHWEN
26731	57099	Α	26884	1	642	
26732	57100	Α	26885	1183	1349	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleoside	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
		<u> </u>				
26733	57101	Α	26886	l I	1371	MSFLIDSSIMITSQILFFGFGWLF
						FMRQLFKDYEIRQYVVQVIFSV
				1		TFAFSCTMFELIIFEILGVLNSSS
l						RYFHWKMNLCVILLIL/VFPMV
						PFLQLAYFIVSNIRLL\HKQRLLF
						SCLLWLTFMYFFWKLGDPFPIL
1						SPKHGILSIEQLISRVGVIGVTL
		1				MALLSGFGAVNCPYTYMSYFL
				İ		RNVTDTDILALERRLLQTMDMI
				ł		ISKKKRMAMARRTMFQKGEVH
						NKPSGFWGMIKSVTTSASGSEN
						LTLIQOEVDALEELSROLFLETA
l						DLYATKERIEYSKTFKGKYFNF
						LGYFFSIYCVWKIFMATINIVFD
						RVGKTDPVTRGIEITVNYLGIOF
1						DVKFWSOHISFILVGIIIVTSIRG
						LLITLTKFFYAISSSKSSNVIVLL
				1		LAOIMGMYFVSSVLLIRMSMPL
						EYRTIITEVLGELQFNFYHRWF
			i			DVIFLVSALSSILFLYLAHKOAP
26734	57102	A	26887	1738	2140	D . II D . O . I D . D . D . I D . I I I I I Q . I
26735	57103	A	26888	81	733	
26736	57104	A	26889	1061	1154	
26737	57105	A	26890	1	3207	
26738	57106	Α	26891	113	367	
26739	57107	Α	26892	2	1391	
26740	57108	Α	26893	154	647	
26741	57109	Α	26894	40	747	
26742	57110	Α	26895	1	3186	
26743	57111	Α	26896	271	491	
26744	57112	A	26897	304	1836	
26745	57113	Α	26898	1	2343	
26746	57114	A	26899	1	765	
26747	57115	Α	26900	318	473	
26748	57116	A	26901	2	426	
26749	57117	Α	26902	1	433	
26750	57118	A	26903	2	1004	
26751	57119	A	26904	125	199	
26752	57120	Α	26905	3	156	
26753	57121	Α	26906	2	397	VDGMGWSQDLFRALGRSLSRE
					1	GKEHVGTDQFGNKYY\*SRSTK
			1			TGEVRWRRGQRLRGQ*LRGQT
						IREKRIVEAANKKEVDYEAGDI
						PTEWEA WIKRTRKTPPFMEEIL
						KNEKHREEIKIKSQDFYEKEKL
26754	57122	Α	26907	1	1350	
26755	57123	Α	26908	I	582	

SEO ID	Tero in No.	Tate:	SEO ID NO:	Maratandida	Nucleotide location of last	A mine and managed Value
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for pentide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequenee	1	
26756	57124	<u> </u>	26909	2	687	G + DOW BOTTONOPOST + KINWS
26/36	3/124	Α	26909	2	08/	GARQVLPGESPCFSSS\AKIVKP
	1			1		NGEKP\DEFESG/LSPQALLEL\E
				l		MNSD\LKA\QLREPELLRPA*GK
		ł				LKVGGCSENLSI/ILLFPVPSN*K
		1				SFPENPQVRA*YRELEKK\FQW
						GSHVGLYRPQRRILP*AQLRKK
	l	1				PVQKNKQKASPRARTLTAVHD
	1	ı				A\ILEDLGLPQAKIVGARESRVK
		1				L\DG\$RL\IKVHLDK\AQQNNVE
		1				HKV\ETFSGVYK\KLTGKDVNF
		L		1-1		EFPRSFNCKQK
26757	57125	С	26910	164	208	
26758	57126	Α	26911	2288	2625	GSEGHLPITKRWSSLWEWRKG
		ı	1			LSEVGSCKRNLVRCLRTAI/LM
	1	1				GGEAGVIHCKGHQKASDPIALG
		1				NAYADKVARQAASSPTSVPHG
		1				QFFSFTLVTPTYSPAETSTYQSL
		_				PTQGK
26759	57127	A	26912	1	400	
26760	57128	A	26913 26914	3	277 630	OCHANICA A PRANCIA CA PERI
26761	57129	Α	26914	1	630	CEIKNRKAAEKVNKTKGKFFEI
		1				NTYPGPIKTGEPSGQTQKWLDI
		1				VRNTLVEEDTSSWSWRAHQPK
		1				STLTGTGRPSTNGTMSSLARTV
		ı				REEPGNQPNYRGKPSPFWFPHL
		1				VRAASTQPVITRLLQHGRLKPI
	Į.	1				NSPYNFPILPVLKPDKPYKLVQ
	]	1				DLHLINQIVLPIHPVVPNPYTLL
	i	1				SSIPASTTHYSVLDLKHAFFTIPL
		ㄴ				HP*FQPLFTF
26762 26763	57130	A	26915	11	384 1319	CO DOMES A DUMENT A CODE WITH TAKE
26/63	3/131	Α	26916	1113		GRDPVSAFYIWLASFPNTIY*IG
		1		i		NPFPIACFSQVCQRSDSCRYAA
		<u> </u>		<u> </u>		LFLRALFCSIDLYLCFGTSTMLF
26764 26765	57132 57133	A	26917 26918	99	2144 470	
26766	57134	A	26918	636	1220	GPGFQAQNCAAIWADTKLAAG
20/00	3/134	I <sup>A</sup>	20919	030		
						IFSHTPVAPGTPVRQNHLLPWD
						APAWSGEECLPLLRLVYVVFPS
		ı				QCKQSCQEV*TGQSPPQLGKAF
						VARLPL*IPSLWAGHLFLEHPV
			1			YCCGCVTAGRQGSWKGQRRH
						GHPFPLPLLLLQMVCCSISYQY
						DYPESSFLLLFLSSLCSAGKSTG
						SHAILLGSAFVLPHLVALRS
26767	57135	Α	26920	10	161	RLRMVRDIKVLLNTRSLRNCLG
		1	1	1		DLTNKGRSIIGPPL*ELSKASVM
				1		VPVGF
26768	57136	A	26921	1	855	
26769	57137	A	26922	5	1442	
26770	57138	A	26923	1061	2332	

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26771	57139	A	26924	804	1100	SPKGGPPDPSHGTKFHSRPCEET TKQAFCEQHGCLFHLGTLGALL G*QRWLHQLSRPSLGCNESKSL FQ*PPLP*E*KEIQCKVPPNLGL GVRSGKGF
26772	57140	Α	26925	3	1186	
26773	57141	A	26926	126	363	SRSKDQGLDPSGTWCKRAFSPG PWPIIPVAAGGGGHSGGGKSET PAHLQKGLHKVKNC*PSTYSVC QTPDAEHPVSNK
26774	57142	Α	26927	1	1125	
26775	57143	Α	26928	401	446	· · · -
26776	57144	Α	26929	332	499	
26777	57145	Α	26930	74	200	
26778	57146	Α	26931	300	416	
26779	57147	Α	26932	324	430	
26780	57148	A	26933	60	381	
26781	57149	Α	26934	2344	2453	
26782	57150	Α	26935	131	274 444	
26783	57151	А	26936			GGGENFSYPWYLLVGCGWFSS SPIVPDVPPFSLLLPAQKKKPAP PK\PEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK
26784	57152	A	26937	540	811	
26785	57153	A	26938	69	375	QHLRPAAVAAATMPKRKAEGD AKGDKAKVKDEPQRRSARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKADAGKEGNNPAEN GDAKTDQAQKAEGAGDAK
26786	57154	Α	26939	9294	9486	SLLYQPRCMAFRIKASS*RGMP GGSASAARKPTG/SPGREGAGR RGQWGPRNCCAGRLPGGESTV
26787	57155	Α	26940	248	613	
26788	57156	С	26941	94	234	
26789	57157	Α	26942	2157	2408	
26790	57158	Α	26943	547	815	
26791	57159	Α	26944	254	467	VFLISVYNGLAISLYLGIHIRQK PVMPRNPLNCFGVLG*G*AGIG *IRSSLRTLVPLDNFSPKYLTFC EQS
26792	57160	A	26945	238	391	
26793	57161	Α	26946	232	1659	
26794	57162	Α	26947	1	951	
26795	57163	Α	26948	1	2046	
26796	57164	A	26949	3	97	SVR/SKFYVREPPNAKPDWLKV GFTLSVEL*M
26797	57165	Α	26950	l	828	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26798	57166	A	26951	224	475	AGPRKMAPSALLRPLSRLLAPA R\LPSGPSVR/STKFYVREPPNAK P\DWLKVGFT\LGTT\VFLWIY\L IKQH\NEDILEYKRRNGLE
26799	57167	Α	26952	I	411	
26800	57168	Α	26953	442	2490	
26801	57169	Α	26954	3	1592	
26802	57170	Α	26955	9	308	
26803	57171	Α	26956	153	227	
26804	57172	Α	26957	1	411	
26805	57173	A	26958	517	825	
26806	57174	Α	26959	6	646	
26807	57175	Α	26960	1	275	
26808	57176	Α	26961	3	272	
26809	57177	Α	26962	1	1002	
26810	57178	Α	26963	1	1791	
26811	57179	Α	26964	2	160	HMTTSLLAQSGFQKTSALNKIT TKGSH*VQFTSLLPPPERVLVS MAERPWGG
26812	57180	Α	26965	1	892	
26813	57181	A	26966	1	549	
26814	57182	A	26967	234	387	SCLEVCDEQGPEK\TRQRALRG VSSVTEDTLNICRLCWQPLPEPL ELWPKAL
26815	57183	Α	26968	269	501	RARSEGAGLWSVVAPSAVSVFF VSDPRCAPFHRSPSCCSP/RRPC LSLSA*SRPRASGVGACLLWQP LPEPLELWPKAV
26816	57184	Α	26969	210	296	
26817	57185	A	26970	71	283	LRLGDLPSEINPLSSCSLLREKD PPTTSGPQT\TSPRNISPISNPDST GNRTVQLTWQPLPEPLELWPK AL
26818	57186	A	26971	1112	1180	
26819	57187	A	26972	71	284	LILGDLPSEIKPLPSCSLLREKEP PTTSGPQT\TSPRNISPISNPDSTG NRTVQLTWQPLPEPLELWPKA
26820	57188	В	26973	1	663	
26821	57189	A	26974		502	MLLTQSLFGGLFTRTHMKFGA VTQIRGPPLGDKSPVLLLFALER QRRHVLSMDPKLRCWSRTGKA AFPWCLIIAEMPDYSPTFQRCQ TTQGRLPWSFTLSSKSRFSGEG ARACYKCQKSDHQAKECPQPG IPPKPCPICAGP!TGNRTVQLTW QPLPEPLELWPKAL
26822	57190	A	26975	233	496	
26823	57191	A	26976	226	543	
26824	57192	A	26977	1478	1744	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
		_				
26825	57193	Α	26978	3	450	VRPRRDACLGPSPLAASPAFLG
						KGQVPQPLISLCPDPLFPHPNLIS
						LRPNPLCPHPDLVSLCPDPFPAF
1		1				LEAHKNFQTTEPQQPGVPPEPP
		1				PTGACYTCRKSGHWAKECPQP
		1				GIPPNHVPSVWDPTENLTVQLT
26026	57104	١.	0.0000	416	724	WQPLPEPLELWPKAL
26826	57194	A	26979 26980	615	1968	
26827	57195	A	26980	227	556	
26828	57196	A		400	548	
26829	57197	A	26982 26983	1	1968	
26830 26831	57198 57199	A	26984	65	741	
26832	57200	A	26984	1	658	
26833	5720I	A	26986	1	666	
26834	57202	A	26987	67	608	NPGKGGCFVL/VLDGLLRDRKA
26834	5/202		26987	67	608	NYGNGGY-IV-VUGGETIFOGWHPQDRPLPAHAI LVAG\UDRPTPPQK*TA\AMGKK KDRPKRSKIKSFCGKCYNY\NH\ LMPHKGTLWDIPLGQNLFVQL RDVFIRDPGSLNKKA\RRGGPRF KFE/REYETGGETKWVLPRKL AGFKNAFGFDSLKIIKKKKKK KKTTKKGRP
26835	57203	Α	26988	1	352	
26836	57204	Α	26989	1	1419	
26837	57205	Α	26990	2	878	
26838	57206	В	26991	75	293 I	
26839	57207	Α	26992	229	724	<b>IIFIVYSSQLTYVKISDSFQTFKF</b>
	i	1		1		CLDFCLFFSEMS\FLSLNISSCS*
		1		1		YSAKVNSCGKFGLTKGSFSAPL
		ł		į.		TPLFFLCFGSELVEGV*ELLAVG
		1				GLHLARIFLCLSISSLC*FTHSCC
		ļ		1		FTRVTPINLASNNSCLLGFRLQS
		1		ł		SSIAPSLGLLDGGVCFIRDLAAA
26840	57208	Α	26993	737	1048	KKYNIQLEKPYFKHLYKNKLL
	1	1				KLSN*NMTSVQQFTIELEGNLS
	1	1			i	LSCIELVC/ILVTHCHLF/CMNK
	1	1		1		AW*QKKNT/WLSILTC*KHWQ
	1				1	YYNLVNSTDFNTSSSFLSKV
26841	57209	Α	26994	I	1209	
26842	57210	Α	26995	2	1683	
26843	572 I I	Α	26996	I	1386	
26844	57212	Α	26997	1	47I	

sible nucleotide nucleotide inscrition) //LRFRRASRVQK //LRFRRASRVQK GYVYGHKGKFG GKLRYANNFIN AYYHKSVMEEL EDDAL WPPDI DEHISFITTSKIG FEGLRVEYYLVQ LHFKIKPI //LHFKIKPI
//LRFRRASRVQK XYYVGHKGKFQ GKLRYANNHW EAYVHKSVMEEL EDDAL WPPPDR DEHISTITISKIG PEGLRVFYYLVQ LHFKIKPI
RYYVGHKGKFG GKLRYANNHN AYYHKSYMEEL EDDALWPPPDR IDEHISFTTSKIG PEGLRYFYYLVQ LLHFKIKPI
RYYVGHKGKFG GKLRYANNHN AYYHKSYMEEL EDDALWPPPDR IDEHISFTTSKIG PEGLRYFYYLVQ LLHFKIKPI
RYYVGHKGKFG GKLRYANNHN AYYHKSYMEEL EDDALWPPPDR IDEHISFTTSKIG PEGLRYFYYLVQ LLHFKIKPI
GKLRYANNH\N AYVHSVMEEL EDDALWPPPDR EDDALWPPPDR EDEHISFTI\SKIG PEGLRVFYYLVQ ELHFKIKPI
EAYVHKSVMEEL EDDALWPPDR IDEHISFTTSKIG FEGLRVFYYLVQ ELHFKIKPI  PVLCQSRANDQE
EDDALWPPPDR DEHISFTI\SKIG PEGLRVFYYLVQ ELHFKIKPI  PVLCQSRANDQE
DEHISFTT\SKIG PEGLRVFYYLVQ ILHFKIKPI  PVLCQSRANDQE
PEGLRVFYYLVQ ELHFKIKPI PVLCQSRANDQE
PVLCQSRANDQE
PVLCQSRANDQE
MPKSKELVSSSSS
KLKRKK\OV\AS
GETS\RALSS\SKO
MFQIGKM\RYVS
LI\DIREYWMDPE
SLNP\QQWEPSL
SKKTCKISEPILI
VLFSIGFCFLNVL
NL
DSCTCAGSCKC
SKWDPLFPLPLP
RGIKAVWGCPIA
GRAGILIPGVAS
R\CCSCCPVGCAK
SDKCSCCA
KEGLLLKH*AL
LVLCITSHTDML
TQ
GATSALAPKIGP
DIAKATGDWKG
RQAQIEVVPSAS
RDRKKOKNIKH
IARQMRHRSLAR
IARQMRHRSLAR FAQSVGCNVDG
T I I

SEO ID	ISEO ID NO:	Mot	SEQ ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.01	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l '			sequence		
		<u> </u>				
26862	57230	A	27015	53	1227	QPPVHTTPASSPCDD\DIAAL\V
						VDN\G\$GMCK\AGFAGDDAPRA
1	ŀ		1			VFPSIVGRPRHQGVMVGMGQK
			l			DSYVGDEAQSKRGILTLKYPIE
						HGIVTNWDDMEKIWHHTFYNE
1	1	1		1		LRVAPEEHPVLLTEAPLDP\RAT
						REKMTQIMFETFNTPAMYVAIQ
		1				\AVLSL\YASG/RVTTGIVMDSG
						DGVTHT\VPIYEG\YALPHAILR
	,			ŀ		LDLAGRDLTDYLMKILTERGYS
				l		FTTTAEREIVRDIKEKLCYVAL
		1	l			DFEQEMATAASSSSLEKSYOLP
	ł					DGOVITIGNERFRCPEALFOPSF
		l				LGMESCGIHETTFNSIMKCDVD
						IRKDLYANTVLSGGT\NMYPGI
					i	ADRMQKEITALAPSTMKIKIIAP
		1				
						PERKYSVWIGGSILASLSTFQQ
		ļ.				MWISKQEYDESGPSIVHRKCF
26863	57231	A	27016	2	438	ADLLQVSNCVVSSCQPPAFLVL
					1	FSSSRLPAGEGRGRPGQTQRPSS
						LEGAWHSVTLERRCLVSHLINL
						REAGMYPSRPCHHLFPDQLV*T
						EGGF*RPRLGWQRCHGTPQQA
						PSQPAFRSKHPRKGMPALQQQP
						GSGLCRPLPCRCR
26864	57232	Α	27017	112	493	AHSRTPARPENRAAASAPRKPR
1		Į				RAMSSPPEGKLETKAGHPPAVK
						AGGMRIVQKHPHTGDTKEEKD
					l .	KDDQEWESPSPPKPTVFISGV\I
	-	1				ARGDKDFRPADAQVAHQKPHA
						S\MDKHPSPRTQHIQQPRK
26865	57233	Α	27018	1	1176	
26866	57234	Α	27019	3	307	
26867	57235	A	27020	86	179	SVKRRC*SLLTWIGMRLQRQHR
l _						ECLAEQVGS
26868	57236	Α	27021	1	948	
26869	57237	Α	27022	3	534	EGAHFRAAHHPRSTGSRCPGSL
						QPSRPLVANWLQSLPEMPVDFT
						GYWKMLVNENFEEYLRALDV
	1					NVALRKI/APTLLKPDKEIVQDG
	i					DHMIIRTLSTFRKLTSWNF\QVG
		İ				KEFEEDLT\GIDDRKVHDKQ*A
1	1	1			I	WDGDKL\QCVQKGEKEGRGW
1	1	1			I	TQ\WIEGDELHLEMRVEGL\VC
	1			1		KQVFKKVQ
26870	57238	Α	27026	1	2400	-
26871	57239	A	27027	294	425	
26872	57240	Α	27028	1	797	
26873	57241	Α	27029	1	173	
26874	57242	Α	27030	1	1047	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	450.40	Ļ	0.004		lioto	Intro a pure ann a lump page a la pur
26875	57243	A	27031	2	1019	PTSAPHSLSPRAVIERRSRALDW
						NASPSLSDPQGLDASLPFPSHKR
		l				SRTASPEPAEHPVMDKNE\LVH\
		ı				KAKLAE\QAERYDDMAACMKS
		i				VT\EQGAELSNEERNL\LSVAYK
		l		I		N\VVG\ARRSSW\RVVS\SIEQKT\
		l				EGA\EKKQQMAR\EYREEIETEL
		1				R\DI\CNDVLSLVGKSSLIPNAFT
		1		ı		SRRSKVF/YILENGKGDYLPFTL
						GWRVAAGWMDQERGLFDPVH
		1				NKAYPRKAFWKSAKKGNGNPT
		1				HP\IRLGL\ALNFSVFYYEILNSP
						EKACSLAKTAFDEAIAELDTLS
		1	1			EESYKDSTLIMQLLRDNFDIVG
				İ		HRDTQGRRKLEGREEGRGENL
						TGPFPTFCSWPHS
26876	57244	A	27032	177	477	
26877	57245	Α	27033	1	1290	
26878	57246	В	27034	49	1112	
26879	57247	A	27035	98	245	
26880	57248	A	27036	1	351	
26881	57249	A	27037	3	471	MAN (DAYO ON A) THE POLICE OF COMMO
26882	57250	Α	27038	I	440	MKMRVGCMLTAESLSDGGNS
						HQRTLSLFEESKESQCEARGEV
i					ł	SKAGVWLVPLEPSSDALPKITS
1						LVRPAVPWRPSSEAGLCEVRGG
					i	VLGKASKAPIKEPQLDRGMGL
1						GAQRRGSSGTEVQSGETLGASG
						SPRGLLEPRPDWVSNNGAGSLG
						FQQLPIVDKIRTIAQAVCGAKDI
						ELCPEAQVKIDRYTQQYYSC*N
						PKLPAPLFETQSGLGSKSPLGLP
		l				LAPRVSPDCTSVP/GAP/SAAGP
		_				RAPCPDPAVAPLWGLCWPFPEL
26883	57251	Α	27039	I	1113	MHQEDLRAWYLDLGLPSHQN
						AQPTAWKCQRAPSPYTHQDMA
		l				LIPSPTARWLSPEKEPKQGEVG
		1				EKSLLPDPTLPLTDPRLTGSTEQ
		1				AHAEGLAALMSALRVSHLQGR
		l				GGVVTLVDSQLGVIAVSSTQFN
		1				KGPSYRLLADVQNRLLPKYDS
		1				QKEAELRSWIKGFTGLSIRPDFQ
						KGLKDGIILCTLVNKLQPGSVP
		1		I		KIN\ASV*NWH*LENLSNFLKA
		1	1			MVSYGM/NPVDLFEANNLFESG
		l				NNMQVRVSLLALAGKAKTKGL
		1				RSGVDIRDKYSEKQNFDDTTM
		1				KASQCVIRLQITNKCASQSGMT
	1	1	1			AYGTRRHLYDPKNRILPPMDNS
						TISLOMGTNKCASOVGMTAPG
			l			TORHIYDTKLGIDKCENSSMSL

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26884	57252	Α	27040	347	1061	
26885	57253	Α	27041	212	386	LQGSWVTSGLERICGSILGTIPL
		1			l	AHEVTDTQHGRMVYQVATAG
						F*SSLGAASIGTQGL
26886	57254	Α	27042	1	1017	MHSRRERARGLRGAHHPLVDN
ļ		1				GPPQSLRAPPLLSPLKTAGAKSI
						WEPLASARRPETPERTPLQKTP
	l	1				EQVPTNFMGALHMKTSAPLSS
		1				RNGEGRRGGTSVASCPWVVGA
	l	l				VCSAERQPCTQRVREALMGGW
						RAGAQNNRAEDQVDEFTEVGF
l						RRWVIKNYDELKEHVLTQCKE
						VKNLDKSIHPEISRLHEFITTTH1
						LPVIGGKVSLLSKCQDNAEQKQ
						SQGCSQEGHEVYDPRLNSSSSS
						SSSGGGQSPGLRRCSTSAAAAA
					ŀ	ALEGAALKPMPVHAGLVGSGE
					1	GGGAGAVAGPCSRWGATTAA
					l	ASSAQPAQPVRGGSSGAQGHR
						GGRRRQAGKGGPAG*TAAAAA
						AP\GRGAEPGAAALLNLGGGSG
1						GAG\SAALKPMPVHAGLVGSG
l						EGGGAGAVAGPCSRWGATTA
1						AASSAQPAQPVRGGSSGAQGH
		L				RGGRRRQAGKGGPAGSS
26887	57255	Α	27043	644	949	
26888	57256	Α	27044	811	1886	
26889	57257	A	27045	1	410	HAHSLNSIILPTPLEIHKV*IQIY
						A*GCKRISNNCWHCHQHLLSIS
ŀ						PDLRINEGKECGPSPWIGVEAR/
						MGGELSSAVGLTSLLLYQQVPF
					Ì	HPHFQSPTFIPRESILLQHASCW
26890	57258	A	27047	1	2445	RQHHLHTGIYSSYLPGWKQEFS
26890	57259	A	27048	1	457	
26892	57260	A	27049	1	873	
26893	57261	A	27050	2549	2728	ATSRSSALITSSKYPGKF*LILI*
20075	37201	,	27030	2547	1-720	RSTLETANSISARLNNPFLRKYP
						SYFSLFMGTTRI
26894	57262	Α	27051	277	394	
26895	57263	Α	27052	2	1394	
26896	57264	Α	27053	1	1091	
26897	57265	Α	27054	1	1404	
26898	57266	Α	27055	2457	2674	ANHCYLLSELQHWSDCPVVLQ
		1				SAG*RH*DRN*DGNQY*SR/SLS
[	l	l		1		*SR*STTK*RNTPCSQVSSLSRLS
1	l	1		1		TRSAP

SEQ ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	1			sequence		
				1		1
26899	57267	A	27056	716	1455	LFPRLLSCLTTPPHCSFSICFVIC
						SRTLILKGNYTSGDNHTLR/DPH
						YVEDKGHKYLVFEANTGTENG
				1		YQGEESLFNKAYYGGGTNFFR
				1		KESQKLQQSAKKRDAELANGA
				İ		LGIIELNNDYTLKKVMKPLITSN
				i		
	ļ	1		İ		TVTDEIERANVFKMNGKWYLF
		1	l	l .		TDSRGSKMTIDGINSNDIYMLG
l	1	1				YVSNSLTGPYKPLNKTGLVLQ
	1			ŀ		MVLIPNDVTFTYS\HFAVPQAK
1						GNNVGIHQATLTN\RGFFEIKKA
				1		TFAPSFL
26900	57268	A	27057	66	197	
26901	57269	A	27058	379	905	AGNFVHITVRKMLWIRRDOOO
1				1		S/DKQDIQTAHRSYSVLKGYND
						MYYGWPCCKVNEISGQLASEP
l	ł			l		A*SLVLPAAG*QAPASGSPWLS
1				i		GGPQQVEDAGAGYGFAPGQPP
				Ì		PPPRTOPRSACSRRAAGSOFHG
						RPLLPROAAKARAPRSLGCGSL
			1			
		<u> </u>		<u> </u>		GRFSTGVRPDKCIFPPETENAA
26902	57270	A	27059	<u> </u>	1608	
26903	57271	В	27060	1	1974	
26904	57272	A	27061	2712	3216	KTGRGPTDKFG\ANDPILKDQT\
1				l		QEWS\GSAPFTS\DGKFRLFYTD
ŀ				l		YSGKHYGKQSLTTAQNVQQFI
	l					DEGNYTSGDNHTLRDPHYVED
	1		l			KGHKYLVFEANTGTENGYQGE
ŀ	1			l		ESLFNKAYYGGGTPFFRKESQK
	1			1		LQQSAKKRDAELANGALGIIEL
	1					NNDYTLKKVMKPLITSNT
26905	57273	Α	27062	l	3066	
26906	57274	Α	27063	1	972	
26907	57275	A	27064	14	273	
26908	57276	Α	27065	42	302	
26909	57277	Α	27066	1	487	MGLSLKGPESAPIPKTPQFNKIL
				1		FKPIAVYNRFTQFRLSETKEITN
				1		PYAMRLYESLCOYORYOLPOS
				ł		YQR\SLTSAAASCRSVLMRSTA
		1		l		ELOCASHTLRKRKAARRLISLS
		1				EMPRKQGDYRTRIWKFEDGLS
						NVLVIQLNKLIICVMCLVRDCD
		1		l		
26910	57278	В	27067	1	1035	VLKTYFHR
26910	57279	A	27068	132	230	CHYFACMWSGCEVYS*SAPG**
26911	31219	l <sup>A</sup>	2/068	132	1230	
	emano.	١	00000	ļ	2001	C*EDLSGMVR
26912	57280	Α	27069	1	2784	
26913	57281	Α	27070	855	980	LSCSGWRAG**ADGCIIQIG*RL
		L				SPNKCL*TWSALCKPIAE
26914	57282	В	27071	85	863	
26915	57283	A	27072	345	500	I

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26916	57284	В	27073	1	1116	
26917	57285	Α	27074	1	1173	
26918	57286	A	27075	1	999	
26919	57287	A	27076	771	908	
26920 57288	57288	A	27077	104	547	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPVDSKGP
					PWLFKFLKNGLNFLLHSVGTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDADDVLSTEVKRVITS SASNITPAFFCS	
26921	57289	A	27078	34	1353	
26922	57290	A	27079	213	338	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26923	57291	A	27080		1246	MVKVGTSYVPINVSFSPKVGPG LPGINRDTRIYLFCEVIFRHERD RESADLGSGOGNGPRWIGED VAAAAADGVTFSVPVTPHTER HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRNRFTQFRLSETKEITIVPYAM RLYESLCYGKPEDGSCVSLKID WIIERYQLPQSYQLYYFELAIPV GYFYPGSFSTASRILLLHPRGLR ATITAVFGKOTYTIRLEPFKINV LEQITKHIEKLQCGGVVKQLSR RGNNQHISSTYDINRADYPG*A RDPHLMLRLAIETVAHDYDVIV JDSAPNLGIGTINVVCAADVLIV PTPAELEPJYSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPWMEEQNSGCRGKTS RVEVPHRDSOFKVIKLVTLRQL VTLYDPVDFQRDDA
26924	57292	В_	27081	1	1041	
26925	57293	A	27082	I	1011	
26926	57294	Α	27083	2	1007	
26927	57295	Α	27084	1	738	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26928	57296	A	27085		1439	MAETAVINIKKRKNSPRIVOSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS ESFPWFIKRAHSPRSGLYSVHIN PYLIPFFIGLONRETOFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPGSYGRV WTPGINCPEPCGYWTPGINCP GAWGHIGPHGSAENTGPLIFIG QLSPRKQNRSLQNIGVTPSLR QLSPRKQNRSLQNIGVTPSLR VPWPKASNVQPIEDGNYTSG DNITLRDPHYVEDKGHKYLVF EANTGTENGYQGESLFNKAY VGGGTNFFRKSQKLQOSAKK RDAELANGALGIELNNDYTLK KVMKPLITSNTVTDEIERANVF KMMGKWYLFTDSRGSKMTIDV PQAKSNNYGITSYMTNRSFED KKATFAPGFENNIKAKTS
26929	57297	Α	27086	345	563	
26930	57298	A	27087	1	1188	
26931	57299	В	27088	1	1186	
26932	57300	В	27089	1	1090	
26933	57301	A	27090	183	410	
26934	57302	Α	27091	1	1557	
26935	57303	A	27092	888	1165	CTRERRIKARGPPAGKRWLLLS GSSGRKHHL*QDPRPGSQTAGD LPEPAR\PIIVIGEGSQMGLDECQ FQFRNGRWNCSALGERTVFGK ELKV
26936	57304	В	27093	I	1027	-
26937	57305	В	27094	1	1117	
26938	57306	В_	27095	1	1377	
26939	57307	В	27096	1	1014	
26940	57308	Α	27097	1040	1285	
26941	57309	A	27098	901	2277	
26942	57310	Α	27099	1	1122	
26943	57311	Α	27100	1	1137	
26944	57312	Α	27101	ı	1881	
26945	57313	В	27102	1	1211	
26946	57314	A	27103	294	506	NRRPGSAATVWAAAAEPSERG NNPALENR*SSGFSWGFFSGYQ RCRESRATTAPGYGNSRTG*AT CWLYN
26947	57315	В	27104	1	1073	
26948	57316	Α	27105	1	1809	

SEQ ID NO:	SEQ ID NO:		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide
NO:	of peptide sequence	nec	09/540,217	codon for peptide	of peptide sequence	deletion, = possible nucleotide
1	sequence		09/240,217	sequence	or pepade sequence	deceasi, i-possible increditae insertion)
	ļ	1				
26949	57317	Α	27106	1688	2187	SYFIMVKVGTSYVPINVSFSPKV
						GPGLPGINRDTRIYLFCEVIFRH
		ŀ				RYLFAISSWSGVTVA\RKDRES
	1	l				ADLGSDGQNGQDLDWGGG\AA
	l	l				AAADGVTFSVPVTPHTFRHSYA
	l	!				MHMLYAGIPLKVLQSLMGHKS
	1	i				INSTEVYTKVFALDVAARHRV
						QFAMPESDAVAMLSF
26950	57318	Α	27107	782	1402	LFPRLLSCLTTPPHCSFSICFVIC
	i					SRTLILKGSSLIKLLFYKIPSMLV
	1					SSVLLLEVKSHIVGPGLPGINRD
	1					TRIYLFCEVIFRHRYLFAISSWS
				ĺ		GVTVA\RKDRESADLGSDGQN
1	ŀ	1				GQDLDWGGG\AAAAADGVTFS
		1		l		VPVTPHTFRHSYAMHMLYAGI
		1				PLKVLQSLMGHKSISSTEVYTK
	1					VFALDVAARHRVQFAMPESDA
						VAMLKQLS
26951	57319	A	27108	197	421	LAMPGAGFSSSLRMASIFSIHSV
				l		GTRDLSRVSTILSPLYNTVAPG
				l		AN*CRELKLVLDADDVLSTEVI
						RVITSSA
26952	57320	В	27109	1	934	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	deletion, \≕possible nucleotide insertion)
26953	57321	A	27110	I	2047	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR
				}		LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI
		l				GVAAHKGGVYKTSVSVHLAO
		l			1	DLALKGLRVLLVEGNDPQGTA
		ı				SMYHGWVPDLHIHAEDTLLPF
		1				YLGEKDDVTYAIKPTCWPGLDI
		l				IPSCLALHRIETELMGKFDEGKL
		1			i	PTDPHLMLRLAIETVAHDYDVI
						VIDSAPNLGIGTINVVCAADVLI
						VPTPAELFDYTSALQFFDMLRD
		}				LLKTVDLKGFEPDVRILLTKYS
		1	İ		i	NSNGSQSPWMEEQIRDAWGSM
	1					VLKNVVRETDEVGKGQIRMRT
					i	VFEQAIDQRSSTDTSLSTPAAP
						MVDSLIARVGVMARGNAITLP
						VCGRDVKFTLEVLRGDSVEKTS
						RVWSGNERDQELLTEDALDDLI
						PSFLLTGQQTPAFGRRVSGVIEI
1						ADGSRRRKAAALTESDYRVLV
1					1	GELDDEQMAALSRLGNDYRPT
	ľ					SAYERGQRYASRLQNEFAGNIS
						ALADAENISRKIITRCINTAKLP
					-	KSVVALFSHPGELSARSGDALQ
1						KAFTDKEELLKQQASNLHEQK KAGVIFEAEEVITLLTSVLKTSS
	1	1				ASRTSLSSRHOFAPGATVLYKG
			l			DKMALNLDRSRVPAYIIRSYIR
					l	CGRKGFASAGVGGCRGWLNY
		1				AASEQIVLRVHHMRCEIPHRCV
26954	57322	A	2711I	1175	1298	LSCSGWRAG**ADGCIIOIG*RL
20934	31322	<u> </u> ^	2/111	1173		SPNKCL*TWSALCKPIAE
26955	57323	В	27112	1	1056	
26956	57324	Α	27113	1979	2217	WLSVRVDGGANSGCLGKHGSK
						KCCT*NG*SW*RSDPDENCF*T
	1	l				EQ*STLFN\GAWRNALSIWEPV
- 60.00		L		222		CN/GNFRSSD*TTLGD
26957	57325	В	27114	320 606	1633 705	
26958 26959	57326 57327	A B	27I15 27I16	1	4118	
26939	57328	A	27117	4048	4051	
26961	57329	A	27117	1791	1884	ADGCIIQIG*RLSPNKCL*TWSA LCKPIAE
26962	57330	В	27119	1	2436	DOM INC
26962	5733I	A	27120	I	2449	
26964	57332	В	27I2I	173	4112	
20904	101002	ייו	2/121	1113	F1112	L

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26965	57333	A	27122	916	1568	HHSHEQQFQWPVGASGVDRW
20,000	31333	1	27122	1,0	1500	AGYLHOFRSLTOFOYGAEPDR
		i				KE*COIFIFMONTLSCLSILGKR
		1				TMSLMO
26966	57334	A	27123	1268	1773	SYFIMVKVGTSYVPINVSFSPKV
		ľ.				GPGLPGINRDTRIYLFCEVIFRH
	İ	l				RYLFAISSWSGVTVA\RKDRES
		1				ADLGSDGQNGQDLDWGGG\AA
		1				AAADGVTFSVPVTPHTFRHSYA
						MHMLYAGIPLKVLQSLMGHKS
	1	ŀ				ISSTEVYTKVFALDVAARHRVQ
İ						FAMPESDAVAMLKQLS
26967	57335	A	27124	606	852	HOILFDRTPVSVDQSVEKKG*D
		1		1		HSVRPQ*AAPGHVHYLTIPEKS
l						SOHYHPRTTSE*TSGRYESSGG
i	Į.	l				LSFSOCMRGALEFCC
26968	57336	A	27125	1	2680	MKLMETLNQCINAGHEMTKAI
	1	ĺ	l			AIAQFNDDSPEARKITRRWRIG
	1	1				EAADLVGVSSQAIRDAEKAGR
		1	l			LPHPDMEIRGRVEQRVGYTIEQ
		1				NHMRDVFGTRLRRAEDVFPPVI
		1				GVAAHKGGVYKTSVSVHLAQ
		1			1	DLALKGLRVLLVEGNDPQGTA
		1				SMYHGWVPDLHIHAEDTLLPF
						YLGEKDDVTYAIKPTCWPGLDI
						IPSCLALHRIETELMGKFDEGKL
		1				PTDPHLMLRLAIETVAHDYDVI
	1			1		VIDSAPNLGIGTINVVCAADVLI
	1			1		VPTPAELFDYTSALQFFDMLRD
		1				LLKNVDLKGFEPDAETSQGAL
				1		GTLANV VTSLANLSESLNNGDT
l	i i	1				SEIQPEDQSASEITRAFDTLAKA
1						LNTTDSSSSPSLADGIDTSGGGS
						IHVISRDQSTPIIEVEGPLLSDTH
		1				VTFKSIREDRNGRSQKTVHTEG
		1				DMNMNIKKIVKQATVLTFTTA
						LLAGGATQAFAKENNQKAYKE
					1	TYGVSHITRHDMLQIPKQQQNE
						KYQVPQFDQSTIKNIESAKGLD
						VWDSWPLQNADGTVAEYNGY
		1	i			HVVFALAGSPKDADDTSIYMF
		1				YQKVGDNSIDSWKNAGRVFKD
	1				1	SDKFDANDPILKDQTQEWSGSA
l	1	1	1			TFTSDGKIRLFYTDYSGKHYGK
	1					QSLTTAQVNVSKSDDTLKINGV
			1		1	EDHKTIFDGDGKTYQNVQQFID
	1		l			EGNYTSGDNHTLRDPHYVEDK
						GHKYLVFEANTGTENGYQGEE
26969	57337	Α	27126	2014	2138	LSCSGWRAG**ADGCIIQIG*RL
		_				SPNKCL*TWSALCNPTAE
26970	57338	В	27127	1	7616	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
		Ļ	0.000	10.40	1710	HSKKLVTLSHGSVMAETAVIN
26971	57339	A	27128	240	719	
l	1	1				HKKRKNSPRIVQSNDLTEAAYS
		1				LSRDQKRMLYLFVDQIRKSDGT
l						LPEHDGFCYIHVAQSAEITGLTS
	1					\GNPVRIYGRH*RVSRGRKVVL
	İ					YRPEEDAGDEKGYESFPWVIKR
						AHRPSRGLFSGHIPPISHSLLYR
26972	57340	Α	27129	1505	3812	
26973	57341	Α	27130	471	566	
26974	57342	A	27131	1	229	
26975	57343	A	27132	121	303	
26976	57344	Α	27133	183	524	MSTPRPPFVPAFVGRRPSLLFVP
						AARLTDVRGRKVRACGLLSPR
					Ì	LRSPSSSSATRVARHSIGRPRVA
		1				RLSTVFVAVCVESPSRQRRWCL
		1				FALAATPRAPGTLA*SCLTDSFS
1		i				A
26977	57345	A	27134	1	1025	MIFVLOIRVRGHDDSFLKNHLV
20777	0,540	ľ	27.55	ľ	1.020	FLVIYGTNGTFNOTLVTDNNGL
ŀ		1				APFTLETSGWNGTDVSLEGKFQ
1	ł	1			l	MEDLVYNPEQVPRYYQNAYLH
	1	1				LRPFYSTTRSFLGIHRLNGPLKC
	i	1				GOPOEVLVDYYIDPADASPDOE
1	İ	1				ISFSYYLIGKGSLVMEGOKHLN
ŀ	ŀ	1				
	1			i		SKKKGLKASFSLSLTFTSRLAPD
i	1	1				PSLVIYAIFPSGGVVADKIQFSV
1	1					EMCFDNQGTDLTSTVRVTRSSA
						SVMVYGASEAIGQRQSSAAKP
1						RRSQSDSLGPEFQGLWERLPGL
l						RINGELITAYPQVVVVRVPTPW
1	1					VQSDSDITVLRHLEKMGCRLM
	1					NRPQAILNCVNKFWTFQELAG
ĺ	}					HGVPLPDTFSYGGHENFAKMID
	1					EAEVLEFPMVVKNTRGHRGMY
1	1	1				ELLVSTMGCSNSGMVTTPIKWL
1	İ	1				SMISVQCLANGTFLSPSLTKCPK
1	ļ	1				GIRASVPLSGGPRSLKARTFSAF
1		1				SGPVRSDEQAEALPEAYEPIEV
1		1				NEFGEIDLLAMVEDEIILALPVV
		1				PVHDSEHCEVSEADMVFGELPE
1		1	1			EAOKPNPFAVLASLKRVRSMA
1		1	1			VOONKPTRSKRGMRRSHDALT
1		1	1			AVTSLSVDKTSGEKHLRHH*SA
1		1				DLAAAPRAPGTLAQGCLTDSFS
26978	57346	A	27135	79	306	SGDLPWEINPLSSCSLLREKDPP
209/8	3/340	Ι^	2/133	/*	300	
		1				MTSGPQTNQPKKHLINFKSGPH
	1	1				WKSDCSTHLAATPKAP\GTLAQ
	<b></b>	1				GSLTDSFSA
26979	57347	A	27136	159	254	
26980	57348	С	27137	63	370	
26981	57349	С	27138	107	408	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
26982	57350	A	27139	210	291	
26983	57351		27140	395	680	
26984	57352	A		157	485	
		Α	27141		507	
26985	57353	A	27142	1		
26986	57354	Α	27143	1	1041	
26987	57355	Α	27144	1	671	GASGAAAYGADMAKSKNHTT
1	1					HNQSRKWHRNGIKKPRSQRYE
		1				SLKGVDPKFLRNMRFAKKHNK
	1	1				KGLKKMQANNAKAMSARAEA
		1				IKALVKPKEVKPKIPKGVSRKL\
l				I		DRLAYIAHPKLGKRARARIAKG
	1			1		LRLCRPKAKAKDQTKAQAAAP
	I			1		PSVPAQAPKDKDTSNIFISNRKR
				ı		GCDFTKKETNIPKVLTISMAPSL
1	1			i		MSLYSVTRNQTTKPPSRHKNLT
1				l		KGOLEPLY
26988	57356	A	27145	6	448	
26989	57357	A	27146	930	1307	
26990	57358	Α	27147	1	675	
26991	57359	Α	27148	142	456	
26992	57360	A	27149	3	175	
26993	57361	c	27150	378	434	
26994	57362	Α	27151	11	792	
26995	57363	Α	27152	li .	578	MVRCVRLVEAGSVVRYLSTSIC
		1		1		RPVVDAGSRALCLQEWADSQQ
1		i		1		VKEKQYSSRDVQRAAALNIYRI
1		1		I		PPSSRKPALCPTPRDRLEYDEDR
1		İ		l		LEHIAYVRARELHTLEVTGLET
				1		VAOSKAHVASLEGLIPEDKVVL
	1	1		l .		LAGSPLONEATLGOCGVEALTT
	1		i	I		LEVVGRRLGASL/HTSASKHTM
	1		1	[		VRALTYCSSREETFTAI
26996	57364	A	27153	1239	1905	SAAAAPATGVPACRAGAWVSA
20990	37304	^	2/133	1239	1903	APPAEGRPARARRHPGRCLEAA
1			l			GPRGQRGAAHGH*ARAGSPQP
1						GAPPCHPLGIPARQPLGLPRRTR
-	1					CFGGIAQRGRAARHCLLSRPSA
				1		KAKRNSSYREPGMGGWRSPQA
				1		LGEYGKGSQAGSARLSGAASQ
	1			ł		GRRARHLRGKAPAWNPAPPPSP
	1					PPPALGLPLRTQREATRKPRRE
1						EARRPRPRPLRPGGANGSPGPP
		L_				RAARA
26997	57365	Α	27154	1	1275	
26998	57366	Α	27155	3	92	EAVDPHSECYSS*RWCVRSFFIL
						VGLWSH
26999	57367	Α	27156	2	367	
27000	57368	Α	27157	98	293	GQTFATASISLLRYATGCGVFP
		1	l	1		RV*IRSPRAIPALSGDWPAPFSV
		1	l			LSEPPRFVCLRAMTKAAAFL
27001	57369	Α	27158	3	211	
		•				

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27002	57370	A	27159	1	519	GOLI/LKDTFITOSAADIRRKFO
2,002	37370	,	27137	ľ	5.5	KQALGPEHNLEALLNLAILVFY
i			ł			NRDQEEQAQKEKRDQRKAAPL
1			l			IMALROTLVVQRGQKMEQANH
1						LIPGYSEIARPLYTLIKEIORANT
			l			HOVEWEPEAETAFKPLKOALV
1			l			OAPALSLPTGONFSLYITERAGI
		1		İ		ALGVLTOTHGTTPOLVAYL
27003	57371	A	27160	72	381	DSHTRSGTTRWGIRCRSGSSPSR
27003	3/3/1	l^	2/100	/2	361	RARWGRWGGLAAVALRRPAP
		l				AAGGTAPRGCLPAA*GSPPAPP
l						SGS*SGSSDRPARMPLVVGLSH
						EFE*GLAGVDGEVLPPSRCVAL
						LLLRVERLHVAVYLPREALHOL
						HPLALDLDLLIARLVCHWLWG
				1		CPTSLSKDSKSYSCSLCDV
	47470	ļ.—	00161		7.7	
27004	57372	Α	27161	515	747	SHGNSGNFQGTRDTISLS*AQLT
				İ		TSTKDPWTDPPALWPRVFPSGG
1						HYNCRAPSSP/TIQQEVARAVIT
		Ļ				QFPTAAGVSCL
27005	57373	A	27162	1	663	
27006	57374	A	27163	1	1980	
27007	57375	A	27164	1	672	
27008	57376	A	27165	1	691	
27009	57377	С	27166	1	1491	
27010	57378	A	27167	830	2592	
27011	57379	Α	27168	1	3744	
27012	57380	A	27175	2	365	QWDWAPWSRGWCSSGRLGPH
		ŀ				RSPRSGGGSG\RRAAGPKPCPSP
1		1				RSDAPAQPRGRSRRVLPLPQVQ
		l				AEPPEPWPVLPAAPKPLARPEA
1		1				GMAGPGGRRTTSLPRRRGCGC
		_				CCPASSCFSSLSC
27013	57381	В	27176	1	1392	
27014	57382	Α	27177	79	1241	
27015	57383	A	27178	3	299	

SEO ID	ISEO ID NO:	Mer	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
27016	57384	A	27179	l Ii	812	I IMPTVLACPAFDSRGSPICRFDPP
27016	37364	^	2/1/9	l'	012	ELTSGVRALEESPNAITLPVCGR
		1				DVKFTLEVLRGDSVEKTSRVW
		1				
1		1				SGNERDQELLTEDALDDLIPSFL
	1	1				LTGQQTPAFGRRVSGVIEIADG
	1	ı				SRRRKAAALTESDYRVLVGEL
	İ					DDEQMAALSRLGNDYRPTSAY
		1				ERGQRYASRLQNEFAGNISALA
					1	DAENISRKIITRCINTAKLPKSV
					1	VALFSHPGELSARSGDALQKAF
	1	1			l	TDKEELLKQQASNLHEQKKAG
	1				1	KRSRRLHHTLLRVVAEIDKPDP
						RDELAGLLQFAGGPLQTLFAW
					i	VSPVEAAEQQRLLLAPSSGSFIP
						EG*DHPVRPQ*AAPGHVHYLTI
						PERSSQHYHPGALQE
27017	57385	Α	27180	306	701	
27018	57386	A	27181	1	396	
27019	57387	A	27182	1	1263	
27020	57388	A	27183	1	873	
27021	57389	A	27184	149	421	
27022	57390	В	27185	23	268	
27023	57391	Α	27186	1	363	
27024	57392	Α	27187	2	398	TKFAARRPALAACAAISKIKAR
		l			l	DLRGKKKEEL\LKQ\LDDLKVE
		l		1	l	LSQLRVAKV/TQGGAASKLSKI
	İ				l	RVVRKSIARVLTVINQTSGKKT
				1	i	FREILTRGKKYKPLGPCGP*GRT
27025	57000	Ļ.	27100	224	647	RAMRRRFKPSTEGEP*RTQGSR
27025	57393 57394	A	27188	224	547 888	
27026		A		1		
27027 27028	57395 57396	A A	27190 27191	280	1170	
27028	57396	_	27191	438	1240	
		A		168	378	
27030	57398	A	27193			
27031 27032	57399 57400	A	27194 27195	2	1362	
27032	57400	A	27195		397	D OD DTI ADD DI WOTOD OVO ODD
27033	37401	A	2/196	38	397	RRCRPTMPRP\WCTCRGYQGPR
				l	I	KAQGG*AQDPKGCQPQARSTC
	l			l		LHCPPQAWE/RVLVPVLPRGSG
						CAGQ/MAKAKAKAKDQTKAQ
1						AAAPASVPAQAPKRTQAPTKA
		<u> </u>				SE*ISLPT*GQKDWCDP
27034	57402	A	27197	1	1206	
27035	57403	A	27198	734	913	
27036	57404	A	27199	3	778	
27037	57405	C	27200	164	274	
27038	57406	A	27201	1	2700	
27039	57407	A	27202	1	747	
27040	57408	A	27203	164	409	
27041	57409	A	27204	152	380	

SEQ ID	SEQ ID NO: of peptide		SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	noa	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27042	57410	A	27205	230	2579	
27043	57411	Α	27206	1	2433	
27044	57412	Α	27207	1	528	NHQIRNDFTISPGVKADSRTSPI
		1		1		PQQPASSFDITEAAVSFAKDSLA
						GGVAAAISKMAVAPIERVK/RV
		1				PKEHGVLSWCGNLASVIRYFP\
						TQALNFTFKDKYKQIFLDGVDK
						RSQFWRYFAGNLASGGATGAT
						SLCFVYPLDFAHTRVAADVGK
		1				AGAERELRGFGDCLVKIYKSDC
		<u> </u>			200	IK
27045	57413	A	27208	ı	292	MTSKDKTSRGTIRQQHSRFKKI
						RCSAATTAGTQANRVWSGPLA NSNRPAAEAGVSTAAAPDGPPP
1						PSVPTVDSDSLESAQFKCDNLK
l						TCHTSHGSVMAETAVINHKKR
						KNSPRIVQSNDLTEAAYSLSRD
		1				OKRMLYLFVDOIRKSDGTLOE
						HDGICEIHVAKYAEIFGLTSAEA
	ļ					SKDIRQALKSFAGKEVVFYRPE
						EDAGDEKGYESFPWFIKRAHSP
						SRGLYSVHINPYLIPFFIGL*PDK
						EGNEIWVDMYTVKPSGWTVRT
1						FDKPRKRFIAFFIAGILFRAIKNH
İ						FLPRETLQCLPYILTGFRRGQSE
						YFSIFSNMDLADTVMFL
27046	57414	Α	27209	1	1452	
27047	57415	В	27210	53	844	
27048	57416	Α	27211	281	624	ACSDVWSKFRLRWSPNPRCQE
						RPSAEKMSPHPPSAARHQASWS
						ARRLTQWPRPCHTQ*GQSEEH
						GHRSGLMPAG\THQLPDEHAIT
						PHLQSTAPIPEPKTLSHKDSSLQ GTGK
27049	57417	A	27212	3	411	GIGK
27050	57418	A	27213	265	480	LDTILTASDGRPTYTPP*FLLLS/
2,030	37410	1	2,213	200	100	CFCYGFFCYIFGCSCRALARAR
						AGGGGVPAAHRAAGRGSRAPE
				1		RIPPH
27051	57419	A	27214	294	620	
27052	57420	Α	27215	1	420	
27053	57421	Α	27216	1	342	
27054	57422	Α	27217	175	244	DLLIEMGSFFVQCRTAIL*RKQN
27055	57423	Α	27218	11	951	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27056	57424	Α	27219	20	1654	ELRFPAACSQLQFSDGLHRVDQ
ĺ		l				PPSSMCVSAADLWLC\EAGKLL
		ŀ				VVPMDGSHWFTMRSVVEKLIL
1	ŀ	l				RGHEVVVVMPEVSWOLGRSLN
1		l				CTVKTYSTSYTLEDLDREFKAF
		l				AHAQWKAQVRSLFSLFLSSSNG
1		l				FFNLFFSHCRSLFNDRKLVEYL
		l				KESSFDAVFLDPFDACALIVAK
		l				YFSLPSVVFARGIGCHYLEEGA
l		1				OCPAPLSYVPRILLGFSDAMTF
j						KERVRNHIMHLEEHLFCQYFSK
ì		l				NALEIASEILOTPVTAYDLYSHT
						SIWLLRTDFVLDYPKPVMPNMI
1		i				FIGGINCHOGKPLPMEFEAYINA
		l				SGEHGIVVFSLGSMVSEIPEKKA
		1		İ		MAIADALGKIPOTVLWRYTGT
						RPSNLANNTILVKWLPQNDLLG
		1				HPMTRAFITHAGSHGVYESICN
		l			ŀ	GVPMVMMPLFGDQMDNAKR
1		l				METKGAGVTLNVLEMTSEDLE
						NALKAVINDKSYKENIMRLSSL
						HKDRPVEPLDLAVFWVEFVMR
					ľ	HKGAPHLRPAAHDLTWYQYHS
1						LDVIGFLLAVVLTVAFITFKCCA
1						YGYRKCLGKKGRVKKAHKSK
27057	57425	Α	27220	1	2022	
27058	57426	Α	27221	124	205	
27059	57427	Α	27222	248	443	
27060	57428	Α	27223	263	415	
27061	57429	С	27224	1	717	
27062	57430	Α	27225	349	1125	
27063	57431	Α	27226	629	796	
27064	57432	В	27227	1	388	
27065	57433	A	27228	2	346	
27066	57434	Α	27229	448	555	OPPURIDADIO DE L'UCIONE DE L'U
27067	57435	Α	27230	2	423	CEPIKVYVVGN\GAVGKTCLL\I
				l		SYTTNAFPGEYIPTVFDNYSAN
		1		I	1	VMVDGKPVNLGLWDTAGQED
				I		YDRLRPLSYPQTDVFLICFSLVS
1		1		I	1	PASFENV/LCKGAVKYLECSAL
				1		TQRGLKTVFDEAIRAVLCPPPV
0-150		<u> </u>	0.0001		1400	KKRKRKCLLL
27068	57436	A	27231	1	1503	
27069	57437	A	27232	1	635	

SEQ ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27070	57438	A	27233	3	1107	AVFLSFGWWPLPGIGFOSAEGE
27070	37430	\^	21233	3	1107	AAWTAAPAPSAPPPSKPRARPP
		1				RPEPAASYLSALPPPPRPSERPS
		1				MOAIKCVVVGDGAVG\KT\CLL
		1				I\SYTTQCHFLGEYIPTVFDN\YS
	ł					A\NVMVDGKTGEIWGLWDTAG
						OEDYD\RLRPL\SYPANRMCS*I
		l				CFS\LVSPA\SFENV/LVQKWYPE
				l		VR\HH\CPNTPI\IPVGT\KLDLRD
						DKRHDSRNLKEKKLT\PITYPA
		1				GS*AMAK/ERLGAVKYLG/CAP
						AAHTSEGLKTVFDEAIRA\VLCP
	1	1				PPVKERGRENCLPVVNVSAPSF
		1				LGSCPLGTFCRLCSKKNKKKKK
	ŀ	l				KKKNNGGAFALNANFLLQINFS
		l				IKPFFEPISNFKVLFVLNVRVOT
	l .	ı				HILLKFSPKMTSLLKALFFK
27071	57439	Α	27234	3	203	THEERISI KMISEEKAELI K
27072	57440	A	27235	1	112	LGNTWG*QPCKRLKIWLSLEFT
2/0/2	37440	^	21233	1	112	KINVIRHMWKKFKRL
27073	57441	A	27236	1	513	OHWGRYLKRAFEOWOVPRFG
2,0,5	37441	l^	2,230	,	313	HMPDPGPVKPLQPVEVETRGN
						DYKFLLFHFWDEWLYKFSADE
						FFIPGKLCAIVF*KRL*RPGAVA
	1					YACNPSTLGSRGRWIT*GOEFE
		1				TSLTNKEVKVLSIDORNFKLRSI
		1				GWGEEFSLSKHPQGTEVKAITY
						SAMQVYNEENPEVFVIIDI
27074	57442	В	27237	125	302	
27075	57443	A	27238	93	432	
27076	57444	Α	27239	3	279	
27077	57445	Α	27240	263	446	
27078	57446	Α	27241	237	369	
27079	57447	Α	27242	389	836	
27080	57448	Α	27243	1422	1580	
27081	57449	Α	27244	103	444	RSLTCPGDMFPVVLVINIQLLLT
	1	l				YANFCSWLESLPRKWDFLFYCI
		l				VRLQIFQTFMLCFLLNTLPLRNF
	1					FYQIP*IISLKFKVPQISKAEAKC
						HQSLCIGRVTFIPVPNKFFISI
27082	57450	Α	27245	3	242	MHRNAQHHVKTAKPWGLHPL
	1	İ				KPQPK*YSGPF*PPLEQLRCKAT
		i				GP*GCTQQGGPGPGPQNNFSLL
						GLQACDGRDCHEGL
27083	5745I	A	27246	506	664	
27084	57452	Α	27247	1	1515	
27085	57453	Α	27248	269	54I	RFPNLNS*LLYTRGLTPHESCQ
1	1	1				GLGLAPSEAMAQTIPWPLLATA
1						RLAVTGNQILMQISAAGLNFSS
1	1	l	1			ENGAFISIALSGCKFFKLLCSAS
27086	57454	Α	27249	1	564	

No.	Ceo III	lego in vo.	Tx4-4	lero in No.	Disease and a	Nucleatide location of lost	A mine only assures ( X-Unbrown		
Requence	SEQ ID								
27087   57455   A   27250   2   235	NO.		nou.						
27088   37456		J. C.			<u> </u>				
27089   37457   A   27252   28   271									
27090   37458					I				
LNNKKTIAEGRRIPISKAVENPT   ATEIQDVCSAVGLINVILKRIKM   YPTEWNRDVQYKGRVRVQLK   QEDGSLCLVQFPSRLYTKPNF   WFLGKSVMILVARABMPKLKTR   TOKTGGADQVFQQGEGS*KGK   GKQKEVT   TOKTGGADQVFQQGEGS*KGK   GKQKEVT   APPGMGAASLCAFGLLVTFAT   ASPRYAMVQPSRLGTKLGQA   EADEPFVSGSVPSFLSPLLPA   APGARG*LQRGDLGROAPPA   PGCAPGLA*GRPPAPIIL*RLCSR   PTFFPPANSSKLALADSPPRQ   LQGARPPVPGRLLTSTGTPRPL   PRPLGP									
ATEIQDVCSAVGLINVIL RIKIM	27090	57458	A	27253	12	485			
YPFEMNRDWOYRIGRWRVQLK QEDGSLCLVQFPSRLYTKPNF WFLGKSYMLYAAEMIPKLKTR TQKTGGADQVFQQGGGS*KGK GKQKEVT ASRMPKLKTR TQKTGGADQVFQQGGGS*KGK GKQKEVT ASRRYAMVQPSFRLGTKLQA EADEPFVSSGSVPPSFLSPLLPA APGARRG*UQRGDLGRQAPPA PGCAPGLA*GRAPPLIFTLSTG PPRPLGP PGCAPGLA*GRAPPLIFTLSTG PPRPLGP PGCAPGLA*GRAPPLIFTLSTG PPRPLGP PRLGP PRPLGP RPLGP PRPLGP			1						
WELGKSVMLYAAEMIPKLKTR TQKTGGADQVFQQEGS*KGK GKQKEVT	1	l	1	l					
TOKTGGADQVFQQGGGS*KGK			1						
GKQKEVT	1	l	1	l			WFLGKSVMLYAAEMIPKLKTR		
27091   37459   A   27254   1689   2176   APPOMGAASICAFGILVTFAT ASPRYAMVQPSFRIGTKIGQA EADEPTVSSGSVPPSTLSPLLPA APGARRO*I-QRODLGRQAPPA PGCAPGIL-A*GPPPILSTRUSK PTFFPPANSSR.ALA.DSPPPRQ LQGAP"PVPGRLITSTGTPRL PRPLGP   PREGGP   PRPLGP   PREGGP   PRPLGP   PSFLSPLLPA   APGARRG*LQRGDLGRQAPPPA   PCCAPGLA*GRPAPHL*RLCSR   PTFFPPANSSRLALADSOPPRO   LQGARP*PVPGRLLTSTGTPRPL   PRPLGP   LQGARP*PVPGRLLTSTGTPRPL   PRPLGP   PREGRAM   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PREGRAM   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PREGRAM   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PREGRAM	1		1				GKQKEVT		
EADEPFYSGSVPPSFISPLIPA   APGARRG*IQRGDLGRQAPPPA   PCCAPGLA**GRPAPHL*RLCSS   PTFFPPPANSSRLALADSPPPRQ   LQGARP*PVPGRLLTSTGTPRPL   PRPLGP   PREGGP   PRPLGP   PREGGP	57459	Α	27254	1689	2176	APPGMGAASLCAFGLLVTFAT			
APGARRG*LQRODLGRQAPPA   PGCAPGLA*GRPPAPILL*RLCSR							ASPRYAMVQPSFRLGTKLGQA		
POCAPGLA-GRPAPHLE-RILCSR   PTFFPPANSSRALADSPPRQ   LQGARPPVPGRILTSTGTPRPL   PRPLGP	1		1				EADEPFVSSGSVPPSFLSPLLPA		
PTFFPPPANSSKLALADSPPPRQ   LQGARP*PVPGRLITSTGTPRPL   PRPLGP	1		1				APGARRG*LQRGDLGRQAPPPA		
LQGARP PVPGRLLTSTGTPRPL	1		ł			1	PGCAPGLA*GRPPAPHL*RLCSR		
PRPLGP   PREGCP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   P	1	1	1				PTFFPPPANSSRLALADSPPPRQ		
PRPLGP   PREGCP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   PRPLGP   P			i i				LOGARP*PVPGRLLTSTGTPRPL		
27093   37461			ŀ			1			
27093   37461	27092	57460	A	27255	263	439			
VKDLFKKNYKPLFNEIKDDTNK WKNIPCL WIGRNILKMAILPKV IYRRNAIPIKLLMTFFTEMENTT FKFMWNQKR/CPHQQDWPKPK EQSWRHAIT-LQTHLQKYSNGM SMG/TWMKLETIILSKLSQGK TKHRMFSLIGGN     27094   57462					1	499	MSELPFTIATKRIKHLGIOLTRD		
WKNIPCL WIGRNILKMAILPKV   IYRFNAIPIKLLMTFTEMENTT   FKFMWNQKRCPHCQDNPKK   EQSWEHHAT-LQTILLQGYSNQN   SMGTWMKLETILISKLSQQGK   TKHRMFSLIGGN   T			Γ.						
FKEMWNQRRCPHQQDMPKPK			1			l	WKNIPCLWIGRINILKMAILPKV		
FKEMWNQRRCPHQQDMPKPK			1				IYRFNAIPIKLLMTFFTEMENTT		
EGSWRHHAT-LQTILGGYSNQN SMG/TWNKLETIILSKLSQGQK TKHRMFSLIGGN		1	1						
SMG/TWMKLETIILSKLSQGQK   TKHRMFSLIGGN			1						
TKHRMFSLIGGN			1						
27096   57463   A   27258   1232   1432     27096   37464   A   27259   168   1189     27097   37465   A   27260   1   1760     27098   57466   A   27260   1   1760     27098   57467   A   27262   873   543     27100   57468   A   27262   873   962     27101   57469   A   27263   8   411   FSRCRCSGRYLCMASCL/CFHH     CWWMASHHWPI*RTQV*CAC     WEGRILGGARKCLSLLGFTRL     LACVL-WLPILGSVIPHIQVSITV     RVLFAAAHDEARASEATFQESC     GPYPLLSTPLILLKAVVVLMLD     AHAS     27101   57469   A   27264   1   552     27103   37471   A   27266   428   655   DQKVPPLEMYFGIEVKSLKQLR     SISA*SLFSSRALKEDSGLKLK     OPRSSGVIPRFIVSWPWKMVR     QPVLFSVG     27104   57472   A   27267   1   855     27105   57473   A   27268   1   1261     27107   27473   A   27268   1   1261     27108   27473   A   27268   1   1261     27109   27473   A   27268   1   1261     27100   27473   A   27268   1   1261     27100   27473   A   27268   1   1261     27100   27473   A   27268   1   1261     27100   27473   A   27268   1   1261     27100   27473   A   27268   1   1261     27100   27473   A   27268   1   1261     27100   27474   27476   1   27476									
27097   57464	-, ., .								
1760   1760									
27098   57466   A   27261   453   543									
27109   57467			-		1.				
27100   57468   A   27263   8   411     FSRCRCSGRVLCMASCL/CFHH   CWWMASHWPIPTQVPCAC   WEGRHLG/CGRKCLSLLGFTRL   LACVL-WLPILQS-WIPTIQVSTV   RVLPAAAHDEARASEATFQESC   GPYPLLSTPLILLKAVVVLMLD   AHAS   A   27264   1   552     57470   A   27265   828   1211     27103   37471   A   27266   428   655   DQKVPPLEMYFGIEVKSLKQLR   SISA*SLFSSRALKEDSGLLKLK   QPRSSGVIPRFIVSWPWKMVR   QPRSSGVIPRFIVSWPWKMVR   QPVLFSVG   27104   57472   A   27267   1   855   27105   57473   A   27268   1   1261   1261     27105   27107   A   27268   1   1261     27107   27107   27107   27107   A   27268   1   1261     27107   27107   27107   A   27268   1   1261     27107									
CWWMASHHWPI*RTQV*CAC   WEGRHLGCAPKCLSLLGFTRL   LACVLWIPLLQSYPINIQVSITY   RVLFAAAHDEARASEATFQESG   GPYPLLSTPLILLKAVVVLMLD   AHAS									
WEGRHLGGAPKCLSLLGFTRL   LACVIWLPILQSVIPHIQVSITV   RVLFAAAHDEARASEATFQESG   GPYPLLSTPLILLKAVVVLMLD   AHAS   27101   57469   A   27264   1   552   27102   57470   A   27265   828   1211   27103   37471   A   27266   428   655   DQKVPPLEMYFGIEVKSLKQLR   SISA*SLFSSRALKEDSGLLKLK   QPRSSGVIPRRFIVSWPWKMVR   QPVLFSVG   QPVLFSVG   QPVLFSVG   27104   57472   A   27268   1   855   27105   57473   A   27268   1   1261   27105   27107	27100	57468	Α	27263	8	411			
LACVLWLPILQSVIPIHIQVSITV	1		1						
RVLFAAAHDEARASEATFOESG	1		!						
GPYPLLSTPLILLKAVVVLMLD		1	1				LACVLWLPILQSVIPIHIQVSITV		
AHAS	1		1						
27101   57469   A   27264   1   552							GPYPLLSTPLILLKAVVVLMLD		
27102   57470   A   27265   828   1211							AHAS		
27103   57471   A   27266   428   655   DQKVPPLEMYFGIEVKSLKQLR   SISA*SLFSSRALKEDSGLLKLK   QPRSSGVIPRFIVSWPWKMVR   QPVLFSVG   QPVL									
SISA*SLFSSRALKEDSGLLKLK   QPRSSGVIPRRFIVSWPWKMVR   QPVLFSVG   1   855   27105   57473   A   27268   1   1261									
QPRSSGVIPRRFIVSWPWKMVR QPVLFSVG   27104   57472   A   27267   I   855	27103	57471	A	27266	428	655			
QPVLFSVG QPVLFSVG 27104 57472 A 27267 I 855 QPVLFSVG 1105 57473 A 27268 I 1261	1	1	1			I			
27104 57472 A 27267 I 855 27105 57473 A 27268 I 1261	1		1			I			
27105 57473 A 27268 1 1261			L				QPVLFSVG		
27106 57474 A 27269 164 260	27105	57473	Α		1	1261			
	27106	57474	Α	27269	164	260			

SEQ ID	Tero in vo.	T34.4	SEQ ID NO:	INteia.	Nucleatide less tion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27107	57475	Α	27270	147	224	RLTLPDHLGSLLDHHR\ALGNS YSGG
27108	57476	A	27271	1	837	
27109	57477	B	27272	184	288	
27110	57478	Α	27273	i	286	
27111	57479	A	27274	1	699	
27112 27113 27114 27115	57480 57481 57482 57483	A A A	27275 27276 27277 27277 27278	1059 2 415	1229 4735 825	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCLRVDGQQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPED PVALETRSVGTWYRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPYRVDTVRVECPREVEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAAATSNVHMVKKISI TERSCDGAAEMKWEDQNIGD SCADFQDVWDQREYTYNRPHT
	57484		27279		1326	ASRRIVLDFLLFPEW/PTFVAFW APLFNPSKRASLYRFSLCISSLSF GSHWGSVPGNWVLTYSWG/SL VISRCMFL*PLSCCLEHSPPFICV KEEHEQLVAISPSGVMGLDNSL EQIN
27116	57485	A	27280	2976	3068	VWTALTNRLGQQVSICG*PGTE
		Ľ				DSKGDWLL
27118	57486	A	27281	78	220	APTSLHS*SYFKNCGHGRLRWV ITHIRLVISWATYLVQNNIIQTR LF
27119	57487	Α	27282	1	1077	
27120	57488	A	27283	307	922	QVVPSSLSAISQSPAPCG/CSP*G PSPGAT
27121	57489	Α	27284	1	4560	
27122	57490	Α	27285	87	237	LLFFQLGGDAFSFKFSSGVNF\R NSLICQAWGKRVFSALLCIILSE YTSPL
27123	57491	Α	27286	1	246	
27124	57492	Α	27287	46	396	
27125	57493	Α	27288	1	552	i avener e rachemana
27126	57494	A	27289	3	418	AEKCPCLGAFGFGWDHPRRPG SWGAWSEGSGSPPARIVKMSLR KQTPSDFLKQIIGRPVVVKLNS GVDYRGVLACL\DGYMNIALE QTEEYVNGQLKNKYGDAFNR GNNVLYNSTQKRPDVRTPKRA TLFIVGYIFL
27127	57495	A	27290	202	450	ILI I GIIIL
~/12/	57475	10	27270	1	1.50	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide Incation of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \≔possible nucleotide insertion)
27128	57496	Λ	27291	304	642	
27129	57497	Α	27292	75	393	
27130	57498	Α	27293	1	678	VFGLGSVAHMLLNKTFGSYLG
1		1				VNLGFGFGVTMGVHMAGRTS
						GAHMNAAVSLTNCALGRVPW
		l				RKFPVYVLGQFLGSFLAAATIY
		l				SLFYTAILHFSGGQLMVTGPVA
						TAGIFATYLPDHMTLWRGFLNE
		1				AWLTGMLQLCLFAITDQENNP
					į.	ALPGTEALVIGILVVIIGVSLGM
1	1	1				NTGYAINPSRDLPP\RIFTFIAGW
ļ		l		l		GKQVFRWHHLPGLHWLHHPT
						GAPEIGGFCGV
27131	57499	Α	27294	2	1694	
27132	57500	A	27295	l	356	GIFVTYLPDHMTLWRGFLNEA
1		1				WLTGMLQLCLFAITDQENNPA
l				l		LPGTEALVIGILVVIIGVSLGMN
1		ı				TGYAINPSRDLPP\RIFTFIAGWG
ł	i	l				KQVFRYFPCPGPIPLSFSVGPLC
						VEGWGVM
27133	57501	Α	27296	1	544	
27134	57502	Α	27297	320	610	LREYTINIHTAHPMEWASKKRA
1	į.	1				PRALKEIRKFAMKEMGTPDVRI
	ŀ					DTRLNKAVWAKGIRNVPYRIR VRLSRK\RNEDEDSPNKLYTLV
27135	57503	A	27298	1	303	TYVPVYHFQK
27136	57504	A	27299	1	1311	
27136	57505	A	27300	1	3126	
27138	57506	A	27300	2	779	NRVLLAMVNPTVFFDIAVDGEP
2/130	37300	^	2,301	ľ	///	LGRVSFEVRGLDTKK*LLI*SIK
			İ			LC*OIG\LFADKGPRGTA*FSLL*
					1	ATGEKGFGL*GVPCFHRIIPGFM
	1					COG/GDFTRH/NGT/GGKSHLW
						GRNLKDENFI\LKHTGPGILSHG
						KMLDPNTNGSOFFICTA\KT\EW
						LDGK\HVVFGKVKERHEILWEA
						MGALLGPRNGKTQQEESPIVPG
						GOLRIKFDLVFYSLTTKIIPFCSF
		l		1		KESTPPPHLLASILESLCSRLQFP
	1	1			1	FGFHVFLVPCHA
27139		+	1	l		
	57507	IA.	27302	143	390	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /~possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27141	57509	Α	27304	2	645	NRVLLAMVNPTVFFDIAVDGEP
						LGRVSFEVRGLDTKK*LLI*SIK
l			ĺ			LC*QIG\LFADKGPRGTA*FSCL*
						SIEEKGFGL*GVPCFHRIIPGFM\
					1	CQG\GDFTRH\NGT\GGKSHPM
						GKKFE\DENFI\LKHTG\PG\ILSH
						GKCLDPNTNGSQFFICTA\KTEV
ŀ						VGMAKHVVFWQK*KKGMKYC
		l				GRPWERFG\SR\NGKTOORKITI
1		ļ				C*LVGOLRNKVLTWWF
27142	57510	A	27305	72	387	VCLQHGPWSSLKHVQGWRDD
						CHGLSLGPRTHVQAGTLPKPTL
l						WAEPGSVITQGSA\VTLWCQGI
						LQTQEYRLYREKKTAPWITRIP
İ		l	ļ			QEIVKKGHDPIPSITWEHTG
27143	57511	Α	27306	1	322	
27144	57512	A	27307	1	1125	
27145	57513	Α	27308	1	1419	
27146	57514	Α	27309	198	1634	
27147	57515	A	27310	78	216	
27148	57516	Α	27311	1	489	
27149	57517	A	27312	18	463	AEGVEPGSPRVVLLESEQFLTE
		l				LTRLFQKCRTSGSVYITLKKYD
į.		l				GRTKPIPKKGTVEGFEPA\DNKC
		l				LLRATDGKKKISTVVSSKEVN*
		l				VFRWLISNLPLGANMDGLKKR
1			1			DKKNKTKKTKAAAAAAAAGP
						AAAATAATTAATTAATAAQ
27150	57518	A	27313	1	1242	
27151	57519	A	27314	147	965	DPPSPVPAPPSSPRDGHFLVPDA
1	l	1				TMAEEQPQVELFVKAGSDGAK
1		1				IGNCPFSQRLFMVLWLKGVTFN
						VTTVDTKRRTETVQKLCPGGEL
						PFLLYGTEVHTDTNKIEEFLEA
						VLCPPRYPKLAALNPESNTAGL
	i	1				DIFAKFSAYIKNSNP\ALN\DNLE
ĺ				1		EGTPGKP*RFLDNYLTSPLPEEV
		1		İ		DET\SAEDERCLSDGTFLDGNEL
						TLADCNLLPK\LHIVQVVCKKY
		1		1		RGFHHPPRPFRGVAFGYL\SNA\
	l			I	1	YARENFRFPPVPDDEEIELAYE
		<u></u>				QVAKALK
27152	57520	Α	27315	]1	933	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nuclcotide insertion)
27153	57521	Α	27316	63	641	FAKMTDHKGERGEATRYMFSR
						PFKKTMGVVPCGHNN*RFYK\K
						GDIVD\IKGMGYCVQNGMP\HK
1						CY\HG\KTGRSLTIVTPACLLPLL
						*TNQF*GKVFS\KRINVRIEHIKH
l						SKSRDSFLKRVKENDOKKKEA
				1		QEEGT\WVQLKRQPAPPREAHF
						V\RTNGKEPEL\LEPIPYEFHGIN
						RCPKKKIKDLWATKKKKK
27154	57522	Α	27317	1	390	
27155	57523	Α	27318	75	394	IWGDVEKGKK\IFIMECSQCHT
ļ		1		1		VEKGGKHKTGPNLHGLFGRKT
l		l l				GQAPWDTPYTAANKNKGIIWG
1		ı				EDTLMEYLENPKK\YIP\GTKMI
1		1			1	F\AGIKKKEERADLIAYLKKSY
27156	57524	A	27319	2	529	ERQTRHAGGVRRGPRPKLQRD
		1			\	KAAAAAVLGAVRKRPSVVPM
		1	1			AGQDPALSTSHPFYDVARHGIL
	ŀ	1	1			QVAGDDRFGRRVVTFSCCRMP
		1				PSHELDHQR\LLEYLKYTLDQY
						VENDYTIVYFHYGL\NSRNKPS
		l				LGWLQSAYKEFDRKYKKNLKA
İ						LYVVHPTSFIKVLWNILKPLISH
						KFGKK
27157	57525	A	27320	287	445	
27158	57526	A	27321	2	362	
27159	57527	A	27322	30	365	EEAETVLVGQLKQLSSCLAVH
		l		1		KYRPETKQEKKQRLLARAEKK
l		l		i		AAGKGDVPTKRPPVLRAGVNT
		l		1		VTTLVENKKAQLV\CRKMGVP
		1		l		YCIIKGKARLGRLVHRKTCTTV
		<u> </u>				AFTQVN
27160	57528	A	27323	]3	432	NSRVDDFVAAQDAKGKKVAP
	1	l	1	1		APAVVKKQEAKKVVNPLFEKR
1	1	1	l	I	1	PKNFGIGQ\QRLLARAEKKAAG
						KGDVPTKRPPVLRAGVNTVTT
1		l	l			LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR
		l			1	LGRLVHRKTCTTVAFT
27161	57529	С	27324	62	217	LUKLVHKKICITVAFI
27161	57530	A	27325	1	1545	
2/102	1030	ΙΛ.	21323	<u> </u>	1343	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27163	57531	Α	27326	2	801	PKGKKAKGKKVAPAPAVVKK
						QEAKKVVNPLFEKRPKNFGIGQ
ŀ			i			DIOPKROLTRFVKWPRYIRLOR
		l l	İ			ORAILYKRLKVPPAINOFTOAL
		l l				DROTATOLLKLAHKYRPETKO
						EKKORLLARAEKKAAGKGDVP
	1	l				TKRPPVLRAGVNTVTTLVENK
İ	1	l				KAOLVVIAHDVDPIELVVFLPA
		l				L\CRKMGVPYCIIKGKARLGRL
	1	1				VHRKTCTTVAFTQVNSEDKGA
		l				LAKLVEAIRTNYNDRYDEIRRH
1		1				WGGNVLGPKSVARIAKLEKAK
	1	1				AKELATKLG
27164	57532	A	27327	550	827	DVSWAGRSEDHRWIFLKEQRT
2/104	31332	<u>۱</u> ^	21321	1550	027	GGPPK/ERSRSESRHOISCMCAA
1					I	STWMERTAYGGSHRELLLQQL
i	1	1				
				ľ		PQEHTRKTLPLQQTSAWTYRLF HTSCEI
27165	57533	A	27328	908	1331	GDMRGRREGGFGLGRRTAMRC
2/165	5/533	Ι^	2/328	908	1331	GCSPGIVREADNLVKLSRPSTV
	l					
		l			i .	RVTRSSASVMVLTMPLAPATFL
		l				RVNCWAG/RGR/C*SQNETVSR
		1				TRCEEGR**KDYRVEEQRLRKN
1						WDLARPGEEQLAPSPEKRDLPL
27166	57534	A	27329	1	1134	RVKDQGRHPCVV
27167	57535	A	27329	62	310	
27168	57536	A	27331	243	578	
27169	57537	A	27332	324	995	NLVPRPGTWIRGLPLGDHSPVL
				I		LLFAP*ERSTYDLRSSDRPAQET
	Ì	l			i	SHOFOIRERORRHVLSVDPKLR
		l				RRSRTGKAAFPWCLIIAGTPL*L
			ł			YTHVSRVSDHAGMPALVLHP*
1		1				R/LSPTFLGKGOHALKGLKPVIT
		1				RLLQHGLLKPINSPFPSPILPVLK
			Ì			PDKAYKLVQNLRLINQIVLPIHP
Į.						VVPNPYTLLSSIPPSTTHYSVLD
1		l			I	LKHAFFTIPLHPSSQPLFAFT
27170	57538	A	27333	I	1860	
27171	57539	A	27334	1	957	
27172	57540	A	27335	97	826	
27173	57541	Α	27336	245	392	
27174	57542	Α	27337	736	1300	
27175	57543	Α	27338	590	891	
27176	57544	Α	27339	1256	1654	VQPVRLVSGMQHPGSGWRRL
						WGQHSTSLTSKEHLHISKRGNI
1	1	1	1		1	DNLVQRNMP\SNEKPKCPELPP
1	1		1		1	FPSCLSTVHFIIFVVVQTVLFIGY
1	1	1			1	IMYRSQQEAAAKKILLTTIFLCT
		L				SSICVQNDVVLREFKYLNCFIV
27177	57545	Α	27340	295	852	

SEO ID	leco in vo	later.	SEQ ID NO:	Nucleatide	Nucleotide logotion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
1.0.	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		, ,
		1				
27178	57546	A	27341	3	446	ILAWFGSIAEAPSAAWLCGSSO
						GRYCSSFNRVVRQNSSDAKVV
		1	l			NVPKTRITFCKK\CGKHQPHKV
ľ					l	TQYKKGKDSLYAQGRRRYDRK
ŀ						OSGYGGOTKPIFRKKAKTTKKI
ľ	1	1				VLRLECVEPNCRSKRMLAIKRO
		1				KHFELGGDKKRKGQVIQF
27179	57547	A	27342	1	565	TELL DEGODIKING CONTROL
27180	57548	A	27343	i	1050	
27181	57549	В	27344	1	2109	
27182	57550	Ā	27345	2916	3229	l
27183	57551	A	27346	3	671	AGILAAIREANMGAYKYIQEL
2/103	37331	^	27340	ľ	0''1	W/RKKPSDVHAFFLRV\RCGOT
l	1			1	1	RSFFVFTGVPRPTRPDKARRLG
	1	1				
l						YKAKQGYVIYRIRVRRGGRKRI
ļ		1		]		VPKGATYGKPVHHGV\NPA*KF
		1			i	ASKALQVPLPEGTEAGR\HCGG
	1		1			S*ESLNSYWVGEDS\TYKFFEVI
			1		l	LIDP/YSHKAIRRNPDTQ\WIT\K
		1				PVHKHREMRGLTSAGRKSRGL
		1		1		GKGHKFHHTIGGSRRAA WRRR
	1					NTLQLHRYR
27184	57552	Α	27347	1	1646	
27185	57553	Α	27348	2	2600	
27186	57554	A	27349	1	2403	
27187	57555	Α	27350	100	520	
27188	57556	Α	27351	1	570	
27189	57557	В	27352	1	837	
27190	57558	В	27353	1	1434	
27191	57559	Ā	27354	1	2379	
27192	57560	Ā	27355	3	952	IDWAPKSDRIVTCGADRNAYV
		1		ľ	l'	WSOKDGVWKPTLVILRINRAA
	1					TFVKWSPLENKFAVGSGARLIS
	1			i		VCYFESENDWWVSKHIKKPIRS
	1	1		i		TVLSLDWHPNNVLLAAGSCDF
	1		1			KCRVFSAYIKEVDEKPASTPWG
l	1		1			SKMPFGQLMSEFGGSGTGGWV
1						HGVSFSASGSRLAWVSHDSTVS
	ŀ	1				VA\DASK\$\VQV\$TLKTEFLPLL
	1	1	1	I	1	SVSFVSENSVVAAGHDCCPMLF
	1	1	1	I		NYDDRGCLTFVSKLDIPKQSIQ
1	1	1	1	1		RNMSA/LWERFR\NMDKRATTE
1	1	1	1	I		DRNTALETLHQNSITQVSIYEV
1		1	l	l		D\KQDCRKFCTTGI\DGAMTIW
1		1		I		DFKTF\ESSIQGLRIM
27193	57561	A	27356	3	134	-
27194	57562	A	27357	1	478	
27195	57563	A	27358	1	623	
27196	57564	A	27359	425	667	
27197	57565	A	27360	121	401	
27198	57566	A	27361	1	1818	
27.170	15,500	٠.	15,501	ı <u>.                                    </u>	1.0.0	L

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27199	57567	Ā	27362	552	2325	<u> </u>
27200	57568	A	27363	693	1270	
27201	57569	A	27364	18	146	
27202	57570	A	27365	270	683	
27203	57571	A	27366	1	1398	
27204	57572	В	27367	1	1152	
27205	57573	Α	27368	40	538	SPSPKDSPGVRVGISCYIGGPCQ
				İ		QRLLSPVRASKMTKKRRNNGR
		l				A\KKGPRHVRGPSPLKFLPPSSC
						HLTVPRCRAQGTRPIKKF\VISK
		l				P*VEAAAV\RDISEASVFDAYL\
						LPKLYVKLHYCVSCAIHKQK*S
						GNRS\REA\RKTRTPPPRFR\PGG
		1				*LPHGPPTKSP
27206	57574	Α	27369	204	401	
27207	57575	Α	27370	3	980	
27208	57576	A	27371	2124	2836	
27209	57577	Α	27372	139	8892	
27210	57578	A	27373	1	2592	MAGLGASLHVWGWLMLGSCL
	1					LARAQVRASAPRHLFSRSLRRG
						LSFSDTEARCARELIHVHTSTN
	1			1		APARTEAYPAGSAEPPRRPRAG
	į.	1				REHSFFSQRYVPLPPLGGALGS
						GPAKLPPPRAPCPVRFCADLET
						LCGALDCYKVRGGAAPARPAP
		1				RPAGGIQVSSLSGFGTESLPGGN
						PFPHRDHRESGTMDSPSLTVAT
		1				PLSLTPPIPRELACGDWRRVGG
		1				GAGGGGLRRRGLGGDKAGKR
		1				KSSDLPCGPGFLQSLLQKRRHW
						ESGLGLPGCGCESELVSGCGAP
		1				TLRQHIIPAEGRNGVKEKSADL
						GCGGSQGLRAKKGTNPGIENG
				1		KRKGKEGMLDAWICRRSAFGP
						GREKLGGEEVGCNDKGKIRFIE
						VKMSKKISGGSVVEMQGDEMT
						RIIWELIKEKLIFPYVELDLHSY
						DLGIENRD/ATNDQVTKDAAEA
						DKKHNV\GVKCATITPDEKRVE
	1	l		l	1	EFKLKQMWKSPNGTIRNILGGT
	1	1		1	1	VFREAIICKNIPRLVSGWVKPIII
				1		GRHAYGDQGFGSNMQNAIMK
	1	1	1		i	KLKWLHLARVGKFSDANAKFY
						CRLYYAGEFHKMREVILDSSEE
	1	1		1		DFIRSLSHSSPWQARGGKSGAA
	1		1			FYATEDDRFILKQMPRLEVQSF
	1			1		LDFAPHYFNYITNAVQQKRPTA
	1		1		1	LAKILGVYRIGYKNSQNNTEKK
ĺ	1	1		1		LDLLVMENLFYGRKMAQVFDL
		_				KGSLRNRNVKTDTGKESCDVV
27211	57579	Α	27374	2	2138	

SEQ ID	ISEO ID NO:	IMe*	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino seid	*=Stop eodon, /=possible nucleotide
110.	sequence	""	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,,,,,,,,,,,	1		sequence		, ,
		_				
27212	57580	Α	27375	1	2355	
27213	57581	Α	27376	249	1544	EIYSLSRFIEVKMSKKISGGSVV
	į.			1		EMQGDEMTRIIWELIKEKLIFPY
l		1			1	VELDLHSYDLGIENRDATNDQ
1	i	1				VTKDAAEAIKKHNVGVKCATI
		1				TPDEKRVEEFKLKQMWKSPNG
ĺ		1				TIRNILGGTVFREAIICKNIPRLV
		i i				SGWVKPIIIGRHAYGDQYRATD
		1				FVVPGPGKVEITYTPSDGTQKV
		1			İ	TYL\VHNFEEGGGVAMGMYNQ
		1				DKSIEDFAHSSFQMALSKGWPL
l						YLSTKNTILKKYDGRFKDIFQE
ŀ		1				M\YDKQYKSQFEAQKIWYEHR
		1				L\ID\DMVAQAMKSEGGFIWAC
		1				KNYDGDVQSDSVAQGYGSLG
		1				MMTSVLV\CPDGKTVEA\EAAH
		1				GTVTRHYRMYQ\KGQGDVHPII
		1			1	LASIFAWGPEGL\AHRAKLDNN
		1				KELAFFANALEESFYETHE\AGF
		1			1	MTKDLAACIKGLPNVQRSDYL
		1				NTFEF\MDKLGENLKIKLAQAK
27214	57582	Α	27377	1	692	
27215	57583	Α	27378	251	2150	
27216	57584	С	27379	93	293	
27217	57585	Α	27380	308	534	
27218	57586	Α	27381	2	856	
27219	57587	Α	27382	3	327	AQELHTFEVTGQETVAQIKAHV
		1				ASLEGIAPEDQVVLLAGAPLED
		1				EATLGQCGVEALTTLEVAGRM
		1			i I	LGG\AKQEKKKKKTGRAKRRM
27220	57588	١.	27383	150	456	QYNRRFVNVVPTFGKKKGPNA
27221	57589	A	27384	651	835	
27222	57590	B	27385	1	2193	
27223	57591	В	27386	109	714	
27224	57592	A	27387	150	458	
27225	57593	A	27388	1	2055	
27226	57594	A	27389	1	804	
27227	57595	A	27390	645	1828	
27228	57596	A	27391	899	1216	
27229	57597	A	27392	79	156	
27230	57598	A	27393	1796	2215	
27231	57599	A	27394	107	724	
27232	57600	A	27395	854	926	PLEIPHEPPPGRG*HAPQLPRGQ
27233	57601	Α	27396	2	413	, , ,
27234	57602	Α	27397	54	442	FAKMTNTNLNRRGTRYMFSRP
	1	1	1			FRKHGVVPLATYMRIYKKGDI
	1	1	1			VHIKGMGTVQKGMPHKCYHG
	1	1	1			KTGRVYNVTQHAVGIVVNKQG
	1	1	1			KGKILAKRINVRIEHITHSKSRH
		1				SFLKRAKENDPEYE\EALENGT

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclentide location of last	Aminn acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27235	57603	IA.	27398	1	1490	<u> </u>
27236	57604	A	27399	150	536	NCKISFLHFCYIFVKALKRISAL
2/250	3/604	A	2/399	150	336	
						SRGKILAKRINVRIEHIKHSKSR
			ĺ			DSFLKRVKENDQKKKEAKEKG
		ŀ				TWVQLKR/QGKNLVYISLVLRA
		1			1	L*G*DLTHHIIILFPFFFL**PAPP
	<u></u>					REAHFVRTNGKEPELL
27237	57605	Α	27400	336	928	
27238	57606	A	27401	13	724	INPPPPPFRPEPPSSSKFAKNDGP
	ļ.	1				QRGKRRGTPIIMFS/RGPFKKTM
	1		1			GVVPLAHIFMR\IYKQRCDFVDI
	İ	1	İ			OGEWGTLFOKGNCPHKVVTHG
				ļ		QNLEGVLPMVTPAMLVGHLL*
						NKOV*GORFLPKRNLMWRI*A
		1				HLRHF*GARD/RASLKTCGREN
						GSRKKERKPKGGKVTWGFQLK
	1					RRHLGFPPQEEATFLLKEPIGGR
	1					EP*ACLEPYFPYWISWGINRVF
						KKKIKGPSGLQKKKKKKVD
27239	57607	A	27402	11	759	
27240	57608	В	27403	1	372	
27241	57609	A	27404	1746	2966	DMKNGAKEGESYLLLQCLPPSP
	1	1	1			LPSPPPSPSPPPPPPPPPSPSSPSPP
	1	1	1	l		PSPPPPPSPSPPPPSPSPSPPPPTSPP
	1	1	-	1		SPSSPSPSPPPSPPSPSPLSPTPPPP
	1	1				PSPSLPPLPSPSLPPPPSPSPSPPPP
		ł		i		PSPPPSPPPSPSPSPSPSPPPPPS
						PPPSPPPSPSPSPSLPPSPSPPPSPSPP
	1	1		1		PSPSPLPSPSPSLSPSLPPSPSPSPP
						нининининининининин
	1	1	i	l		нинининининининини
				1		нинининининин
	1	l	i			
						нининининининин
1	1			l		ннинснининниконнин
i						HHHHHHQHHHPQTLH*PSESQ
	1		ì	1		HIVGAQ*MLHCHSLCVYIQGSH
	1	1	1	1	1	SVRKFLVLKQKLSMGMVLPPG
	1	1	1		1	GDLEHCGACLDCDQDWRCAM
				0		PSHKYPPKHAHCCEGCLC
27242	57610	A	27405	150	462	ICEGRTCIFEEPCNCSSLYVRSN
2,242	2,010	<u>'</u>	2,403	1	102	GGNHSHSTTTFKYNGSNWIPR
	1	I		I		WQGPSGSTQPSKARRPVAFSQG
	1	1		1		
		1		1	1	NCAMEKGN*SDILGTTEHWL*A
	L	L	L	L		DIDSRGPKMSLQSSS

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27243	57611	A	27406	142	1285	SRMSKAFGLLRQICQSILAESSQ
l						SPADLEEKKEEDSN\MKREQPR
		l				ERPRAWD\YPHGLVG\LHNIWT
1						DLACLNSLIQVFVMNVDFTRIL
ŀ		l				KRITVPRGADEQRRSVPF\QML
						LLLEKMQDSRQKAVRPLELAY
						CLQKCNVPLFVQHDAAQLYLK
1						LWNLIKDQITDVHLVERLQALY
		1				TIRVKDSLICVDCAMESSRNSS
		1				MLTLPLSLFDVDSKPLKTL\EDG
		l l				LHCFFQPRELSSKSKCFCENCG
						KKTRGKQVLKLTHLPQTLTIHL
ļ						MRFSIRNSQTEKDLATPLYFPQS
						LDFKPRSFQLKRESC\DA\EEQS
		l				GGQYELFAVIAHVGMADSGHY
		l				\CVYIRNAVDGKW\FCFNDSNIC
		1				LVSWEDIQCTYGNPNYHWQET
		1				AYLLVYMK\MEC
27244	57612	Α	27407	1	1077	
27245	57613	Α	27408	3	242	
27246	57614	Α	27409	213	928	EGPARQRLLSPVRASKMTKKR
						RNNGRAQKRAAAHVRGPSPLK/
			ŀ	1		CFPSGPLPPNCAR\CVPQGTRPI
		1				KKF\VIR\NIVGGRSRQGHISEAS
ŀ						RLRMPISLPKL\YVKLH\YC\VSC
	1					AIHKQK*FR\NRS\RESPAKTRTP
		1				PPRF*DLAGGCPTVPPPKAHDL
						GPEYCRHQTCVNWVCCRQATI
i						LGKELCGQIRKLPSQQMSPGWL PSGYSCWLYKYKTEATTALOS
ł		1				
27247	57615	A	27410	1	267	RGEVYHPLQALWSRPPGRDPL
27248	57616	A	27411	257	322	
27249	57617	A	27412	2	176	
27250	57618	A	27413	218	923	
27251	57619	A	27414	2	429	TKFAARRPALAACAAISKIKAR
		ľ		1	1	DLRGKKKEELLKQ\LDDLK\VE
1		1		1	1	LSQLRVA*VTGGAASKLSKIRV
				1	İ	VRKSIARVLTDINQTSGKKTFR
		l	l	1		EILTRGKKYKPLGPCGP*GRTR
1		1	l	1		AMRRRLNKHEENLKTKKQQRK
				1		ERLYPLRKYAVKA
27252	57620	Α	27415	I	1146	
						<del></del>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
27253	57621	Α	27416	2	670	IAGEITRRGSRARPRPGPOCPPG
12.233	37021	1		[	l***	PPGTAMIKAILIFNNHGKPRLSK
						FYQPYSEDTQQQIIRETFHLVSK
						RDENVCNFLEGGLLIGGSDNK\
1						LIYRHYATLYFVFCVDSSESEL
						GILDLIQVFVETLDKCFENVCEL
					]	DLIFHVDKVHNILAEMVMGGM
						VLETNMNEIVTQIDAQNKLEKS
1				l	l	EAGLAGAPA\RAVSAVKNMNL
						P\EIPRNINIG\DISIK\VPNLPSFK
27254	57622	A	27417	5	379	T CH KINING DISKITTI KETSI K
27255	57623	Ā	27418	536	675	LEWSSAKFPTAVGVSLLLSSVC
12.200						RSQ*FLMDAMSRMDLVRYTSA
						RVS
27256	57624	A	27419	2	1220	
27257	57625	Α	27420	435	552	
27258	57626	Α	27421	5	379	
27259	57627	Α	27422	1	1062	
27260	57628	Α	27423	17	467	
27261	57629	Α	27424	105	355	
27262	57630	Α	27425	283	466	APRSARPIVHGVKATRPKPRNL
i	1	1				LDKDMFSKSDPLCVMYTQGME
1	İ	1				NKQWR\EFGRTEVIDNTLN
27263	57631	С	27426	167	379	
27264	57632	Α	27427	164	1185	
27265	57633	Α	27428	1	873	
27266	57634	В	27429	20	523	
27267	57635	Α	27430	3	1225	
27268	57636	A	27431	1	884	GTRDATAEENRVLLAMVNPTV
		1				FFDIAVDGEPLGRVSFEVRGLD
1		1				TKK*LLI*SIKLC*QIGGSSIFITS
	1	1				D*KNSCLPLIVQQCLLFLRILP\L
		i	1			FADKVPKTAENFRALSTGEKGF
	ĺ	1				GL*GVPCFHRIIPGFM\CQG\GDF
		1				T\RH\NGTGGKSIYGEK\FEDENF
		1				I\LKHTGPGILS\MANAGP\NTNG
1		1				SQFFICTAKT\EWLDGKP\VVFG
		1				KVKE\GMNIVEAMERF\GS\RNG
		1				KT\SKKITIADCGQLRIKFDLVF
		1				YSLTTKIIPSGSPRESTPPTHLLA
		1				SILESLCSRLQFPFGFHVFLVPS
27269	57637	Α	27432	27	410	LQDEATGCQKLIEVDDERKLRT
		1				FYEKRMATEVAADALGEEWK
1		1				GYVVRISGGNDKQGFPMKQGV
		1				LTHGRVRLLLSKGHSCYRPRRT
1		1			1	GERKRKSV\RGCIVDANL\SVLN
		1				LVIVKKGEKDIPGLTDTTVPR
	1				<u> </u>	

SEO ID	SEQ ID NO:	Met	SEO ID NO.	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		ᄂ			I .	
27270	57638	Α	27433	93	866	TVSFPATGC\QKLIEV\DDERKL
						RTFYEKRMATEVA\ADA\LGEE
						WKGYVVRISGGNDKQGFPMK
		ı				QGVLTHG\RVRLLL\SKGHSCY
		1				RPRRT\GERK\RKSSSVGCI\VDS
l		1				KSWSVLQLGLLLKKKKK*RRIF
1		1				PG\LTDTTVPRRLGPQK/RASRIR
1		1		l		KLFNLSK\EDDVRQYVVRKPLN
		1				KEGKKPRTKAPKIQRLVTPRVL
1		1				QHKRRRIALKKQRTKKNKEEA
		1				AEYAKLL\AKRMKEAKEKRQE
						QIAKRRRLSSL\RASTSKSESSQ
27271	57639	Α	27434	2	401	
27272	57640	Α	27435	1373	1838	
27273	57641	A	27436	1	257	MNRQLSDSYTEDTKEPSDVTTS
l	1			1		ERTRSPPGSAKTTMIDTLKKLQ
				ľ		DV\QKLRTPKIPQSQQQICWNN
		1				MSRLRDQS*RSSKKRQRLWK
27274	57642	Α	27437	247	831	
27275	57643	A	27438	1	993	
27276	57644	A	27439	267	281	CNCPNIFEARWVNLKSLSKIHE*
						RPFQP
27277	57645	A	27440	274	482	
27278	57646	Α	27441	1	219	
27279	57647	Α	27442	1	681	
27280	57648	Α	27443	11	1094	
27281	57649	A	27444	51	65	NNTFLKYC*IDFND*DCGGEDIS
		_				PN*LGLPIPLSMVLCEIIHF
27282	57650	Α	27445	1	1563	
27283	57651	A	27446	3	318	
27284	57652	A	27447	1	294	
27285	57653	A	27448	7	259	
27286	57654	A	27449	29	191	WOODING NATION OF THE PROPERTY
27287	57655	A	27450	2	519	KSQDYKSLNATCAGGTSFSGC
						ARRLLLSTCSSGWRSGGLSLRG
						GKMELEA\MSRYTQPSEPQLSS
						PHLTVVLLAIGMFFT\AWFFVY
						EVTSTKY\TRDIYKEAPHPP*VA
						LTPSMGFGVLF\LLL\WVGIYRV
						SHPRVTTQNGFHWKPAFCKINF
						FFYLFAWEVFPPAAHNKVQML
27288	57656	A	27451	144	386	VCECKMPKVQPNFTHWSRS*N
						DDLNRSSLWQA*PQAASVEIIIL
						RS
27289	57657	A	27452	462	672	
27290	57658	Α	27453	1	475	
27291	57659	A	27454	1	741	
27292	57660	Α	27455	62	390	
27293	57661	A	27456	549	641	
27294	57662	A	27457	456	774	
27295	57663	Α	27458	2852	2935	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
27296	57664	A	27459	699	761	
27297	57665	Α	27460	399 ·	434	
27298	57666	Α	27461	683	1661	
27299	57667	Α	27462	1	95	
27300	57668	Α	27463	3	517	
27301	57669	Α	27464	6	401	RGLTEVPETSGGRVSVGAMAK
						HHPDLIFCRKQAGVAIGRLCEK
İ						CEGKCVICDSYERPCTLVRICDE
						RNYGSYQGRCVICGGPGVSDA
						YYCKEVHHPGERTRDGC\SKIV
						NLGSSKTDLFL*TAKNTGFQER
27302	57670	Α	27465	1	321	
27303	57671	A	27466	67	348	
27304	57672	Α	27467	1	642	
27305	57673	В	27468	193	445	
27306	57674	A	27469	32	216	AGPSQPTNQTTGKSPQLQQDYF
				1		PRRSYRCSHRLIICLNVIGDAV*
						STVQLKALMLRGRNYK
27307	57675	A	27470	214	440	QDRWGLAPHPPAPGLPLPGPTN
						QTTGKSPQLQQDYFPRRSYRCS
				l		HRLIICLNVIGNAL*STVQLKAL
						MLRGRNYK
27308	57676	Α	27471	35	3801	
27309	57677	Α	27472	1	2901	
27310	57678	Α	27473	1	I317	
27311	57679	A	27474	1698	3255	RVACPCVVWLCWAHWELWRT
						EEVEGGIAGTDVAR/EASDFILT
					ļ	DAIFSSIVKAVMASLQRRGSRE
				l	1	L*LPAAGVWKLQTDF*AQSI/AE
						EGIECKSIKPVLAKYLVWTRLF
				ł		VGLLAELRDESAPETTPAGRRR
				l .		QPQVWSGARQTCGQRTERLAG
						GLGEMQACSGNLGAEKEKQSK
		1				KLAGGWPMSPTSLHALGPKLV
	1					PAKSQRHRAEHMSTWQVGVVS
						SSYFTGNLVGTLLTGYVIKRIGF
	1					NRSYYLASFIFAAGCAGLGLMI
		1			i	GFWSWLAWRFVAGVGCAMIW
1	1	1				VVVESALMCSGTSRNRGRLLA
1	1	1				AYMMVYYVGTFLGQLLVSKVS
		1		l.		TELMSVLPWVTGLTLAGILPLL
	ł	l				FTRVLNQQAENHDSTSITSMLK
1		1		I		LRQARLGVNGCIISGIVLGSLYG
						LMPLYLNYKGGKSSPTPAVRPA
	1			I		RHNSLPGPEAKKYRPGFIIGLTS
		1				CIAFSVQAANVDEYITQLPAGA
						NLALMVQKVGASAPAIDYHSQ
				l		QMALPASTQKVITALAALIQLG
1				1		PDFRFTTTLETKGNVENGVLKG
					L	P. D. I. T. I. D. I. KOIV ENGVERO

one In	long to vo	15.	SEO ID NO:	Do a con	Nucleotide location of last	78 10
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27312	57680	A	27475	152	468	GLGIQ*LLCCSSFCFQLLPEKKE
						GRLAGDAGAARPAKSGRFLGL
						TSGLPSEWSARTGPEPPKSLSG
						GGELNGSSLGFGTODGRGTRE
						GRDRGLHPARPPQYQHSP
27313	57681	Α	27476	541	4172	
27314	57682	Λ	27477	3	1110	
27315	57683	Α	27478	340	1032	
27316	57684	Α	27479	2	779	
27317	57685	Α	27480	3	281	
27318	57686	Α	27481	519	737	VPDLLLQLPNAGLCGHFCDPGD
	ŀ					SLQCLCHQGPGFQAQNWAAV
						WADTKPAAGAEAREPGDLA*L VPPTWSPTR
27319	57687	В	27482	1	915	
27320	57688	Α	27483	68	145	
27321	57689	Α	27484	1281	1433	
27322	57690	Α	27485	171	708	
27323	57691	Α	27486	1	270	
27324	57692	Α	27487	278	588	VYIKRMPKKKV/SEGTIKEEPKR
						RLAQLSAKPAPAKVEAKLKKA
	1	1				AAKDKSSGKNVQTKGKRRAK
1	1	ı				GKQAKVANQETKEDLPAENGE
		1				MKTEESPASDEAGEKETKSD
27325	57693	Α	27488	304	513	PVRHGAFFQDKSSDKK\VQTKG
		l				KRGAKGKQA\EVAN\QETKEDL
		l				PVD\SGETKT\EESPSLLIEAGEK
		L.				EAKS
27326	57694	Α	27489	1	435	
27327	57695	Α	27490	3	273	
27328	57696	Α	27491	9	293	
27329	57697	Α	27492	1	504	
27330	57698	Α	27493	1	529	IPPPRLFLPVATEVARVRLLPPP
		l				PPQNAARDALTSPSYLAWASPR
		l	l			KQTPSPPAAKDIK\KILEQRGYP
	l .	1				KADDDR\LNKVI\SEAEWKYTL
	ļ	l			1	KDVIAPGVLASLPSVP\AGGAV
	i	l	1	1		AVSACPQALAAPCCLGSAPA\A
1		l				AEGEEKMKKKEEVLKES\DDD\
	1	ı				MGFGPFELKSLPPLQIKGLFYTS
	L	L.				R
27331	57699	A	27494	1	396	
27332	57700	Α	27495	2		
27333 27334	57701	Α	27496	1060	702	
27334	57702	A	27497	46	216	HPLOLSVIPFLPVK*HVDOMGF
2/335	37703	l <sup>A</sup>	2/498	40	210	
	1			I	1	AD/CVLSN*VNCLASRFLAVSV ALRSSRFIFTMVP
27336	57704	A	27499	1	1152	ALKOSKILIMAA
27336	57705	A	27500	126	184	
27338	57706	A	27501	238	498	
21338	37700	M	27301	230	490	

SEQ ID	ICEO ID NO:	Mar	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	l '		1	sequence	' '	,
		<u></u>				
27339	57707	Α	27502	1	852	
27340	57708	Α	27503	3	171	
27341	57709	Α	27504	1064	1302	
27342	57710	A	27505	449	668	SPGDYFISLMAAMGRPQVGYW
1	ľ					APELLQKMMRKRMNR/VKKLI
						QNYKQLK/CSLTLNNHVKLVRT NLRFHLAGLLG
27343	57711	Α	27506	1	2454	
27344	57712	Α	27507	2	408	
27345	57713	Α	27508	205	715	
27346	57714	Α	27509	1	813	
27347	57715	Α	27510	1	864	
27348	57716	Α	27511	17	396	
27349	57717	Α	27512	3	428	LTNYAAAYCTGLLLARRLLNR
						LGMDKIYEGQVEVPGNEYNVE
		l				SIDGQPGAFTCYLVADLARTTT
1		l				GNKVFGAPEGAVDGGLSNPHS
1		1				SKRFLGLSIPHSTK*ILGYDSEN
		l				KEFNAEVRRKHIMGQKFADDL
		1				HCLIEEDENASKK
27350	57718	A	27513	164	431	EFFFSTSNIGVYLQIIHIVGKPI*H
1		1				/YLV*ILSY*HLAARTISSKIKSN
1		1				SLVPCASNRGDVGSTRRPRVTR
		1				RSVRYSAPAAPLRSPLFAR
27351	57719	Α	27514	1307	1947	TNEGSGNSAPLFSGARNQTRMI
						VRGTNR/DIICQIAYARTEGDMI
					l	VCTAYVHELPKYGVKVDLTNY
						AAAYCTGLLLDRRLLNRFDMD
		1				KIYEGQVEATGDDYNVVSIDG
		1	ĺ		Į.	QPEVHRKHIMGHNVADYMCY
		1				LMEEDEDGYKKQFSQYMKNSV
		1			1	TPDMMEEMCKKAHAAIRESPV
	ŀ	l				CEKKPKKEVKKKKWNRPKMS
		l				LAQKKDWVAQKKASFLRAQE
		l				RAAES
27352	57720	Α	27515	1	987	
27353	57721	Α	27516	1521	1641	
27354	57722	Α	27517	2	614	ILSRVVEFPLTAEVPPELLAAAG
		l				FFHTGHQDKVRCFFCYGGLQS
1		l				WKRGDDPWTEHAKWFPSCQFL
	1	1			I	LRSKGRDFVHSVQETHSQLLGS
1	1	1			1	WDPWEEPED\EPLWPPPSLPLG
1		1			1	TLSCPHPGERSSLKVPRSQEGSV
1	1	1	1		I	QPRPRGRGGFLSPQ/DARDVEA
1	1	1			1	QLRRLQEERTCKVCLDRAVSIV
1	1				1	FVPCGHLVC\AECAPGLQLCPI
	1			1		WQKPPSRSR
27355	57723	Α	27518	3	89	
		_				<del></del>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nuclcotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nuelcotide inscrtion)
				sequence		
27356	57724	A	27519	1	1618	I
2/330	3//24	^	2/319	1	1018	YNKWSRPVANISDVVLVRFGLS
			l			IAQLIDVDEKNOMMTTNVWVK
l		1				
						QEWHDYKLRWDPADYENVTSI
						RIPSELIWRPDIVLYNNADGDFA
						VTHLTKAHLFHDGRVQWTPPA
l		l				IYKSSCSIDVTFFPFDQQNCTMK
l		l	l			FGSWTYDKAKIDLVNMHSRVD
l		ļ				QLDFWESGEWVIVDAVGTYNT
						RKYECCAEIYPDITYAFVIRRLP
		1				LFYTINLIIPCLLISCLTVLVFYLF
						SECGEKITLCISVLLSLTVFLLLI
		1				TEIIPSTSLVIPLIGEYLLFTMIFV
		l		i		TLSIVITVFVLNVHHRSPRTHTM
		1				PTWVRRVFLDIVPRLLLMKRPS
		l		1		VVKDNCRRLIESMHKMASAPR
		l				FWPEPEGEPPATSGTQSLHPPSP
		l				SFCVPLDVPAEPGPSCKSPSDQL
ł		l				PPQQPLEAEKASPHPSPGPCRPP
ł		l				HGTQAPGLAKARSLSVQHMSS
ŀ		l		1		PGEAVEGGVRCRSRSIQYCVPR
l		l		l		DDAAPE\QMARLPAPWPLATPT
		l		ł	0.	RLSSHPQTSPLRANAHARRSPL
						RCPRVPRSRPAAPKHRPRTCPC
27357	57725	A	27520	1	3158	
27358	57726	Α	27521	2	237	
27359	57727	A	27522	76	254	PLHITFFSRACFPSLHNCCEY*Q
	1	l		i		PGF*TS\KTPQLWCQLRQYSFK
		L.				HSFLVVPTCPVPLLG
27360	57728	A	27523	86	376	SLEGRLSDYTPTFQGCQTTQGR
		l				LPWSFTLSGKSRFSGEGARACY
l		l				KCQKSDHQ\ARNACSPGFLLSRI
		l				PSVRDPTGNRTVQLTWQPLPEP
			·			LELWPKAL
27361	57729	A	27524	1	167	MPEPQRPGVPPEPPPGACYAC
		l			1	RKSGHWA\RNARSPGFLLSRVP
		_				SPPGPSRTPSFG
27362	57730	С	27525	1	381	
27363	57731	Α	27526	243	437	VTSTVRQTPATSPAHKNFQMPE
1	1	1	l	I		PQRPGVTPEPSPPGACYKCQKS
		L				DYQA\RNACSPGFLLSRVPSV
27364	57732	В	27527	88	1485	
27365	57733	A	27528	1	3759	
27366	57734	Α	27529	36	438	RNDRVRPHRDVYSLQGRLSDH
		l	l			SPTFQGCQTTQGRLPWSFTLSG
		l		l		KFRFSGEGATTSPAHKNFQTPE
	l	I	ĺ	l		PQWPGIPPEPPPTGACYTCRKSG
1						HWA\RNARRPGFLLSRIPSVWD
						HWA\RNARRPGFLLSRIPSVWD PTENRTVQLTWQPLPEPLELWP

SEQ ID	ISEO ID NO.	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
27367	57735	Α	27530	314	691	SLQGHLSDYTLTFQGCQTTQGF
	l .				\	LPWSFTLSGKSRFSEEGTKGDV
	1	1				SGSQDNCGERVSRQTREQRSLH
	į.	l				HRQGACYTCRKSGHWA\RNAR
		1				CPGFLLSCVPSVWDPTENRTVR
		1				LTWQPLPEPLELWPKAL
27368	57736	Α	27531	383	2907	RSPTSKTKDICHRSWRRGL/WV
İ	1	1				NKASEDGEDLDRDVSVASNIEP
						WTGWCRAAPLQADLGPNSSSA
1				ľ		SAPPPYNPFITSPPHTWSGLQFR
		1				SVTSPPPPAQQFTLKKVAGAKG
		1		ľ		IVKHALKRLKPVITRLLQHGLL
		1				KPINSPYNSPILPVLKPDKPYKL
		1				VQDLRLINQIVLPIHPVLGIIGLT
		1				SSVRRDAGQDLKRDRAEFLLG
		1				DEVHHPHRRRIAEARRLLLGOH
		1				FDPLHRLIGQVLELGEARYAPP
	İ	1				VEOHHRLAPARRTGORLHPLE
	İ	1				OFGOAGRAORRNRLGIEHRDR
						LDRPDDGAGNALAGDGDFRRG
						CLFAGIGIRPRYCRYROSODDR
						RPSHAAPRPRALPIPHRPATPIA
		1				DVMVMFSVAIMSQLRLVLRHI
		1				DGISRWPPAVVFITDVKIWLVY
	1	1				PSDDCRIRSNDRDDMQGEAPA
	1					MSMNAAARVGDPIGHSFSQGL
	İ					FGEALDGLFFARRSEVDMRAG
1	1	1				NLGRLIARGLSGGRWTPADGO
1	l	1				LTLGSRDVFINGPPATMTIRSTG
	1	1				QCRQHSGLRTVTRTETDSIGPIE
		1				VPADAYWGAQTERSLENFPFG
İ		1			l .	AREOMPIGIVHALAIVKKAAAR
		1				INRGHGLAGEKADAIESAAHDV
1		İ			j	IEGRHDDQFPLVIWQTGSGTQS
						NMNANESSNDTFPTALHVAAA
						LAVTKQLFSALDRLHAALDAK
						AKEWDSIVKIGRTHLODATPLT
					i	LGQEFSGYVQQLANARDRIEGT
27369	57737	A	27532	929	1227	PENGTFEFSILQVLDNSCHKMG
2/309	13/13/	l^	21332	747	1221	KWS/RGA*RPGILLHIGPSLVSA
		1				PNVTHPKSFFFLSFLFLRSPPQV
						PSPLNPSFLWTHLTSPLLPRLLL
25250	68830	ļ.	08500	0.0	410	ARLSQVPILT_
27370	57738	A	27533	98	412	LGSGDLPWEINPLSSCSLLCEKH
1		1	l			PPTTSGPQTDQPKKHLTNFKSG
		1	l			ACYMCRK\SGHWA/RANARSPG
1		1	l			FLLSRIPSVWDPT*KFGLVQLTL
	68820	ļ.	0.004	ļ	240	GKPLPEPLELRP\RLSD
27371	57739	A	27534	14	249	
27372	57740	A	27535	49	341	
27373	57741	A	27536	392	571	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
27374	57742	A	27537	1	1590	MPNGTNESHRYNASERSOTOK
2/3/7	37,742	1.	2,33,	,	11370	DEOTGKTVGPPEWTPLVRRNG
					GDSGLDFHFFAEKLKIIVDSAG	
1						RAGTGHMRPPAVHFGHRGOA
ľ						MITLSPLRAKQKAVLQKPPPLT
ł		İ				STYSLMLPLFLPDKRPPTTEWF
İ						LPVMEDAHELTLAWLMLALYR
					1	KPNASVQGSAQEETLCVFRVKE
		1				PLEWQALFADVHSGVNDKGPN
		1				INCSLYEHIKNVSEIVLNLAQTQ
1						KNPAHSDPSSTPAGCM\PGTTA
						GGSAVMSACCPSPAAPGPLPGP
						ATGSC/SPSAAPRPPDPPPGHPE
	ŀ	1				GIMAIRAAPSCLGACITLQDEET
		1				CEQTHTHSRIYMIYLFARCLLH
1						AIARGRSRKCAASAGGTCPHVR
	1					VPGGGSYFRVSLQGQQTHWMR
		1				PENGFSTCVRTKSRRCPIIREQH
	1	ı				PTKIPKALTANANQAFFLLVNG
Į.		1				HSMVASPHQSQRRADLGGFWR
1		1				DASSSLLANSQVQVCGSLRKRP
		ł				HGWVVPFSLRCVAPLTADDSR
	1					LRTASLEMSTPPMHVQDDWQL
1		1		1		RRGLPAGNTAVTVSELIYLNAN
		1				GRLOVEKFLF
27375	57743	A	27538	279	759	GREQVERIE
27376	57744	A	27539	443	696	
27377	57745	A	27540	1	179	
27378	57746	A	27541	3	1237	
27379	57747	A	27542	4	152	
27380	57748	A	27543	760	908	
27381	57749	Α	27544	203	570	
27382	57750	A	27545	312	500	
27383	57751	Α	27546	1	441	
27384	57752	A	27547	1	630	
27385	57753	Α	27548	1	1254	
27386	57754	C	27549	236	408	
27387	57755	C	27550	220	398	
27388	57756	C	27551	254	445	
27389	57757	Α	27552	1	2742	
27390	57758	Α	27553	1	744	
27391	57759	Α	27554	1135	1751	RPGSTLQVRQNYHQGLRRPPIN
		1				R\QINLE\LYAS\YVYLSMSY\YF
	1	1	1		1	DRD\DVALKNFAKYFLH\QSHE
			1		1	E\REHAEKT**KL\QNQRRLAEF
					1	FLQDYQRNQD\CDDWGRAGLN
		1				VA\MECALAFWKKNVESSHYW
		1			1	NLHKL\AT\DKN*PPIWCDFHW
		1			i	RHIYLE*AG*KAIKRIWGDHVN
1		1			l	QTFA/RKMGSAPNLGFGEYLF*
	1		1	1	i .	OSTPWGDSDNESSPWG

SEQ ID	ICEO ID NO.	Mat	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27392	57760	A	27555	224	547	
27393	57761	В	27556	22	130	
27394	57762	A	27557	1	408	
27395	57763	A	27558	1	1011	
27396	57764	A	27559	56	822	
27397	57765	A	27560	146	411	
27398	57766	A	27561	1	885	
27399	57767	A	27562	115	1200	
27400	57768	A	27563	791	1114	
27401	57769	A	27564	67	401	RLGSSGREVIHPGERGLENNVC
						H*SSGNQENELEMNKTANGDC
		1				RRDPRERSRSPIERAVAPTMSLF
		i i				GSHLYTSLPSLGLEOPLALTKN
		l				SLDASRPAGLSPTL\TPGERQQN
27402	57770	l <sub>A</sub>	27565	109	345	HPLFIFPDPLPPPTFHPLIGPRMC
	I			1	1	FSPGLALCPHPNLILNCSSHNSY
						VLWEGPGGK*FESWGRFPHDT
		1			1	VLVIVNKSHKI
27403	57771	С	27566	63	167	
27404	57772	A	27567	231	314	
27405	57773	С	27568	99	323	
27406	57774	Α	27569	1	1347	
27407	57775	Α	27570	192	269	WFYKGEFLCTHS/HCLLPRKTC
		l		1		LLPAAM*YCDSQFSMAGETSQS
		1				WOKAKEEORHILHGGROKARL
		ı				TWQQAGECVHRNSPL
27408	57776	A	27571	107	797	AQWRRAAPPAAGVTCPFRLQP
		1				GMETPLDVLSRAASLVHADDE
ŀ		1				KREAALRGEPRMQTLPVAS\AL
		1				SSHRTGPPPISPSKRKF\SMEP\G
		1				DEDLDCDNDHVSKMS\RIFQPP1
		1				LNKTANGRLARRDPRERSRSPI
		1		1		ERAVAPTMSLHGSHL\YTSLPSL
		1				GL\EQPLALTKNSLDASRPAGLS
		1				PILTPGERQQNRPSVITCASAG
	1	1				ARNCNLSHCPIAHSGCAAPGPA
		1				SYRRPPSATCV
27409	57777	Α	27572	1	1686	
27410	57778	A	27573	1	1614	
27411	57779	В	27574	208	366	
27412	57780	Α	27575	15	1729	
27413	57781	Α	27578	1	1614	
27414	57782	A	27579	308	464	KAHHHWSLEKCKSEPQ*DTISW TWMKLETIILSKLPQEQKTRNC MFSLISGS
27415	57783	A	27580	291	378	IMI SEISUS
27415	57784	A	27581	291	91	
27416	57785	A	27582	439	519	
27417	57786	A	27582	2	91	
27418	57787	A	27584	2	91	
27419	57788		27584	2	91	
2/420	3//88	Α	12/303	<del>-</del>	71	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27421	57789	Α	27586	50	394	
27422	57790	A	27587	1	666	
27423	57791	A	27588	2	91	
27424	57792	A	27589	5	91	
27425	57793	A	27590	884	991	
27426	57794	A	27591	290	460	
27427	57795	Α	27592	86	349	
27428	57796	A	27593	2	89	
27429	57797	A	27594	723	882	
27430	57798	A	27595	255	352	TGTWMKLETIILSKLTQE\QKTK HCMFSLISGS
27431	57799	Α	27596	1	1685	
27432	57800	В	27597	82	263	
27433	57801	A	27598	491	816	RHRGAQRKAFLQRVNCGLCCT WNLCPQKLRGRK WPVQVS\PA AGRDPGGPLL*PEGTLWGAPFC LGAPPPLLTAACAPAAGRAGGT RGAAPACPEDRTNAHSQHHHP HV
27434	57802	A	27599	645	1142	
27435	57803	A	27600	218	326	
27436	57804	A	27601	181	2316	
27437	57805	A	27602	2	238	
27438	57806	A	27603	709	1416	
27439	57807	A	27604	3	501	SSRALRLLGVVVRIRQAGTMA VTKELLQMDLYALLGIEEKAA DKEVKKAYRQKALSCHPDKNP DNPRAAELFHQLSQALEVLTDA AARAAYDKVRKAKKQAAERT QKLDEKRKKVKLDLEARERQA QGQGG*GGRESRSTRTLEQEIE RLREKGSRQLEEQQRLI
27440	57808	Α	27605	1	963	
27441	57809	Α	27606	135	384	
27442	57810	A	27607	349	679	SETYWFFPRESQHLDLDVWPPR SEHHSQSTGTHSGVSESLSPRYF QRCNAHSPSQGHEEQYLAPWK HRLYQRMSDLPLNDIR*FQYSK GHHRCQSNEAVQNPKQLQSLL
27443	57811	Α	27608	1590	2758	
27444	57812	A	27609	123	2312	
27445	57813	Α	27610	1	1809	
27446	57814	C	27611	79	309	
27447	57815	С	27612	77	325	
27448	57816	Α	27613	1	606	

SEO ID	ISEO ID NO.	Ixiat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27449	57817	IA	27614	12	1686	L SQCAELSASPLSPAPGLPRHSRL
2,	3.0	Ι΄.	2.0	l"	1	HALLGLAMPVDLSKWSGPLSL
	1	1	1	1		QEVDEQPQHPLHVTYAGAAVD
	1	1		1		ELGKVLTPTOVKNRPTSISWDG
		1				LDSGKLYTLVLTDPDAPSRKDP
		1				KYREW\HHFL\VVNMKG\NDISS
		1				GTVLSGIVG\SGP\PKGTGLHRY
		ļ.				VWLVYEQG\RPLKCDEPIL\SN\
		1				RSGDHRGKIORWASLPVKK\YE
i		ı				
		1				APGPPVAGHRVTPSPKWDEPM CPQTVTKQLSWGK
27450	57818	A	27615	446	1300	CrQTVTKQLSWGK
27451	57819	Α	27616	2	346	
27452	57820	A	27617	li -	305	MAISTSGSSVPWPSA/PSGPHGR
				1		GS\PWGFCLATCWQSIRGQGGD
	1	1		i		PWSAGSGHPGTKGASAPGPGE
		1			1	GQSGGDSGSA/GR*GSHHLPGP
l		1				ASFRAGSGQAWDGKGK
27453	57821	A	27618	287	475	
27454	57822	Α	27619	37	314	
27455	57823	A	27620	I	367	
27456	57824	С	27621	360	610	
27457	57825	Α	27622	604	980	
27458	57826	В	27623	8	442	
27459	57827	Α	27624	I	2268	
27460	57828	Α	27625	296	398	APPGPTLPWASTPSRGCT*APPG
						PTLPWASTPSRGCTSSWFMLPA
			1			MRRCGAPC
27461	57829	A	27626	1	3633	
27462	57830	Α	27627	1853	3809	
27463	57831	Α	27628	1	656	MTHNQEKNKSTNTEMTMMMK
	1	ļ				LADKDDKTAMINMLQVVKKV
						EEAMSMMRRNKDVKNIHGRA
		1		1		RWVKPMIPALWEAKEVEGKYS
						AHNFWGSWKFKSSSRSSSSGPE
						SPARTHASFCQPDGGPTNKLGT
						KAFRVSPASSLLVDLNTQEVEII
		1		1	1	NVRKATPTCSLELGRKRRDGA
		1		İ		AERAALDVVVVIYQLAPAAAP
					1	NCLNPVTSRR/PPQTPAPEGQGR
						RQSFEE
27464	57832	Α	27629	127	273	
27465	57833	Α	27630	3	405	AAFHARGHRAGLSASSCSWRC
			1			CPSSSAPCAPYAAPAARMLQTC
						LKQSPAGMPPASPSSPAAHSWG
		1				STSFSKYSPRSTSTSCCPCISSCW
				1		ESWPCPTPSSPL*NKFFPASFPN
						RQYQLLFTQGSGENKEKDHQL
27166	57024	١.	27621	100	007	
27466	57834	A	27631	689	987	
27467	57835	Α	27632	228	527	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
27468	57836	Α	27633	108	44 I	
27469	57837	С	27634	156	287	
27470	57838	Α	27635	2	363	RFTKVEMKEK\MLSAAREKGR
1				1		VTHKGKPISLKADLSAETLQAR
1		l		1		REWGPIFNILKEKNFQPRISYPA
	1					KLSFISEQEIKYFTDKQMLRDFV
				i		ITRPALKELLKEALNMERNNW
		_				YQPLQKHAKL
27471	57839	Α	27636	2	367	
27472	57840	Α	27637	1	936	
27473	57841	A_	27638	1	865	
27474	57842	A	27639	1	1287	
27475	57843	Α	27640	I	2565	MGPGARLAALLAVLALGTGDP
ł		l				ERAAARGDTFSALTSVARALAP
		l				ERRLLGLLRRYLRGEEARLRDL
		l	1			TRCNDETITYLLDKRLTVLTAA
		l				NIPYSSPENGAKRRRQDAFPPIH
		1				YNTQDALLQYLSGVGWGAPPA
		1				AQAHRDAPFVDSIAQVLLRTSG
	1					GSAEASGWSLRSRWAVGGATG
1						SWVLSKGDRASLGERVVTGWA
1						TLNVGRSFAYCLTTCVQPPLDV
1	1				İ	GPRKEHAPRPPSLSPTSTRQRGQ
1						SERSQDANGRRKQKTKSEPERF
1						EDAVLLAGFKVEEEPVQRPRRK
1			İ			EWFQGPSPGHCCPAQPQDSAPC
1						ILATHAPARAQNAPGTAWAAA LEGTSTVSLDHFHVVGVVVVS
1			Į			
						GGEIILLLSFRFYDKVLSLHEDS TTPVANPLLAFTLIKRLQSDWR
		ł				NVVHSLEASENIRALKDGYEKV
1			1			EQDLPAFEDLEGAARALMRLQ
		l		i		
						DVYMLNVKGLARGVFQRVTGS AITDLYSPKRLFSLTGDDCFOV
				ł		GKVAYDMGDYYHAIPWLEEA
						VSLFRGSYGEWKTEDEASLED
1						ALDHLAFAYFREQSSSPATEQS
1		ĺ				WMENDFDELREEGFRRSNYSE
						LOEEIRTNGKEVKSFEKKLDEW
1						ITRITNAEKSLKDLMELKTKAR
1				I		ELRDECRSLSSRCNQLEERVSV
1				l		MEDEMNETKRGEKFREKRIKR
1				l		NEQSIQEIWDYVKRPNLRLIGV
1				l		LESDRENGTKLENTLQDIIQENF
20106	57014	L.	00641	210	451	
27476	57844	Α	27641	219	451	APAAEGAGRIS/PCSRHSPAGLE/
						WLCPHLCALF*QCPP/PTCHQSA
1	1			1		SPR\WP*G/RPAAGPHPPAATVA
27475	57045	ļ	27642	227	561	PKRKGKTKSSTRE
27477	57845	Α	27642	237	561	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
l	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, :=possible nucleotide insertion)
				sequence		
27478	57846	Α	27643	3	461	TRTRRGSRTAEAR*CTPGWRPA
						GRRSALCSRGHLGP*RPPRTRS
		1				GAAPGPHSPCGRPDGAPCSRLP
		1				PHRSRSPPHGSHVPAAGWLSAC
		1				PHQRWPAAAAGPGTDQCRVVC
		1				PERASPHIWKGSTVPFLPSWTFL
		1				RVLSVPGCSLPRCCWLGHCQ
27479	57847	Α	27644	2	159	
27480	57848	Α	27645	1	243	
27481	57849	Α	27646	219	462	
27482	57850	Α	27647	256	427	
27483	57851	Α	27648	1	954	
27484	57852	Α	27649	2	4690	
27485	57853	Α	27650	1	1275	
27486	57854	Α	27651	1	867	
27487	57855	Α	27652	1	472	110000
27488	57856	Α	27653	2	1215	
27489	57857	Α	27654	3	401	
27490	57858	A	27655	712	1245	
27491	57859	Α	27656	2	1178	
27492	57860	A	27657	278	339	
27493	57861	Α	27658	1	1407	
27494	57862	Α	27659	1	687	
27495	57863	Α	27660	484	776	
27496	57864	A	27661	299	1318	
27497	57865	Α	27662	<u> </u>	960	
27498	57866	Α	27663	122	282	
27499	57867	A	27664	1	600	
27500	57868	В	27665	1	375	
27501	57869	A	27667 27668	356 49	439 360	
27502	57870	A	27669	2	580	GRVGCGGPWAARVGERIPNMA
27503	3/8/1	A	2/009	12	1380	GRKLAS*KPTD*VAFARD/IIPO
		ì				NPKAPLPSFLKS\WNGDPSPSRL
		1				AALP*ESHPAI\DWA*LPRPNVA
		1		1		QGLAWVDDFE\KKFNAAERFPC
	ļ			1		
			1	1	I	PEDK\YTAQVDA\EEK\EDVKSL C/AEWVSLSKA\RIVEYEKEME
			1		I	KMKNLIP\FDQMT\IEDLNEAFP
						ETKLDKKKYPYWAHQP\IENL
27504	57872	A	27670	1	675	DIRECTION OF THE PERSON OF THE
27505	57873	c	27671	137	1357	
27506	57874	Ā	27672	1	1032	
2/300	13/0/4	1^	12/0/2	T,	L1002	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
İ				sequence		
27507	57875	Α	27673	3	938	MANNPGANGQ\PGGPGGPGMG
		1		ŀ		KPRCF/RGEVFGIVIRGRGSRP/R
	1	l	1			GRGRGR\GRGARGSKGRG*RD
l		i	1			W\VPVHQVGAALVKDH*RSKF
		l				PWKEIYLFSLPH/IKESEIIDF\FL
		1			i .	GGLLSKDEGFE*LCPVQEQ\TRA
		l	1			GPAATR\FKAFCCYPGTTNG\IIV
		1				G\LGVKCSQE\VAHRPFRGAI\IL
		1				AKL\SIVPVR\RGYWGNKIRKP\
		1				HTVP\CKVT\GRCGSVLVRLIP/S
		1				QPRGTGIVSAPVPNKL\LMMAG
	ļ.	1		ŀ		IDDCYT\SARG\CTATLG\NFAK
	ļ	ł		ŀ		AT\FD\AISKTYSYLTPDLWKET
	1	1				VFTKSPYQEFTDQLVKDHTRVS
		1				VQRTQAPAVATT
27508	57876	Α	27674	1	864	
27509	57877	A	27675	2	752	RRAHACARRRRKKEMLGVNVL
		l		l		TSHSSQERMKLTFKKKAVNFA
		l		l		DAAAAQGPLLPAMVNPTMFFH
	1					IAVDGEPLGCVSFEVRGLESKK
	1	l		l		*LLI*SIKLC*QIG\LFADKVPKT
	1	l			ŀ	AENFHALSTGEKGFGYKGSCFH
	1	1				RIIPGFMCQGGDCE/RHHNGTG
		1				GKSIYTEKFEDENFILKHTGPGI
	ł	1				LSMANAGPNTNGSQFFICTAKT
1						EWLDGKHVLFGKVKEGTNIVE
1		1				AMERFGSRNGKTSKKITIADCG
						QLLISLTCVLS
27510	57878	Α	27676	3	327	AQELHTFEVTGQETVAQIKAHV
ł		1		l		ASLEGIAPEDQVVLLAGAPLED
	ŀ	1				EATLGQCGVEALTTLEVAGRM
1				1	1	LGG\AKQEKKKKKTGRAKRRM
1					İ	QYNRRFVNVVPTFGKKKGPNA
27511	57879	Α	27677	567	838	

Fa			Tana Tan			
SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	
1.0.	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27512	57880	A	27678	3	1923	ATMAQGLEVALTDLQSSRNNV
		l				RHHTEEITVDHLLVRRGQAFNL
		l				TLYFRNRSFQPGLDNIIFVVETE
	1	1				DAVYLDSEPQRQEYVMNDYGF
		1				IYQGSKNWIRPCPWNYGQFED
1		l		1		KIIDICLKLLDKSLHFQTDPATD
						CALRGSPVYVSRVVCAMINSN
						DDNGVLNGNWSENYTDGANP
						AEWTGSVAILKQWNATGCQPV
ļ		l				RYGQCWVFAAVMCTVMRCLG
		1				IPTRVITNFDSGHDTDGNLIIDE
ŀ		l				YYDNTGRILGNKKKDTIWNFH
		1				VWNECWMARKDLPPAYGGWQ
ŀ		1				VLDATPQEMSNGVYCCGPASV
		l				RAIKEGEVDLNYDTPFVFSMVN
		1				ADCMSWLVQGGKEQKLHQDT
		1				SSVGNFISTKSIQSDERDDITEN
	ł					YKYEEGSLQERQVFLKALQKL
1		1		l		KARSFHGSQRGAELQPSRPTSL
	ł	1				SQDSPRSLHTPSLRPSDVVQVSL
	į.					KFKLLDPPNMGQDICFVLLALN
	l	1		l		MSSQFKDLKVNLSAQSLLHDG
	1	1				SPLSPFWQDTAFITLSPKEAKTY
		1				PCKISYSQYSQYLSTDKLIRISA
		1			l	LGEEKSSPEKILVNKIITLSYPSI
						TINVLGAAVVNQPLSIQVIFSNP
						LSEQVEDCVLTVEGSGLFKKQQ
İ	1			1		KVFLGVLKPQHQASIILETVPFK
						SGQRQIQANMRSNKFKDIKGY
27513	57881	Α	27679	1	756	
27514	57882	Α	27680	1	2601	

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide		in USSN	location of first	codon for last amino acid	
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	İ			sequence		
		_			1677	
27515	57883	Α	27681	I	1677	MARKDLPPAYGGWQVLDATP
İ			1			QEMSNGVYCCGPASVRAIKEG
		1				EVDLNYDTPFVFSMVNADCMS
	l					WLVQGGKEQKLHQDTSSVGNF
	1					ISTKSIQSDERDDITENYKYEEE
	İ					HFEAFQSVAQ\LPITRPFSWILRP
		1				F*RP*RKISTSFIRPLFTFL/LRLM
	i					NAHPEFRMAMKDAKTYPGKIS
	ŀ		Į	i		YSQDSQDLSTDKLIRISALGEEK
						SSPEKILVNKIITLSYPSITINLLA
						RVLSPSLPGPAGLASRSEYGPA
	i					KPTPTGNSSWPASAARSPGSRP
						CLSLHTSPQAEGAGSGLDQPRE
		1				RLPQCSGELKGSSSAARMGAE
						NEEAPRASEGCQGCQQAVTSQ
		ı				QDGGPLLQNRFFWDCGDENGA
						DAVYLDSEPQRQEYVMNDYGF
	1	1				IYQGSKNWIRPCPWNYGQAASF
						WRYGQWWVFAAVMCTALGIK
						SCDFQAARNNEEHHTKALSSRR
						LFVRRGQPFTIILYFRAPVRAFL
						PALKKANKGKLESFSYICFFSIV
		1				FGSKNSYAKVAYLEVAYPATL
						QNGALRKYLVLGAAVVNQPLS
				1		IQVIFSNPLSEQVEDCVLTVEGS
				l		GLFKKQQKVLIP
27516	57884	Α	27682	1	1653	
	57885	A	27683	3	2170	
27518	57886	Α	27684	2	244	ACPSTSTSHCRGATCSCSRTS\C
						SGVLQHSLRHCASGRGFSSRCP
	i					ACCGSPGLGLPAALPPAAWGL
						QIAPSPQGTPGNSQS
27519	57887	A	27685	618	851	
27520	57888	Α	27686	78	240	
27521	57889	A	27687	860	1246	
27522	57890	В	27688	1	2301	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27523	57891	A	27689		1719	MINTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTOSKT VVAKRNREHGKKERSSSPAME QSWMENDFDELREEGFRSNYL ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQFRSKIDTLTSQLKELEKQEQ THISKAGRROETIKIRAELKEIET QKTLQKINESSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTIDTFEQTTIREYYKHLYA NKLENLEEMDIFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSFGPOGTTAEFYQRYKEEL HINRAKDKNIHMISIDAEKAFD KIQOFFMLKTLNKLVLEVLARA DDMIVYLENPIVSAQNLLKLLS NFSKYSGYKINVQKSQAFLYTN NRQTESQIMBELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNIPCSWVGRNI VKMAILPKVIYRNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA

SEQ ID	SEQ ID NO:	Met				Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27524	57892	A	27690	11	1902	MNAKALPTLSPLPOATTESVSL
2,524	3,072	ľ`	1,000	ľ		TOERSSSPATEOSWTENDFDEL
		1			\	REEGFRESNYSELREDIRTKGK
İ		1				EVENFEKNLEECITRIINTEKCL
1		1				KELMELKTKARELREECRSLRS
		1				RCDQLEERVSAMEDEMNEMK
	i	1				REGKFREKRIKRNEQSLQEIWD
1		i				YVKRPNVRLIGVPESHGENGTK
			1	ì		LENTLODIIQENFPNLARQANIQ
				ł	1	IQEIQRTPQRYSSRRATPRHIIVR
						FTKVEMKERMLRAAREKEIQT
		1		1		TIREYYKHLYANKLENLEEMD
					i	KFLDTYTLRRLNOEEVESLNRPI
						TGAGIEAIINSLPTKKIPGPDGFT
		ı	1	1		AEFYORYKEELRIKYLGIOFTR
1		1		1	1	DVKDLFKENYKPLLKEIKEDTN
		1		1		KWKNIPCSWVGRINIVKMAILP
İ		1				KVIYRFNAIPIKLPMTFFTELEK
	ļ					TTLKFIWNQKRARIAKSILSQK
1			1	i		NKAGGITLPDFKLYYKATVTKT
1		1	1			AWYWYONRDIDOWNRTEPSEI
1		1		1		MPHIYNYLIFDKPEKNKORGKD
i				1		SLFNKWCWENWLAICRKLKLD
		1				PFLTPYTKINSRWIKDLNVRPKT
				1		IKTLEENLGITIQDIDMGKDFMS
	1			1		KTPKAMATKAKIDKWDLIKLK
1		1	ŀ			ELLTAKETTIRVNRQPTKWEKI
		1	1			FTTYSSDKGLISRIYNEL/KQIYK
		1		1		KKTNNPIKKWAKDM
27525	57893	A	27691	I	2781	MGKKQNRKTGNSKKQ\$ASPPP
1		1		1		KERSSSPATEQSWMENDFDEM
1		1		1	1	REEGFRRSNYSELREDIQTKGK
1		1				EVENFEKNLEECITRITNTEKCL
	İ	1		İ		KELMELKTKARELREECRSLRS
		1		I		RCDQLEERVSVMEDEMNEMN
		1				DGENGTKLENTLQDIIQENFPN
		1	İ			LARQANVQIQEIQRTPQRYSSR
		1	1			RATPRHIIVRFTKVEMKEKMLR
1		1		i		AAREKDFKPTKIKREKEGHYIM
1		ŀ				VKGSIQQEELTILKIYAPNTGAP
1						RFTKQVLSDLQRDLD
27526	57894	В	27692	I	756	
27527	57895	В	27693	I	1743	
27528	57896	Α	27694	I	1407	
27529	57897	Α	27695	3	391	
27530	57898	A	27696	604	955	SSVFLGDPPILIGNKEMCLSSVL
1	1	1	1	1		LINGSINFLHPFREDKGAVDVP
	1			1		GVATQQLILLNDPVLTASEILG\
1		1	1			LVSSLSK*TSPPIPGPGGNA*AR
	1	L.	L			QPSCP*KGELSWRSAPSLVQFSS

SEO ID	SEO ID NO:	34.4	SEQ ID NO:	North-Mar	Nindestide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
110.	sequence		09/540.217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,			sequence		
27531	57899	Α	27697	I	1783	MGARAGGSCSCLMWLLLASG
						HFMGCVAAGDTVGPEKFRSCY
						TITLLQSKLSYSFGKNNKNFQL
						RKCLQTVDNLFVPNQNGYYCH
				ł		SQTSLDRAQIDLNGRIRNGSVY
						SAHSTNSLNNPQPYLQPSPMSS
				l		NPSITGSDVMRPDYLPSHRHSA
				l		VIPPSYRPTPDYETVMKQLNRG
					l	LVHAERQSHSLRNLNIGSSYAY
i		1		1		SRPAALVYSQPEIREHAQLPSPA
		ł				AAHCPFSLSYSFHSPSPYPYPAE
1						RRPVVGAVSVPELTNAQLQAQ
1				1		DYPSPNIMRTQVYRPPPPYPPPR
	}	1		1		PANSTPDLSRHLYISSSNPDLITR
						RVHHSVQTFQEDSLPVAHSLQE
	ľ					ERSSSPATEQSWTENDFDELRE
		!		ŀ		EGFRRSNYSELREDIQTKGKEV
ì		1				ENFEKSLEECITRITNTEKYLKE
						LMELKTKARELCEECRSLRSQC
						DQLEERVSAMEDEMNEMKRE
l		1				GKFREKRIKRNEQSLQEIWDYV
1		l			l	KRPNLRLIGVPESDGENGTKLE
1		l		i	1	NTLQDIIQENFPNLAKQANVQI
		l			1	QEIQRTPQRYSSRRATPRHIIVR
				1		FTKVEMKEKMLRAAREKGRVT
1	l				1	LKG/ITHQT/RQRISRQKLYKPEE
					1	SGGQYSTFLKKRIFNPEFHIQPN
27532	57900	Α	27698	3	1046	
27533	57901	Α	27699	I	3585	
27534	57902	A	27700	937	1119	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nuclcotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
		L				
27535	57903	Α	27701	1	2231	MGKKQSRKTGNSKKQSASPPP
						KERSSTPATEQSWSENDFDELR
						EEGFRRSNYSKLQEEIQTKGKE
				1		VKHFEKNLDECITRITNREKCL
						KELMELKAKARELREECRSLRS
i						QCDQVEERT\LARLIKKKREKN
1						QIDAIKIDKGDITTNPTETQTTIR
	i	l				EYYKHLYTNKLENLEEMDKFL
						DTYTLPRLNQDDVESLNRPITG
ŀ		ĺ				SEIEAINHSLPTKKSPGPDRFTA
		ļ.				KFYQSLPSSCDYGHAPAHPDVF
						RVSSFWWVRGLAGSGVKLQTF
		1				AVSVTALKAARLELFIPPDSGA
		ı				QLASPSGSLTRTGGGAACQSHA
						VCPHSSAFGWSMGLGAMEQG
						AALIGEARASREPMEEVGGSG
		ı				MAACRSQALPRGQLRPSEKSRA
1		1				APEHSSSPAMEQSWMENDFDE
		1				LREEGFRRSNYSELREDIQTKG
		1				KEVENFEKNLEECITRITNTEKC
		1	i	1		LKELMELKTKARELREECRSLR
1	İ	l		]		SRCDQLEERVSAMEDEMNEMK
l		l	1			QEGKFREKRIKRNEQSLQEIWD
		l				YVKRPNLHLIGVPESDGENGTK
		l				LENTLQDIIQENFPNLARQANIQ
		l				IQEIQRTPQTYSSRRATPRHIIVR
		l	1			FTKVEMKEKMLRAAREKGDSV
		l				ERSFSNKAELLFQLHGHQRESL
		l				SKKEAQVWRDKGLYFRKGLLD
		1		1		QAQSWSRQVASILGAQIQVEGS
İ		l		i		PEORLENVELAGGHLNTLKAIP
		l		l		MVAVAGGISFKCGAVLLLGAA
27536	57904	A	27702	596	1593	KPRLENYVKNAEASGANAINW
2,330	3.704	ľ.		1	1.555	KKGY/LVMEDEMNEMKOEGKF
		1				REKRLKRNEQSLQEIWDYVKR
i		1				PNLRLIGVPESDGENGTKLENT
		1				LQDIIQENFPNLARQATVHIREI
1		1				ORTPORFSLRRSTPRHIVRFSKV
		1				ETKEKMLRAAREKEIQTTIREY
		1				YKHLYTTKLENLEEMEKFLDT
		1				YTLPRLNQKEVESMKRPITSSEI
1	l				1	
1	l	1				EAVINILPIKRSPGPDGLTATFY
1	1	1				QRYKEELERSSSPATEQSWMEN
1	1	l				DFDELREEGFRRSNYSELREDIQ
1	1	l		I		TKVKEVENFEKNLEECITRITNT
1	1	l				EKCLKELMELKTKARELREECR
	L	ᆫ				SLRSRCDQLEERVSAMEDEMN

sequence 09/540,217 codon for peptide o sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) STGRKAPHHTYSKIDHILGSKA
sequence		
27537 57905 A 27703 717	1803	CTCDVADIUTVCVIDIU COVA
		ISTURNAPHHTYSKIDHILGSKA
		LPSKCKRT/E/IITNCLSDHSAIKL
1 1 1 1 1		ELRIKKPTONPSTTWKLNNLLL
		NDYWVNKEMKSEIKMFFETNE
		NKNTTYONLWDAFKAVCRGK
		FIALNAHKGKQERSKIDTLTSQ
		LRELEKQEQTHSKVSRRQEITKI
		RAEPKEIETOKTLOKINESRSWF
		FERINKIDRRLARLIKKKREKNO
		RDAIKNDEGDITTDPTEIOTTIR
		EYYKHLYANKLENLKEMDKFL
		NTYTLPRLNOEEAESLNRPIAGS
		EIVAIINSLPTKKSPGPDGFTAEF
		YORYKEKLVFGAGYFGMWAL
		AALPSNLLKLSOLCOEAAEVNV
		LVOFVCICPAQEPTEIDVLFSVL
		PPLSLILN
27538 57906 A 27704 407	1696	NILRNAVPHQQQNKA*RRMTL
		TS*EKKASDDQTTPSYRRKFKA
		KAKKLNT/YEKNLDECITRITNR
		EKCLKELMELKAKARELREEC
1 1 1 1 1		RSLRSOCDRLEERVSVMEDEM
		NEMKREGKFREKGIKRNEQSL
		OEIWDYVKRPNLHLIGVPESDR
		ENGTKLENTLODIIOENFPNLAR
		OANIQIQEIQRMPQRYSSRRATP
		RHIIVRYTKVEMKEKMLRAAR
1		EKGRVTHKGKPIRLTADLLAET
		LOARREWGPIFNILKEKNFOPRI
		SYPDKLRFISEGEIKYFTDKOML
		RDFVTTRPALIEALKEVLNMER
		NNRSPSSSPATEQSWMENDFDE
		LREEGFRRSNYSELREDIOTKG
		KEVENFEKNLEECITRITNTEKC
		LKELMELKTKARELREECRSLR
		SRCDOLEERVSAMEDEMNEMK
		REGKFREKNNKKK
27539 57907 A 27705 2597 5	5904	
	675	
	1357	
	1032	1114

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27543	57911	Α	27709	3	959	MANNPGANGQ\PGGPGGPGMG
		1		1		KPRCF/RGEVFGIVIRGRGSRP/R
				!		GRGRGR\GRGARG\$KGRG*RE
						WNAVHQVGAALVKDH*RSKFP
						WKEIYLFSLPH*RNQRIIDF\FLG
			l			GLLSKDEGFE*LCPVQKQTRA\
						GQPHPGFKA\FVAIGDY\NGHV
				l		GLG\VKCSKE\VATGHPVGAII\L
	İ			l		AKLSIRPRCAEGYLGNKVLAKP
				l		\HTVPLQGDKGRCG\\$VLVRLH
,				1		PLHPRG\TGI\VSAPVA\KKLLM
						MA\GIDDCYTLS/ARGCTATLG
ŀ	1					QIWPRAT\FDAISKTYKLP*PPD
		1		l		LWKETVFTKV\PYQ\EFT\DHLV
						KDPHPESSVQQDSELQLVATT
27544	57912	В	27710	50	1598	
27545	57913	Α	27711	1	3916	
27546	57914	A	27712	334	462	PAFITVNKCSSARKLIQV*GPVA
						CRVHILPLVVRCPPKPGTTG
27547	57915	Α	27713	256	654	
27548	57916	Α	27714	i	855	
27549	57917	A	27715	211	436	
27550	57918	A	27716	19	319	
27551	57919	A	27717	987	1392	RHCLCSPSRSSESLQPTASSSSA
		1				RSSPSPPASQPVPPGPAGAAAAP
l						HPPCCPPESTCWTWPC*SPLCH
		1				WAVA*ARSGPGPLGECFETHGP
	l l	1				HGCPPGQSPRPPQ*APSAWWTE
						VQPR*PRPAPEGSSRRPPPPGAP
27552	57920	A	27718	285	1266	RSQIQRGTDRAPKCTSGPP\HRV
						AOPODDAPREEPPYLPNGMPPG
	l .	1				RDAPHLPDWAASQRGSSHPRR
	1	1			ŀ	WPPSORRSLLPRRVADRPEAAI
	i					SALWEAKAGGWETLPEMEITIH
		1				NKTRQSKRITHQTNRPNTSSKTI
		1				RITKTDLTSWETQSPGSPDRHR
					i	KPSTATKHNRFSKIYSRFSIFOC
		1				DOGLNGRCGQGKGAGKEQRM
						QEQGENFQAPPFQSHPALRSLQ
ľ		1				MOOVOTEEHFGTLECGKLAQC
ŀ						SFHPTREEDRNQDGKTDMLHF
ŀ						KLELPLOSTEHVLGVOLILTFSY
						RLHSCGIPSVLSRYPYFSMLAFG
						ILSRTLRRFVTVSSLLITGI
27553	57921	A	27719	1518	1779	ARSGPGPLGECFETHGPHGCPP
27333	3,921	1"	2,,,,,	1510	'''	GOSPRPPQ*APSAWWTEVQPR*
l	1				1	PRPAPEGSSRRPPPPGAPCPAQP
l	1				1	PTRRCPGRHQTPPAAGAAVP
27554	5 <b>7</b> 922	A	27720	507	1114	. Hatel Glary III Alloway
27555	57923	C	27721	80	223	
ددداعا	21923	1	21121	lov	LLJ	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27556	57924	A	27722	li .	2373	
27557	57925	A	27723	2	272	RARTPPLWPRARGPGSRVSGAP
						WFLLDLAGGGFLPPAVLCDLSA
						ASSTVSGRSNPHC*AWGGLEFF
				l.		GEVERAESGFPVPEPSLISEMPH
27558	57926	Α	27724	195	489	
27559	57927	Α	27725	210	1308	
27560	57928	Α	27726	203	474	
27561	57929	Α	27727	224	892	
27562	57930	A	27728	l	457	
27563	57931	Α	27729	3	1325	
27564	57932	A	27730	322	512	
27565	57933	Α	27731	621	737	
27566	57934	Α	27732	441	588	
27567	57935	Α	27733	1	792	
27568	57936	Α	27734	8	488	SGCRNSARADADPSLHASPPAP
		1				TMATVQLLEGRWRLVDS\KGF
		ł		l		DEYMKE\LGVGIALRKMG\AMP
		1				KP\DCIITCDGKNLT\IKTESTLK
		1				TTQFSCTLGEKFEETTADGRKT
		1				QTVCNFTDGALVQHQEWDGK
		1				ESTITRKLKDGKLVVECVMNN
						VTCTRIYEKVE
27569	57937	Α	27735	861	2161	
27570	57938	Α	27736	349	625	
27571	57939	Α	27737	1	630	MAQETNHSQVPMLCSTGCGFY
	1	1				GNPRTNGMCSVCYKEHLQRQN
	1	1				SSNGRISPPATSVSSLSESLPVQC
	1	1				TDGSVPEAQSALDSTSSSMQPS
	1	1	l	ł		PCIK\QSLLSESVASSQLDSTSVD
						KAVPETEDVQASVSDTAQQPSE
		i				EQSKSLEKPKQKKNRCFMCRK
		ŀ		ì	1	KVGLTGFECRCGNVSCES\HRY
			l			SDVHNCSYNYKADAAEEN/LE
				l		KENPVVVGEKIQKI
27572	57940	Α	27738	1	1089	
27573	57941	A	27739	41	334	AGKMTKLEEHLEGIVNISPQ*S
	I	1				VRKGHFDTLSKG\ELKQLLTKE
	I					LANT\IKNIKDKAVIDEIF\QG\LD
	İ	1				ANQDE\QVDFQEFIS\LVAIALK
						AAHYHTHKE
27574	57942	Α	27740	1	519	
27575	57943	A_	27741	28	314	
27576	57944	A	27742	208	421	
27577	57945	Α	27743	619	890	
27578	57946	A	27744	113	328	LGSGA WGGGDLPWEINPLSSCS
						LLREKDLLTTSGPQT\TSPRNISP
1						ILNRDPTVQLTWQPLPEPLELW
		_				PKAL
27579	57947	Α	27745	501	680	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
27580	57948	Α	27746	166	405	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQ\PRNISPISNRD PTGKWTVQLTRQPLPEPLELWP KALRLTPSQIFSA
27581	57949	Α	27747	425	484	
27582	57950	Α	27748	448	520	
27583	57951	A	27749	3	679	GGGFSDRDRTIALDPOQQIWM WGIGKQVGCCGWLRGKNRVV GAAKDQSGTGEKPYFIPKAMG AMEGSQRRTLPDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLREKD PPTTSGPQTVTSPRNISPILNPELA TLAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP EPILEWRALD
27584	57952	A	27750	3618	3848	NLCKEPSSRRSIHKESLLNFPLM GLDPRPQEGFPRDSPR*REESTS LHDPMASSSSTVFWGLKRQKY FLWPFRAST
27585	57953	Α	27751	1	297	
27586	57954	A	27752	244	420	RKETKERSRTPP*SPRTGQMTP CKLQPGVLSFPRTAQSWEPPAV PQSPLKNELRRKYLT
27587	57955	Α	27753	1993	2205	
27588	57956	Α	27754	138	833	
27589	57957	Α	27755	1	875	
27590	57958	Α	27756	1	1041	
27591	57959	Α	27757	3	1447	
27592	57960	Α	27758	23	3257	
27593	57961	A	27759	2	168	GKAGCWPRSRARKCRTSSPSIW AAWRPPTR*LTVTSRPGTSGSE PWAMAAASRWQ
27594	57962	Α	27760	85	1271	
27595	57963	A	27761	5871	6056	TSSAASTAPRWRRKPHGHQKSL PASLRFPGR*TPQPDLPGPPAQP PAQPGPPQAATVPGRW
27596	57964	Α	27762	1	280	
27597	57965	Α	27763	1	714	
27598	57966	Α	27764	2	558	IRRAHACARRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IA VDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG`LFADK VPKT AENFHALSTGEKGFGYKGSCFH RIIPGFTCQSGDFTRHT/GIGGKS ICREKFDDKNFILKHTGPGILSM ANAGPSYNV

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	ł	
27599	57967	A	27765	11	927	GTRDATAEENRVLLAMVNPTV
		1		1		FFDIAVDGEPLGRVSFEVRGLD
i		l				TKK*LLI*SIKLC*QIGGSSIFITS
						D*KNSCLPLIVQQCLLFLRILP\L
						FADKVPKTAENFRALSTGEKGF
						GL*GVPCFHR\IIPGFM\CQG\GD
		ĺ				FTPP*MAPGGKSIYGEK\FEDEN
						FI\LKHTGPGILS\MANAGPNTN
		1				GSQFFICTAKTEWLDGKP\VVF
		l				GK\VKKGLNIVEAMERFGSRNG
		l				KTSKKITIADCGOLLISFDLCFIL
		l				NHQDHSFCALLSGEHPSTPFAR
		1				RILRILWLSLQFLWGSMFSLFPP
		ı				MPSWIAAVKFMIIEIKTK
27600	57968	A	27766	1	798	
27601	57969	Α	27767	1	575	PTRPPTRPPTRPIMAODOGEKE
		1				NPMRELRIRKLCLNICVGESGD
ł		l				RLTRAAKVLEQLTGQTPVFSKA
1		l		1		\RYTVRSFGIRRNEKIAVHCTVR
		1				GAKAEEILEKGLKVREYELRKN
l						NFSDTGNFGFGMQDHIDLGIIY
		1		1		DPSIGIYGLDFYVVLGRPGFSIA
			Ì			DKKRRTGCIGAKHRISKEEAMR
				1		WFQQKYDGIILPGK
27602	57970	Α	27768	1	1695	
27603	5797 I	Α	27769	1	228	
27604	57972	Α	27770	1098	1938	IWPRPRDC/RVSYTTVFPPATVT
						APV/VSGGSHDHIQQYSDIEDFR
						QATAASSVMVARAAMWNPSIF
				1		LKEGLRPLEEVMQKYIRYGGM
				1		GAALLSDPDKIEKAPSMGTLM
ļ						GVYLPCLQNIFGVILFLRLTWM
				l		VGTAGVLQALLIVLICCCCTLL
1						TAISMSAIATNGVVPGYLHTLV
				l		QNLVNNGYVRDETVRAAPYD
l						WRLEPGQQEEYYRKLAGLVEE
						MHAAYGKPVFLIGHSLGCLHLL
						YFLLRQPQAWKDRFIDGFISLG
27605	57973	L	22771	1	1710	APWGGSIKPMLVLASGSGTRA
27605	57973	A	27771	163	1659	
27607	57975	A	27773	3	297	
27608	57976	A	27774	3	447	SSPHSSRSLSAPPLPGLPLWRHL
[		1	I	ľ.		RSPSAHRCTVGAPFWAGEGRSP
I			l			LPQLAGRCGGRRASGNRG\ARG
l				1	1	ACGPAGVPGGRGLGGPALGAA
			1	I	1	GRPGP*LPSRGAGLGTA/GPPCL
			İ			SLPPPPWVPVOPEPPRRAPPPAP
l						RRPVPSTAQGLRSASA
	<u> </u>	_	L		L	INQUERONON

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27609	57977	IA	27775	13	197	RPDA VPARSLEMKRFPMPPPPP
				[		G*FSPGASLDVNPGCYKOAPSC
						SLAQILSNLSNLWSSAVSNF
27610	57978	A	27776	77	379	GRLLDKAGIPH/PPFPSGGLGCO
2,010	51770	1	2,,,,	1"		H*RRSPLHEHPSSGP\PAGLKPS
1		İ		1		LSCLPAGQGSGPAARY/GLSLPP
1		1				TPWAPVOPEPPRRAPPPAPGRS
				l		VPSTTOGLRSASA
27611	57979	A	27777	177	444	RGGQGSGPAACYA*/RLPPTPW
		Γ.		1		APVRPEPPORAPPPAPRRPVPST
	1			1		TOGLRSASTRRVTGRQLHLQP
		i		1	l	WCGIHWVKPAGLLSLVGRWRV
						LMS
27612	57980	Α	27778	165	591	ORAGSPHSPRSLSAPPLPGLPLW
				1		RHLRSPSAHRCTVRAPFWAGO
ł		ı				GRSRLPQLAGRCGGRGASGNP
1		1				G\SHGACGPAGVPGGRGLGGPR
				1		TGSSOLALPAPGNEGLSTPASG
		1		ı		RRKKLRTHPSIRRNKLQTRYLK
		1		1		SCNTHREGPRLH
27613	57981	Α	27779	1	1605	
27614	57982	Α	27780	2	1970	
27615	57983	Α	27781	1	3522	
27616	57984	C	27782	183	254	
27617	57985	Α	27783	39	346	QYISELQFLASTVRQTPATSPAH
		1				KNFQTPEPQQPGIPPEPPPGAC
		1				YKCWKSGHQAKECLQPGIPRK/
		ı				HASHLWQPLPEPPGTLAQGSLT
		<u> </u>				DSFPDLLGLAAED
27618	57986	Α	27784	1	354	
27619	57987	A_	27785	72	299	
27620	57988	Α	27786	273	530	LGSGDLPWGINPLSSCSLLREK
				1		DPLTISGPQTHQPKEHLTNFKSG
			1			PH*KSDCSTAPG\ATPRAPGTLA
						QGALTDSFPDLLSLAAED
27621	57989	Α	27790	1	1068	
27622	57990	Α	27791	148	527	
27623	57991	Α	27792	2	1910	
27624	57992	Α	27793	1	1047	
27625	57993	Α	27794	96	488	WDRMAGGSSNTFGFPPPPLPYR
-						SCER*QRDGGPRSPGSLSVPPW
ŀ						PR/PPILAALEEPFSPPLHRGRPS
		1		1	1	LGWPRPELAPSAQRSAAS/RPEA
1		1		1	1	SKDHEPTRKKE/PTPDTQP*EL*
	<b></b>	1		<u> </u>		HSLPRSSASLALGPHYLYEL
27626	57994	A	27795	3	2086	
27627	57995	Α	27796	3	412	
27628	57996	Α	27797	2	390	

SEQ ID NO:   Met   SEQ ID NO:   No:   Nucleotide	t codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
sequence	ide of peptide sequence	deletion \=nossible nucleotide invertion)
	I	
27620 67007 A 22708 I	li .	
	1629	MKVGLDQIIEVVPSHSVTSGAA
27025 37777   1 27750   1	025	AGECGGVHCDSVCAEGRWGPN
	l	CSLPCYCKNGASCSPDDGICEC
		APGFRGTTCQRICSPGFYGHRC
		SQTCPQCVHSSGPCHHITGLCD
	ŀ	CLPGFTGALCNE/RLFTVCPSGR
		FGKNCAGICTCTNNGTCNPIDR
		SCQCYPGWIGSDCSQPHCADKC
		VHGRCIAPNTCQCEPGWGGTN
l <del>  </del>		CSSVKKQSTVCES
27630 57998 A 27799 108	1071	YPLFLSSISACDGDHWGPHCTS
		RCQCKNGALCNPITGACHCAA
		GFRGWRCEDRCEQGTYGNDCH
		QRCQCQNGATCDHVTGECRCP
		PGYTGAFCEDLCPPGKHGPQCE
	i	QRCPCQNGGVCHHVTGECSCP
	ł	SGWMLSFPGWRPI*FSKSL*MQ
		GTVCGQPCPEGRFGKNCSQECQ
		CHNGGTCDAATGQCHCSPGYT
		GERAAVPDVRK\CQDECPVGTY
		GVLCAETCQCVNGGKCYHVSG
		ACLCEAGFAGERCEARLCPEGL
		YGIKCDKRCPCHLENTHSISLIA
1 1 1 1		AKKSNSLHAIALDFRAQCQSVK
		DRCHASDLPIDIVSTETLR
27631 57999 A 27800 243	1296	ETQEESSEFLPCGSHQPNG*LLF
		CSTYKRCLCNWGPC*AY*RACF
		CPALQQCPDI/CPQAQLAIPCAP
1 1 1 1 1		QQQQLSRCLSFPSSLLQDPNTP
		G/EYRKDEGRAGSRGAGEKQC
		THNSPRWLQNTVSNQGSSMPG
		FQSHVPSLLGAFVQCTNCTRVC
		SSPANKIFTTFRLGDPLVSPCHO
		GFGSNTHCCVESWQSSCSGMH
1 1 1 1		KDLGALHTPAPGSPTNVAATO
		ARREPRCRLAVLSTLDRSTROK
	į	VNKDIQELNSALHQADLTDIYR
1 1 1 1		TLHPKSTEYTFFSEPHRTYSKTD
		HLVGSKGLLSKCKRTEIITNCLS
		DHSAIKLELRIKKLTQNCSTTW
	1	KLNNLLLNDYWVHNEMKAEID
27632 58000 A 27801 552	827	
27633 58001 A 27802 70	200	
27634 58002 A 27803 18	1057	
27635 58003 A 27804 652	960	
27636 58004 A 27805 1	474	
27637 58005 A 27806 1	140	
27638 58006 A 27807 1	1260	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
	<u> </u>	丄		l		
27639	58007	A	27808	126	893	EDGSGGGKFPEGARQGGTGQR
						RRRKAMRRTGAPAQADSRGRG
	1	1				RARGGCPGGEATLSQPPPRGGT
	i					RGQEPQ\MKETIMNQEKTRHTC
		1				RHKVRIGGKGTARKKKKVVHI
	1		l			TATA\DDKK\LQFLLKGS*GVN
						NISGIE\EVNMFTNPRNKLIHF*Q
						PLKVQGISWAANTFHHLQGHA
	1					*DKSSWTEMLPSIFKPSLGAG*V
		1				*LVLRRLA\EALPQTNLWDGKS
	1	1				TTLLLGEDDGDDDESSQILWEY
l		1				FGWRVPRNEANLNLSSTF
27640	58008	A	27809	180	589	KELPLLIFCRWOFESLHELNVPF
2,040	20000	1	2,000	100	507	FKVGSGDTNNFPYLEKTAKKG
						SPNGDLPVGCKSNGHP*SKFIRS
						VKPLNPOLLASLOCTSAYPLOP
						EDVNLRVISVSRREGVPFLGHL
	i	1				LWGRRSLFYNONSNKHGILYN
27641	50000	<del>-</del>	27010	623	1002	LWGRRSLFTNQNSNRHGILTN
27641 27642	58009 58010	A	27810 27811	548	1082 645	
27642		A	27811	329	510	
27644	58011	A	27813	3254	3628	
27644	58012	A	27814	3254	960	
27646	58013	A	27815	349	681	PMASNRAITLTAWPKIPFLGICE
27646	58014	l <sup>A</sup>	2/815	349	081	
	1	1				AKNPRSENMRL/AHHFGSGLPP
1		1				SWELWEQGPPGNSSRYIEFLNK
l	1	1				HTYIKGTLRVYTKKFCMLVIKS
		_				FESKSCVWRYDFDSKSSVNVTV
27647	58015	Α	27816	240	473	
27648	58016	Α	27817	825	1043	
27649	58017	Α	27818	2	418	GKVVCFEAFLQQILGKHQFYW
	1	1				CLEGLGHCHHHIGAKYPEDIVD
	1					EESAQQDAASADIVEVQELYSI
	1	1				KGEGQAKKVVGNPVLPQQVPD
	1					ANDAAQAQAHQVLGVKFIIDD
	1					L*AERPGKSTP*GRATPPTFLVF
						PRTLCEGI
27650	58018	A	27819	2	427	
27651	58019	В	27820	51	672	
27652	58020	Α	27821	43	667	
27653	58021	Α	27822	516	1056	WSRAPAPQQCQHWLHPAGRTL
		1				HLRCLLGIWHQCDGDSGQVLR
						GTNENLVFPQDLLEKGLEANNF
	1					AMLGTWEMSSFPGIFIALLLRF
1	1	1	1	I	i	DISLKKNTHTYFYTSFAAYIFGL
		1			1	GLTIFIMHIFKHAQL*GVKS*GS
1	1	1		1		SGSDRIQRGNRGISIEGAGEERE
		1		I		MMQLVPEPLRARPDRWGLGPH
		1		1		RRA
27654	58022	A	27823	1	1019	
27655	58023	A	27824	1061	1258	
27055	150025	1~	2,027	1.001	12.0	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
Ì	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27656	58024	Α	27825	44	621	
27657	58025	Α	27826	406	727	
27658	58026	Α	27827	2	1337	
27659	58027	Α	27828	1236	1391	
27660	58028	Α	27829	228	502	
27661	58029	Α	27830	I	1035	
27662	58030	A	27831	146	392	GHRSHQSPEETPNLIPRTPIPPLG
ŀ				•		TGTSIRSTRIPRTEASGPNGLN\
		1				WYLTPTPPGGQRPSSAASPRGF
						PPTNNSSRLPAEPE
27663	58031	A	27832	15	300	
27664	58032	С	27833	289	414	
27665	58033	A	27834	3	576	AALAERWLGEVLVRVGVRVPG
		1		-		GSGGLRHWCPCGLLGRGLGOA
					l .	PEHKVRLSMEFCSTCTADHISLS
1						SFWRSSFQQPLVPAVSLQSPDR
						RLSHDPAASSWSGFCGISPAFSA
1	l			İ		FSECSPSSLRSHPPALLOAAES*
	1	l				FAASSSPSPTWSLSGSGTRKPW
		l				S/VACNWLLSDSSSHRRSFWES
						GIITMVLALTLEELV
27666	58034	A	27835	h	231	DELLVGGNPRGDAAEEGRCPP
27000	38034	<u>۱</u> ^	27033	i'	231	GGVGVRYQIQPIWPRRLCSRNP
i	ŀ	l				GAAD*GPGS*RWDRCPRDEIWR
						FLGALVGSVSSG
27667	58035	A	27836	18	398	KVRWERSWSESESESQEGRRR
27007	38033	<u> </u> ^	27830	l'°	398	AQALVPSVAS*/SSRPWDRPPST
		1				K*GCLWSSAARAOOTIYHSVPS
1		1				GGHPSSSHWLPAVSLOSPDRRL
1		1				SHDPAASSWSGFCGISPAFSAFS
		1				ECSPSSLRSHPPALGSF
27668	58036	A	27837	1059	1446	AVWSLPAPPAPCLLAGLLCTCC
2/008	38030	Ι^	21631	1039	1440	RTP*TASLCARGPVPRPRA*EAT
1				}		RGTSA*ALHSPPGTLTPTVTRTS
						PSHLSARAAAPSHPARPTASRSS
		1				
		1	ļ			RLPAWLAVRLSIPPRRGSLGGA
		L				GAQAAAASTRFTCCS
27669	58037	Α	27838	1	211	ATALAERWLGEVLVRVGVRVP
		1				CGEWRAQALVPIVAS*ATRPSG
		1				RGPPTQQT*RTSRIGRS*QTTMR
		_				HART
27670	58038	Α	27839	316	537	
27671	58039	Α	27840	255	475	RPWVRAPYKLLPALLHAPLCAP
		1		1	1	PSSPWRPV/PASAPSFKLLKS*IF
		1		1	1	CKQLSLLPTWSLSGSGTRKPWS
		<u></u>				GPVTGS
27672	58040	Α	27841	622	1127	
27673	58041	Α	27842	364	666	

SEO ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
27674	58042	I <sub>A</sub>	27843	37	299	ILLCSVOTLPLLRREFYGHIPKC
2/0/4	30042	l^	2/043	P'	247	OOSLNIICSPSSLRIPGFLHRNRL
		ŀ		1		STPFHVQQPQREHF*YCRSQIH
1	i	1		1		GENSAWHIRSHHAEKAHF
27/75	50042	<del> </del> -	07044		428	PAEIERSTAKTPGPPGSLEMGLL
27675	58043	Α	27844	84	428	
				1		TFRDVAIEFSLEEWQCLDTAQR
1		1		1		NLYKNVILENYRNLVFLGIAVS
		1		1		KQDLITCLEQEKEPLTVKRHEM
		1	ľ			VNEPTGPRQKRRVTSSR**MKR
		_				YVII
27676	58044	A	27845	1	719	
27677	58045	Α	27846	669	830	CLVQNQNIFC*ILS*WSSLV*QS
		1		1		ACRQLMPLLHLPNDQQAPVWT
				1		ENQPGGHWR
27678	58046	Α	27847	223	382	CLVQNQNIFC*ILS*WSSLV*QS
		1		1		ACRQLMPLLHLPNDQQAPVWT
						ENQPGGHWR
27679	58047	В	27848	1	491	
27680	58048	Α	27849	1	1113	
27681	58049	Α	27850	505	1105	ITCTLYPSLRIVYEAFPATGDNM
l		ı	i		1	FRRIIKDALFRTIQFCQIMNRSQ
l	1	ı		1		YMFTCRCRTEMQVPQHRRKKT
		1				FKPTVLLNHFVMEIIVLTAGRID
1	1	1	Ì	1		AAFQDEVAASEGFLKQPVGKD
1		1				YKFGGPSVKDEKLFGVGTGMG
}		1	1			HHN*LSV*TSIQHLLSNTQG/CL
ŀ	1	1			1	RVCPALRL/HSRNLSAMVISFSF
		1				SCGARSAISPINARKRWASPVC
27682	58050	A	27851	1	2697	
27683	58051	Α	27852	1	1998	
27684	58052	A	27853	864	1025	CLVQNQNIFC*ILS*WSSLV*QS
		1				ACROLMPLLHLPNDQQAPVWT
		1	į			ENOPGGHWR
27685	58053	Α	27854	1605	1766	CLVONONIFC*ILS*WSSLV*OS
		1	ł			ACROLMPLLHLPNDOOAPVWT
		1	i			ENOPGGHWR
27686	58054	A	27855	677	735	
27687	58055	A	27856	1126	1568	SSSSTGRSRHKEVSPGCOODGL
		1				RCQEWWSVRPG\YEATGGVWG
l		1	ł			KOLGIPASGLPGRRSSESPRKSC
1		1				TPVTSRTGLPVCPWAALSPESR
1		1				SFSLSVRPVCVC\CVGTKMSCA
		1				PECCFFLVSLSLLSLFLRLLGL
1		1			1	AAHCOFFPAVPLCIL
27688	58056	A	27857	1142	2450	MAINCOFFFAVELCIL
27689	58057	A	27858	1142	1131	
27690	58058	A	27859	229	402	
27691	58059	A	27860	505	597	<u> </u>
27692	58060	A	27861	1303	657	-
27692	58060	A	27862	248	382	QPPKITLLYQQWIQTKKKSLKS
2/093	28001	^	2/802	248	304	FLP*QEFRKMQKKHSTKSSITL
				1	L	LEL GELVUMÁVVUO I VOOLIT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27694	58062	Α	27863	1	1341	
27695	58063	A	27864	1	739	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSOHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTTVQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKTSRQEITKIRAELKEI ETQKTLQKINECRSWFFEKINKI DRFLARLIKKREKNENDOJIKN DKGDIITDPTEIQTTIREYYKHL
						YGNKLENL*H*MPTRESRKDLK LTP*HHN*KN*RSKSKHIQKLAE GKK*LRSEQN*RK*RHKKPFKK SMNAGAGFLKRSTKLIDR
27696	58064	Α	27865	1	1920	
27697	58065	Α	27866	444	763	
27698	58066	Α	27867	1	651	LE L. D. W. L. OR D. D. G. W. W. W. W.
27699	58067	A	27868	94	964	VNADWVLQRELEQTSLWSSKQ ARACCI.SHVVGIRMISSCTTRKM AEEEQRKIPLVPENLLKKRKAY QALKATQAKQALFGKEGAEER KRAQWFKELESFLHDSLAAET *QG/RISROLEVQPHALELPDKC SLAFVVRIKRIDGGSLLVQRTIA KLCLKKIFSGVFVVKAPPRIQKW LRIVEPYVTWGFPNLKSVRELIL KRGQAKVKNKTIPLTDITVME EHLGKRGVICLEDLIHEIAFPGK HFQEISWVLRPFHLSVAHHATK NRVGFLKEMGTLGYRGERINQ LIRQLN
27700	58068	A	27869	176	334	
27701	58069	A	27870	3	452	AASTGGGSHLLLSIMAALRPLV KPKIVKKRTKKFIRHQSDRYVK IKRNWRPRGIDNRVRRFRGQ ILMPNIGYGSNKKTKHMLPSGF RKFLVHNVKELEVLLMCNKSY CAEIAHNVSSKNRKAIVERA\A QLAIRVTNPNARLRSEENE
27702	58070	A	27871	2	423	
27703	58071	В	27872	193	1698	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27704	58072	A	27873	263	714	KLNVPIIKATNTIMNMTMNLK MSLTAPPSDICRGPKLSFAGKIQ
			l	l		AIPEKLKTTATAORPLDTIGLEV
					1	PVPAAWLLSAVRNCSKLRATS
						GPNLDTMNGSRROTGSWTEGS
			i	l		RSSMKPHLLSDITGALR/SPKVS
1				l		*AFCRLATWPFNFLQSGILS
27705	58073	A	27874	347	902	
27706	58074	A	27875	17	1178	
27707	58075	A	27876	1	1155	
27708	58076	Α	27877	3	1109	EKETMQSLNDRLASYLDRVRS
ŀ						LETENRRLESKIREHLEKKGPQ
						VRDWSHYFKIIEDLRAQIFANT
						VDNARIVLQIDNARLAADDFRV
		1				KYETELAMRQSVENDIHGLRK
		ł				VIDDTNITRLQLETEIEA\LKEEL
		t			İ	LFMKKNHEE\EVKGLKTPNYA
		1		1		ALG*T\VEVDAP\KSQDLAKI\M
		l l				ADIR\AQ\YDELGSERTERKLDK
	1	1				YWSQQIEESTTVFTTQSA\EVGA
		l			l	AETNLHRSLKRTV\QSLEDRPW
		l				TSMRNLKAQLGEQP*GEVEAPL
		1				RPTRWSQLNGILLHLES\ELAQT
		l				RAEGQRQA\QEYEALLNIKVKL
i		l				\EAEIATYRRLLEDGEDFNLGD
		l			1	ALDSSNSMQTIQKTTTRRIVDG
		Ļ				KVVSETNDTKVLEALSQQKAG
27709	58077	A	27878 27879	209	1305 560	
		A				
27711 27712	58079 58080	A A	27880 27881	219 528	512 803	
27713	58080	A	27882	3	432	SSPCVEFSTSMGACLRPATARSP
2//13	38081	l <sup>A</sup>	27002	3	432	SATCTAWTCTGWRRGRPWWR
		l				WTPENSGVAGGDGTSEEDSEE
		l				VEGAEWWGRRRRQRRGERCG
		l				GLRRAPCQGAPGKCLCPRPP\GP
		l				SPC*/CEALGAQRAS*PHRRELK
		l				VGGPGPGCELSPMV
27714	58082	A	27883	117	483	, act of Goldon M v
27715	58083	A	27884	1	1497	
27716	58084	A	27885	228	776	
27717	58085	A	27886	1012	1677	
27718	58086	Ā	27887	194	562	
27719	58087	A	27888	1	423	
27720	58088	A	27889	232	308	
27721	58089	A	27890	1	1692	
27722	58090	A	27891	186	2191	
27723	58091	A	27892	2	141	
27724	58092	A	27893	1	1692	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1		1		sequence		
27725	58093	<u> </u>	27894	186	2192	I ORRPRPFPSOGISMTECFLPPTS:
21125	38093	Α	27894	180	2192	PSEHRRVEHGSGLTRTPSSEEIS
		l				
1						PTKFPGL\YRTGEPSPPHDILHEI
1		l				PDVVSDDEKDHGKKKGKFKKI
1						EKRTEGYAAFQEDSSGDEAESF
		1				SKMKRSKGIHVFKKPSFSKKKE
		l				KDFKIKEKPKEEKHKEEKHKEE
						KHKEKKSKDLTAADVVKQWK
						EKKKKKKPIQEPEVPQIDVPNL
		1				KPIFGIPLADAVERTMMYDGIR
ł		1				LPAVFRECIDYVEKYGMKCEGI
			!			YRVSGIKSKVDELKAAYDREES
		1				TNLEDYEPNTVASLLKQYLRDI
		1	l			PENLLTKELMPRFEEACGRTTE
		1				TEKVQEFQRLLKELPECNYLLIS
İ		1				WLIVHMDHVIAKELETKMNIQ
1		l				NISIVLSPTVQISNRVLYVFFTH
						VQELFGNVVLKQVMKPLRWSN
						MATMPTLPETQAGIKEEIRRQE
		1				FLLNCLHRDLQGGIKDLSKEER
i		1				LWEVQRILTALKRKLREAKRQ
	1	l				ECETKIAQEIASLSKEDVSKEEM
	l	l				NENEEVINILLAQENEILTEQEE
i		l		1		LLAMEQFLRRQIASEKEEIERLR
1		1				AEIAEIQSRQQHGRSETEEYSSE
1		1				SESESEDEEELQIILEDLQRQNE
		1		}		ELEIKNNHLNQAIHEEREAIIEL
						RVOLRLLOMORAKAEOOAOE
1						DEEPEWRGGAVQPPRDGVLEP
1		1	İ		ĺ	KAAKEQPKAGKEPAKPSPSRDR
27726	58094	Α	27895	12	413	PSRAPGLQKACTGHEGMAVHP
1						PRIPVQSDHLISIEGLLCKLPCA
						GQVTKESGLVSFSLRPVLPQNT
						LSNSFYLFPFGYASPYVETFLPG
						AHSGPAPPGLPVRTPRTAKRL/C
1	1				l	VAVAPSPTF*ISPRALRSTFVSN
27727	58095	Α	27896	I	361	
27728	58096	A	27897	2	162	
27729	58097	A	27898	248	381	
27730	58098	Α	27899	73	254	
27731	58099	A	27900	li .	729	<u> </u>
27732	58100	A	27901	i	762	
27733	58101	A	27902	2	334	
27734	58102	A	27903	3	369	
27735	58103	A	27904	669	1006	
27736	58104	A	27905	3	250	
27737	58105	A	27906	721	876	
27738	58106	A	27907	3887	4013	
27739	58107	A	27908	3423	3627	
21133	150107	1~_	2,,00	12.22	2021	L

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27740	58108	A	27909	3	226	HETGCCGQAAERDSCWERPPIP LLLPSLSGDYETVRNGGLIFAG LAFIVGL\ILLSRRFRCGGTKKR
						RRINEDEP
27741	58109	A	27910	67	264	
27742	58110	A	27911	161	851	
27743	58111	A	27912	139	351	GGRRIETGGWERPPIPLLLPSLS GDYETVR\NGGL\IFAGLAFIVG\ LLILL\SRRFRCGGNKKRRQINE
27744	58112	A	27913	2	431	
27745	58113	A	27914	217	289	
27746	58114	A	27915	255	389	KPNIACSHS*VGTEQ*EHMDTG RGTSHTGACREALDRGPAWEK L
27747	58115	A	27916	14	460	NCLTRRRRRRRTFLEEERLKP SRKKITKKHTKKRTASLILHAM ICCRSLNSSKTKNTKCLNSINOR LKILSLQKOLMCGTAGRCKTLT EQ*LNTTAITLCLLREARKTL MTHQSTWTWMKLETIILSKLTC EOKTKORNFSLISGS
27748	58116	A	27917	503	1046	
27749	58117	A	27918	3	198	
27750	58118	Α	27919	54	320	
27751	58119	Α	27920	443	477	
27752	58120	Α	27921	1	963	
27753	58121	Α	27922	1	2292	
27754	58122	A	27923	3	736	SCCLISRI.VRARRILRRAVAVM AAQCVRLARRSI.PALALSVRPI FFGLLCTATK!QRTSAKNI.KGD MGQSEQRADPPATEKTIL.UEK VKLIEEQLKETVJEKYKRAL.AU TEELTGRGSQNLLREAKLLRHF KPFCKDLLEVADVLLEKATQCV PKJEEIKDDNPHLKNPLWRGLIV MTEVQIQKVFTKHGLLKI.NPV GAKFDPYEHEALPHTPVEGKEP GTVALVSKYGKLHGNTLRP ALVGVVKEA
27755	58123	Α	27924	253	363	
27756	58124	Α	27925	235	318	
27757	58125	Α	27926	1	426	
27758	58126	Α	27927	146	254	
27759 27760	58127 58128	A	27928 27929	61	1401 457	LESTLATAERFLIPSYPSSTGN*L VCFCTT*GQECYSVTRRSLGYG SPGCLYA*SSLIPCWRWGTPRL CCEKPFTTHFCLRFVSPSKLAVS RWHIPLGSEEKRRSMSAGTISL HFIWMKSPTRTSFOHFCT
27761	58129	A	27930	1	567	HEIWINGS IN ISPQUICT

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27762	58130	Ā	27931	128	586	
27763	58131	A	27932	271	465	HLTRPGTLLRONFORNDOAAT
						LAVHOYPLLCSNRC/CIPROT/W
1		İ				VWSGPPANSNRPAAEGPDC*KE
		1				N
27764	58132	Α	27933	1	375	MQKSPIFCVAHAGSCRLELFLF
į .		1				GHLGGHHPDTKPGRDTTRKDN
		1				FRPISLMNIDAKILNKILANRIQ
		1		İ		QHIKKLIHRDQVGFISGVQGWF
		1				NIRKSINVIQHINRTKDKNHMII
						SIDAEKAFDKIQQGFMLKILNK
		1				LGIDGMYLKIIRAIYDKPTAKIIL
						NGQKLEVFPLKTGTRQRCPLSP
			1			LLFNIELEVLARAIRQEKEIKGI
		1	1			QLGKEEVKLSLFAHDMIVYLEN
		İ				PIVSPQNLLKLISNFSKVSGYKI
i						NVQNSQAFLYSNNRQT*AIAGA
						PPPASLPPCSLISDCCASNE*GSV
i						GIGPSKPGAGYNLLLCHLISPSIS
			1			PTSSPKSDTCPIADFSNKSPDRSS
		l				AGDILLAMQSLGSMAIFTILILP
		<u></u>				THEHGMFFHLFVSSFISLSSGL
27765	58133	Α	27934	1	1059	
27766	58134	Α	27935	1	533	LSKQGHLNLQRF\LLPFG\C*CLF
		1				LRGGV\YRGRQ\ASLSCGGLHP
		1				V*AS\RQLCLPTQALA\MAGTPP
	1	1				PASLPPCSLISDCCASNERGSVG
	1	1				MGPSEPRCGNNNLVVC\RFLSL
1		1				SEKRSSIRVGVTRFS\RCHLSQL
		1				CLATKGNSLTPCTSQVRRCLTL LQLTLGAMQPLSCGLPTLSDKP
27767	58135	A	27936	140	426	LQLILGAMQPLSCGLPTLSDKP
27768	58136	A	27937	1	918	
27769	58137	A	27938	54	102	
27770	58138	c	27939	244	462	
27771	58139	A	27940	234	282	
27772	58140	Α	27941	328	1212	
27773	58141	В	27942	245	338	
27774	58142	Α	27943	483	635	
27775	58143	A	27944	9882	10134	
27776	58144	Α	27945	2	370	
27777	58145	A	27946	1682	1945	
27778	58146	Α	27947	1172	1732	ESTAAEADTRFGCSWAVWAVE
	1		1	1		AEGEDCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
1	1	1			1	CCCCCCCCCCLPPSAGGRGP
	1	1				SGSARYFALIDAAQREDGGDA
1	1	1			1	YRVGLAAALEVNAAETVACGG
		1			l	LEGGEAPTDAGTRYVLEPEAPQ
	1				I	LSVLWKRVEVQRLVPVRVVVA
1					1	AWHAARKARAWLRRAARPGP
1	1	1	1	1		PASCALRRPSGYAAARN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27779	58147	A	27948	272	393	
27780	58148	Α	27949	333	622	
27781	58149	A	27950	11	1850	
27782	58150	Α	27951	1	1107	
27783	58151	Α	27952	1	1348	
27784	58152	A	27953	3	431	KLQNELLLLHVSHPGHADAKG GFPWP*AAPPLWLCRVQPSFWI LSWAGIEGLWLFHTHDTSCQW
						YHSGVALADVLHESPALQQTS VWTSRSFHTSSEIQAEVPKPQLI TSVHAQAQYSMEAPKAWGLYI LKPWPELYLGPF
27785	58153	A	27954	364	1117	EGHRAEGQCTGSVVLLTSSIGG SGKQSSGCHFWLLOHQICTCPS RVMGPRKKHRPTARGSRPPQPI PSGFPSAGAMGQVHCLAAPHS LERVRNPRQTO;PPGWEG/PPTR ANLALLPTPPAATATNSSIPDSP PGSDGSVPAGLTTWLAVLTLD CPKAFGKVASQACLLWKGEQP PKTPPVTPSRVSLLASEPNTIRL KNVFPRVFPACTWKSHRHSTPA HESSQKGLYPAKPQGWSCPRL WEPTSCISVTWM
27786	58154	A	27955	1	224	QWRHCNRSLLPVQGKSGALEG IGPPRVF\PPE*RAFGGQRAPPDI P\PPSPRHPTKDRRTAARSGPRR KRGQTNE
27787	58155	A	27956	681	879	LQISHPGHADASGGFPWPWAA PPLWLCRVQSPS*LLSQPGVECI QLFQAHSASRHLNSMRPQMNS S
27788	58156	Α	27957	835	1482	
27789	58157	Α	27959	1	522	
27790	58158	A	27960	2	396	
27791	58159	Α	27961	1	1501	
27792	58160	A	27962	473	860	
27793	58161	Α	27963	370	3675	
27794	58162	Α	27964	52	117	
27795	58163	A	27965	3	290	PRKTVQFGGTVTEVLLKYKTG ETNDFELLKNQLLDPAIRDD\QI NWLLEFRSSVMYLTK\DFE\QLI SIILRLPWLNRSQ\TVVEEYLAF LGNLVSA
27796	58164	Α	27966	1	2988	
27797	58165	Α	27967	1	666	
27798	58166	Α	27968	274	930	
27799	58167	С	27969	13	231	
27800	58168	Α	27970	46	386	
27801	58169	Α	27971	3	451	
27802	58170	Α	27972	160	494	

SEQ ID   SEQ ID NO: Mets   SEQ ID NO:   Mets   Met	deletion, \sigma 2406 1069	on, /=possible nucleotide possible nucleotide insertion)
sequence         09/540,217         codon for person squence           27803         58171         A         27973         I           27804         58172         A         27974         201           27805         38173         A         27974         450           27806         58174         A         27976         329	of peptide sequence deletion, \text{\text{del}}  2406  1069	
27804         58172         A         27974         201           27805         58173         A         27975         450           27806         58174         A         27976         329	1069	
27804         58172         A         27974         201           27805         58173         A         27975         450           27806         58174         A         27976         329	1069	
27805 58173 A 27975 450 27806 58174 A 27976 329	1.1.1	
27806 58174 A 27976 329	647	
2,000	697	
27807 58175 A 27977 141	1506	
27808 58176 A 27978 I	1773	
27809 58177 A 27979 3		GVPISRGTL*SVFP*PS*
[ [ ] [ ] [ ]		SLGSCTTACQVRCQPC
		APPERTTSAPAAQSPSR
		APLVSACPTCSPATHP
		STHTPCCRGSSPRPRGS
		WTICPKASKADPKAP
		1PFYAQTQTLGET
27810 58178 A 27980 1		MSKTPKAMATKAKIDK
27010   20170   11   27700   1		KSFCTAKETTIRVNRE
		UFTTYSSDKGLISRIYN
	1	KKKTNNPIKKWVKDM
		EDIYAAKKHMKKCSP
		MQIKTTKKLMLYYDVI
		HKELEOKLAAFLGMED
		FDANGGLFETLLGAE
		LNHASIIDGVRLCKAK
		NDMQELEAAYRRSTR
		SFRSRVLTEFRVCPCL
		GGNLMRLSARSLWQR
		KLEGIIEEY/ALLV/WR
		VNLSPNPGLVDRINFG
		ALEDFHRSALAIQGWL
		ACSAEMAPEAVLHGL
		CEGDMFRATAGVNTH
	KGSIFSL	GLLCAAIGRLLQLNQP
		CSTAASFCRGLTDREL
	RTNNSO	LTAGQRLYQQLGLTG
		AGYPLVINHALPHYLT
	LLDOGL	DPELALLDTLLLLMAI
		ASRGGEGGLRWLORE
	l laotilo	KGGIRTPADLDYLRQF
		GSSRVDCSVWELCRA
		MAVAAKTKNAGKWH
		DINPGDRLYDQGGRA
		THHQKYYRHRSRR
27811 58179 A 27981 1	1974	
27812 58180 A 27982 344	508	
27813 58181 A 27983 3	492	
27814 58182 A 27984 65	261	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nuclcotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27815	58183	IA	27985	3	529	DAWAFHKMAPKAKNEAPAPP
		'			· ·	KA\EAKAKGF*RAKKGSF*KVS
l		l				HSH\KKKKIPHVHPTFRAGRRPL
	i.					R\LRRQP\KYPSGRALPWRNK\L
1		ŀ		l	i	DHLCLSIKFP\LTH*VLPMKKIE
			Ì			DN\NTLVFIVDVKANKHQIKQA
		1	l			VKKL\YDI\DVAKVNT/LWIRPD
1		1				GEKNGICSDLAP\DYDA\LDVA
	1	1				NKIGII
27816	58184	A	27986	105	241	PFFFFEMESPSVAQAVFSLVFRS
2,010	20101	ľ.	2,,,,,,	1.00		PHCGGIQAHLFNL*RDLFKIWT
27817	58185	c	27987	175	363	THE STATE OF THE S
27818	58186	Ā	27988	724	958	
27819	58187	A	27989	3	823	
27820	58188	Ā	27990	1	877	
27821	58189	A	27991	487	786	
27822	58190	A	27992	147	623	RSAVANGLTKRRMGLKLNGRY
27622	36170	ľ.	21772	1-7/	023	ISLILAVQIAYL\VQAVRAAGKC
1						DA\VFKGFSGLFCSSLGDTMAQ
					ĺ	LPAGPGDDKTNIKTVCTYWGG
						ISHSCT/VTALTDCQEGAKNMW
		1				DKLRKESKNLNIQGSLFELCGN
						GNGAAGSLLPGFPVLLVSLSAA
		1			1	LTTWLSF
27823	58191	A	27993	213	579	ASLLLLAFLAELASLKAGLOKS
2/823	38191	^	21993	213	3/9	REYSCSSFISSLSSTDAHCVLSE
	1			l		YARPLS/ORPAPNGSSPRCOASE
1	İ					AOSPGHRPPPPLFSSPLAALOLD
1		1		İ		SHRFPSDPNGKDESRPPRLCTKL
				l		GRGCAGCGK
27824	58192	A	27994	1	800	S.KOC/LOCOK
27825	58193	В	27995	54	165	
27826	58194	A	27996	46	313	
27827	58195	c	27997	30	151	
27828	58196	Ā	27998	169	1173	
27829	58197	A	27999	456	651	
27830	58198	A	28000	487	833	RNKFCDDQTEGNKIKNRREEK
2,350	20178	1	20000	[""	1000	HRCRGOSKLNIIIDNVVKAVNG
	1	1		I	1	GKSQREQAEFADCITFGIRHNTS
1	Ì		l	I		PKMSRVRGGG/TTPWAVLGMA
				1		EASSSLOSSSONPGQAGWQTGP
					1	WVVSLGC
27831	58199	В	28001	1	2268	
27832	58200	A	28002	1	639	
2/832	138200	IA.	120002	11	037	L

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27833	58201	Α	28003	1913	2388	PIIHNTTAMKKAAKAEPPFTTIV CTE*AILSQRTCSL*FTVINDICP
						GPRAH/VVQDIHGKLFTGSAIA NRFQDAMAIPFLGTQGKRVPR
						NGMAIPFPGNRNVIAGAFIPHR
						QHLGOIQLNPVRQCSNLFAHLL
		ŀ				AORSEAIFHMRRHHRIRDTVKK
						TILF
27834	58202	Α	28004	1	1566	
27835	58203	Α	28005	951	1217	
27836	58204	Α	28006	1294	3108	
27837	58205	Α	28007	I	1896	LFDWLVSQNELKANPAKGVSA
i		ŀ				PKAPRHLPKNIDVDDMNRLLDI DINDPLAVRDRAMLEVMYGAG
		1				LRLSELVGLDIKHLDLESGEVW
		1				VMGKGSKERRLPIGRNAVAWI
		ļ				EHWLDLRDLFGSEDDALFLSKL
		l				GKRISARNVOKRFAEWGIKOG
						LNNHVHPHKLRHSFATHMLES
		1				SGDLRARGAYLCAKLLSGAAQ
				i		VPEWRSAFAWFARCAEQARQN
	1					QYLQVSSCVPALEGCDVNGAS
		1				FTLEQMLAWRDHPQVTGLAEN
		l				MDYPGVISGQNALLDKLDAFR
						HLTLDGHCPGLGGKELNAYITA
						GIENCHESYQLEEGRRKLQLGM SLMIREGSAARNLNALAPLINEI
						NSPOCMLCTDDRNPWEIGHEG
						HIDALIRRLIEQHNVPLHVAYR
						VASWSTARHFGLNHLGLLAPG
	1				1	KQADIVLLSDARKVTVQQVLV
						KG\EPIDAQTLPAEEIGRLAQFA
		1				PAYGNTIGRQPLSASDFALQFTI
	i	1				GKRYRVIDVIHNELITHSHSSVY
		ľ				SENGFDRDDVSFIAVLERYGQR
						LAPACGLLGGSGLNEGALAAT
		1				VSHDSHNIVVIGRSAEEMALAV
						NOVIODGGGLCVVRNGQVTSE
		1				GAKERMMGKRYKETSGSIGLK VPAPLNLNLSLQPREQLGGQST
27838	58206	A	28008	1	3257	VIAIENENESEQFREQEGGGST
27839	58207	A	28009	i	2145	
27840	58208	c	28010	193	363	
27841	58209	Ā	28011	1	397	
27842	58210	A	28012	2	405	FVSAQGPGGKRFGTAPATPGCL
						VHDLS*APCLRWYQHPTEEELR
		1				ILAGKQQKGKTKKDRKYNGHI
						ESKPLTIPKDIDLHLETKSVTEV
						DTLALHYFPEYQWLVDFTVAA
					1	TVVYLVTEVYYNFMKPTQEMN
	L		L	L		ISLV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27843	58211	A	28013	13	353	GYIEKRISCIALLF/SF*IPVNFLR
2,013	30211		20015	1		FHDTF1*FCYSS*SIIOLSLWOSOI
						LLCV*LLRSIDFLYLIW*PLTYN
l						EHASILLSLRAPYOLFDL*NDRS
						HIRYSATLVNNPAVCFAVGHD
27844	58212	A	28014	106	1814	
27845	58213	Α	28015	37	2847	
27846	58214	A	28016	1	2430	
27847	58215	Α	28017	1 .	2660	
27848	58216	С	28018	80	328	
27849	58217	В	28019	1	1074	
27850	58218	Α	28020	602	853	
27851	58219	Α	28021	505	649	
27852	58220	Α	28022	672	1903	
27853	58221	Α	28023	3	319	
27854	58222	Α	28024	1	219	
27855	58223	Α	28025	2	508	
27856	58224	Α	28026	1	1011	
27857	58225	Α	28027	1	699	1
27858	58226	Α	28028	175	351	
27859	58227	Α	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	С	28031	115	231	
27862	58230	A	28032	2	139	
27863	58231	Α	28033	1	788	
27864	58232	Α	28034	115	358	LIVVRSRRGTSRSGSPRATAMA
		1				FKDTGKTPVEPEVAIHRIRITLT
						SRNVKSLEKVCADLIRGAKEKN
	1	1			!	LKVKGPVRMPTKVK*IVVRSRR
						GTSRSGSPRATAMAFKDTGKTP
i	1	1				VEPEVAIHRIRITLTSRNVKSLE
	1				1	KVCADLIRGAKEKNLKVKGPV
						RMPTKVK
27865	58233	С	28035	179	283	
27866	58234	Α	28036	57	431	
27867	58235	Α	28037	54	440	RVPELWVGTEVKERKNARSGV
1		1	1			PSTQRLECGSAESAAGAPASVS
l		l				VQVTAVPAPLFPGWTGGGRAV
1			1	1		NLTEAERMRVVINSVCHWRLY
1		1	1	l		E*TANRFS*KQDVGKLTNCVCH
1				1		PEGMLKAVTTQAQVFLVIRHN
27868	58236	Α	28038	1	2693	
27869	58237	В	28039	131	350	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27870	58238	Α	28040	1	594	MLDITNDQGNASQNHNAIPPYS
			1			CKNGHNQKIKAGGLWTTVHSL
						LLFOLEORTOOGYGPITHPKTP
						LHPPALLAVDRGSRSSVPATDS
	ŀ					LPSAHDROQOFHTWVCSRLLA
						TVRADPADGQQPQARADVCGC
						RGTGFINLVMIHLMGFEVGRIQ
		1				QLEQVAPRPQGVSWEVDSSDH
						LQGSPRVEPPGTWDLRVLCSQG
						O*EAVNCGPOTPGLD/SFDYGH
		l	İ			SCRSKVVSHCGFDLHFPDH**C
						KNGHNQKIKAGGLWTTVHSLL
						LFQLEQRTQQGYGPITHPKTPL
i						HPPALLAVDRGSRSSVPATDSL
						PSAHDROOOFHTWVCSRLLAT
1	l				1	VRADPADGQQPQARADVCGCR
	1		ŀ			GTGFINLVMIHLMGFEVGRIOO
	ł					LEOVAPRPOGVSWEVDSSDHL
						QGSPRVEPPGTWDLRVLCSQG
27871	58239	Α	2804I	1	285	
27872	58240	Α	28042	I	1059	HNLSSSNSFPKMSFPNSSPAANT
						FLVDSLISACRSDSFYSSSASMY
		l				MPPPSADMGTYGMQTCGLLPS
		l				LAKREVNHQNMGMNVHPYIPQ
		l				VDSWTDPNRSCRIEQPVTQQVP
		i				TCSFTTNIKEESNCCMYSDKRN
		1				KLISAEVPSYQRLVPESCPVENP
		1				EVPVPRYFRLSQTYATGKTQEY
		l				NNSPEGSSTVMLQLNPRGAAKP
		1				QLSAAQLQMEKKMNEPVSGQE
		1				PTKVSQVESPEAKGGLPEERSC
		I				LAEVSVSSPEVQEKESKEEIKSD
		l				TPTSNWLTAKSGRKKRCPYTK
		l				HQTLELEKEFLFNMYLTRER/R
		1				ALEISKSVNLTD\RQVKI\WFQN
						RRMKLKKMSRENRIRELTANL
27873	58241	Α	28043	358	2292	
27874	58242	A	28044	2	300	HSLS/SFFFFFFFFFFFFFFFFFFF
1		1		l		FFFLFFFFFLLLLLFVSFSFSFSFS
						SFSFSFSSFSSFSFFFLLPSSSSS
						SSSFFFFFFLLLLPFFFFFEMEH
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	<del></del>
27878	58246	Ā	28048	3	212	
2/0/0	155240	<u>.,</u>	120000	1-	l***	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27879	58247	Α	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP
						NNNNFFFFFFFFFFFFFFF
i		1		1		FLLLPLLLPLLLLLPLLPLLPLLP
1		1				SSSFFFLLLSSSHSSPSSPSSPSPS
		l				SPSSPSSPSSSSSSSSSSSSSSSSS
İ		l	ľ			SSSSSSSSSSSFSFSFSFSFSFSFSF
j		1				SFFFFFFFFFLFED
27880	58248	Α	28050	544	729	
27881	58249	Α	28051	1667	1896	
27882	58250	Α	28052	1	477	
27883	58251	Α	28053	25	448	RSQFFFFFFFFFFFFFFFF
l		1				ILLVLLLVLLVLLLLLLLLLLLLL
1		l		1		LLLL/ASSSSSPSPPSPSPSSSSSSS
		l				FSSSSSSSSSLSLGAYVLYFMVT
		l				HSSPVLCCLCNLIINNI*EE*FFR
İ		1				FRHNCDLFLAASTLGVDWLLL
27884	58252	Α	28054	47	376	
27885	58253	Α	28055	1	1740	
27886	58254	Α	28056	3	1464	
27887	58255	Α	28057	}	394	
27888	58256	Α	28058	143	429	STLQKKEARARHLVTPLDILQL
l		l				FNGFPLLVDCYKLLRYSRVHSF
		1				PRFWIFFSIKDHIGFPKENTQRK
		ı		1		MRLHPPPQS*TPPRE*VPSFSSG
						VGKSS
27889	58257	Α	28059	165	408	
27890	58258	В	28060	21	253	
27891	58259	Α	28061	1	150	
27892	58260	Α	28062	1081	1303	
27893	58261	Α	28063	147	437	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27894	58262	IA	28064	107	2499	PIEDPEGRRRMREFILRSIOGVI
		1				RMAPQIQPKPLLTKSSTSVSQA
	1	1				RL/TSKQKALLPRQCSGSAKAQ
		1			1	AEREKIEETCQVGMKPPVPGG
						TLQGKWITTFCNQVQLDTIKIN
		1			Į.	GCLKGKLIYLLGDSTLRQWIYY
		1				FPKVVKTLKFFDLHETGIFKKH
						LLLDAERHTQIQWKKHSYPFV
	į.					FQLYSLIDHDYIPREIDRLSGDK
					İ	NTAIVITFGQHFRPFPIDIFIRRA
		1				GVQKAIERLFLRSPATKASVSK
	ł	1				LKCFWEPTRGTQKYEASQVTG
	İ	1				AFPLRPKKGAATPSQLVIVNSS
		1				DAHNKCDEESEVRIKSTLGLKI
	l	1			Ì	DCKKGTALTKGTKEDEEDGAN
		1				SGVDQLCLLSSVDSSGRPQLM*
		1			ļ	DWHGVKGQFSCFKCGEEKELG
		1			i	QKRKLTGKGWNVFFMVLEVG
		1	-			KTKIKALEVLASGKGTASWFIG
	1	1			1	DFLAVNSSHGRWGKKEEFLFQ
						KWKVDPWLPVRWELVQTGTL
	1	1				THLVPEGRSDSVTCAWMPLGS
		1		1		KOVYKEPAGFPDMLRLRGSRV
					i	RMAVVTVHSQLRNLSLGDQHF
		1				NYPLPLKKKKKKKKKKDTLIYP/
	1	1			i	DWLESCQSDNLSLAERDLVLV
						LRLALCALYGLLAPGNGNTES
					i	ELHPGDKTEAQRPMALFKVTR
	1					PLNERPGDLASHVSRFAKSFLK
		1				PAMESLECPOSRLVGEARKGH
		1				ELVEKIERGCESTVGEGTTRKG
					İ	SKRDHLDSQCKLGQRSQPWGQ
27895	58263	A	28065	1	1770	
27896	58264	Α	28066	85	204	SPCSTSPFRQLA**RRGPHRSPF
					1	TVAHLIGEWRLMRNAG
27897	58265	Α	28067	1280	1531	
27898	58266	Α	28068	1	882	
27899	58267	В	28069	77	1188	
27900	58268	A	28070	1016	1400	
27901	58269	Α	28071	1091	1770	CRGGSGCAVCAELAPGAVHTV
		1				AAERAGAQEAAAGAGPPQLGC
		1				LIAWATHLQHSAAVPLLSQRM
						CHTCCLSPRKLVIGCRAAKSLS
	1	1				SPCGKWLCAALIRQPSVKGLPS
	1	1	1			CGVPLPLSLSRIQMCSSEATSSV
		1	1			ELNPDFGEAATSP**ESGF/LQS
		1	1			VVSTALLPDNTTGETFHHDGRA
		1		1		DIGSQFIHRFLVCCHLLVLRWL
	1	1		1		TLDTKADVVDIGHRLRCFDCRO
		ļ			1000	VDSTICD
27902	58270	A	28072	1568	1819	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27903	58271	A	28073	778	879	LALIVGNRS*MKPYOTTSVTPR
		1		1		CLOOWOORCANY
27904	58272	Α	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT
		İ				LKVLIIGKLSSGRKLSRILPLLRS
	i					SSM*PTRAPN*SSASFTFTSVSG
27905	58273	Α	28075	355	614	CMRRPSCSCPASTRDNTAPHSR
						TLKVLIIGKRSSGRKLSRILPLLR
		i	1			SSSM*PTRAPN*SSASFTFTSVSP
		l				L*NFIRLHPVY
27906	58274	A	28076	1	2226	
27907	58275	Α	28077	31	117	
27908	58276	Α	28078	1	547	
27909	58277	Α	28079	290	730	
27910	58278	Α	28080	3	267	TLVKVKDAEDQLGARVGYIEL
						DLNSGKILESFRPEERFPMMSTF
İ						KVLLCGAVLSRIDAGQEQLGRR
						INTILRMTWLSTHQSQKSILRMA
27911	58279	Α	28081	1	1785	
27912	58280	Α	28082	551	685	
27913	58281	Α	28083	2	211	
27914	58282	Α	28084	1407	1874	PRAAAAPTNLSPELSASPRPRV
		l			\	ACASAWGAGTDVTGWEAAMP
	ļ	l		ĺ		RVGRCLPRTGLGSARRLRRPEL
		l				GGGAGPAPEAMRGFGADAGST
		l				EQPRLPARS*PRLPQRPRRPRKS
		l				ERPAGLAPRLRPPQPAEPPGLGS
}		1				QERGRGTDRAAADPGLPRTSPE
						ss
27915	58283	Α	28085	1284	1786	
27916	58284	Α	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR
						CL
27917	58285	Α	28087	423	676	
27918	58286	Α	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR
		_				CLQQWQQRCANY
27919	58287	В	28089	743	852	
27920	58288	Α	28090	1	1100	
27921	58289	Α	28091	548	652	LALIVGNRS*MKPYQTTSVTPR
1		1	1	i	1	CLQQWQQRCANY

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino neid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
	sequence	1	02/340,217	sequence	or pepade sequence	detection, repositor nucleotide insertion
	<u> </u>	<u> </u>				
27922	58290	Α	28092	1	2438	MRLFGYARVSTSQQSLDIQVR
		1				LKDAGVKANRIFTDKASGSSS
						RKGLDLLRMKVEEGDVILVKI
		1				LDRLGRDTADMIQLIKEFDAQ
		i				VSIRFIDDGISTDGEMGKMVV
	1	1				LSAVAQAERQRILERTNEGRÇ
		1				AMAKGVVFAENDKKMLSNA
		1				ETADFRTLIETDDRTIVVGRRO
		1		i		GSFNLARAATRLLWRYAMLN
				l		IASYISSHYKLSSQISSETLLNE
		1		l		LKKWNSAQGDILRKCRLVAK
			İ			YLDENNPEESIGDLQFNLNISE ENNIVSLLERSDRKVVILMDK
	1			ŀ		DEAYEPDNIGIG\IIAGLAYASI
	1	1				LNOKAKCIRPIIFLRDNIFRSLS
	į.	1				EDPDYSRNIEGQVIRLHWDW.
						OLLMLSAKRMKVAFKLDIEK
					QRVWDRCTADDP*KGGNGFI	
	1				CLOFTLYRPRDLLSLLNEAFF	
		1		i		FRENRETIINTDLEYAAKSISM
						RLEDLWKEYQKIFPSIQVITSA
	1					RSIEPELTVYTCLKKIEASFEL
						ENGDPKITSEIQLLKASGILQS
						YSVGFVGIRDKNTSSYSFCHD
						RTPDKGFESNEKLLIHPCYWL
						LNLNRNALAPEEAEEINDEYD
						NIISDNSAIRNKTIGQITTHLDO
						PIGNEGATEFEQWCLDALRIV
		1		İ		ASHLTDIKSHPNGNAVQRRD
	1			1		GTNGGKSDFWKRVLEDYKT
						VVFDAKNFEELGPSEYRQLQS
						LTGPYGKLGFIINRDESEVVR
27923	58291	Α	28093	673	916	
27924	58292	В	28094	1	4725	
27925	58293	Α	28095	959	1387	CMRRPSCSCPASIRDNTAPHS
				1		LKVLIIGKRSSGRKLSRILPLL
				1		SSM*PTRAPN*SSASFTFTSVC RCMSAVMVMAVLTIACRFLK
						TVSVGHICSLNFALQTSTTAM
						VPAAATRASRAQPNGRHPWF
27926	58294	С	28096	997	1302	CWKTQKA
27927	58295	A	28097	659	2534	
27928	58296	A	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	
27932	58300	A	28102	40	198	QAARTTGFYAHLLRHYKTPV
		1		1		HS*Y*WKLHGENKSSAFAVC*
		1				TCRNPFIDCW
27933	58301	A	28103	390	1186	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
27934	58302	Α	28104	2	1287	GRVGFASTAQSPRILRSEPVRTP
			1			PIPAFSPLKTLRIMSLHQFLLEPI
			1			TCHAWNRDRTRPVCLDYYSLV
1						VSFEIKK*IALSPNNHEVHIYKK
				ł		NGSQWVKAHELKEHNGHITGI
1						DWAPKSDRIVTCGADRNA YVW
			1			SQKDGVWKPTLVILRINRAATF
						VKWSPLENKFA VGSGARLISVC
						YFESENDWWVSKHIKKPIRSTV
						LSLDWHPNNVLLAAGSCDFKC
		1				RVFSAYIKEVDEKKASTPWGSK
		l				MPFGQLMSEFGG\SGTGG\WVH
1		1				GVSFSASG\SRLGWGSATDSTV
		1				SVCWMPSKS\LQVSTLKTEFLPL
		1				LSVSFVSENSVVAAGHDCCPM
		l				LFNYYDRGCLTFVSKLDIPKQSI
		l				QRNMSAMERFRNMDKRATTE
						DRNTALETLHONSITOVSIYEV
i						DKODCRKFCTTGIDGAMTIWD
ı		1				FKTLESSIQGLRIM
27935	58303	c	28105	198	362	,
27936	58304	A	28106	1	915	
27937	58305	Α	28107	403	519	
27938	58306	Α	28108	88	237	
27939	58307	Α	28109	527	1205	
27940	58308	Α	28110	2	272	
27941	58309	Α	28111	39	543	
27942	58310	Α	28112	1	789	
27943	58311	Α	28113	401	912	
27944	58312	В	28114	147	653	
27945	58313	Α	28115	586	650	KIQCLCLWLLFLIIFLHAFQETIL
		1				ALRVLNVFNKRINSLGKNLAFN
i		l				LFVYNKANSMP*RLLWKAPRS
		l				DK*IQ*SLRIQNQCTQISSTAVH
		<u>L</u>				STVTKLRIKSRTQPLLQQL
27946	58314	A	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL
		i i				KSGSGKVYQGPAKGAADTTIIL
						SDEDFHGRWSGASLTLRRHSLV
		_				AG
27948	58316	C	28118	183	254	
27949	58317	A	28119	98	445	LGSGDLPWEINPLSSCSLLCEKH
		1	1	l		PPTTSGPQTDQPKKHLTNFKSG
				1		ACYMCRKSGHWAEECPQPGIPP
				1	-	KPRPICVGPH*KSDCSTHLAATP
				l		RAPGTPAQGSLTDSFPDLLGLA
						AED
27950	58318	Α	28120	32	143	L

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop eodon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	detetion, \=possible nucleotide insertion)
				sequence		
27951	58319	A	28121	139	346	QYISELQFLASTVRQTPATSPAH
21931	36319	l^	20121	l''	340	KNFOTPEPOOPGIPPEPPPPGAC
		1				YKCWKSGHQAKECLQPGIPRK/
						HASHLWOPLPEPPGTLAQGSLT
						DSFPDLLGLAAED
27952	58320	A	28122	159	306	LGSGNLP*EINPLSSCSLFREEDP
21932	30320	^	20122	139	300	PTTSGPQTNQPKEHLTNFKSAA
		1				ED ED
27953	58321	c	28123	80	106	LD
27954	58322	Ā	28123	166	423	RPRSERLLWGTSPLS/CALTL*G
21934	36322	^	20124	100	723	DPPTTSGPQTNQLKEHLTNFKS
		1				GPHWKMDCPTHPAATPRAPGT
		1			]	LAQGSLTDSFPDLLGSAAED
27955	58323	A	28125	1	354	LAQUSETDSTYDEEGSAAED
27956	58324	A	28126	1	702	
27957	58325	A	28127	317	427	
27958	58326	A	28128	467	640	SARKRFOLSP**NKITLLKPASS
21936	38320	^	20120	407	040	AISALAATPRAPGTLAQGSLTD
		l				SFPDFLSLAAED
27959	58327	В	28129	1	320	SFFDFESLARED
27960	58328	A	28129	1	605	
27961	58329	A	28131	273	529	LGSGDLPWGINPLSSCSLLREK
2/901	36329	^	20131	2/3	329	DPLTISGPQTHQPKEHLTNFKSG
		1				PH*KSDCSTAPG\ATPRAPGTLA
		i				OGALTDSFPDLLSLAAED
27962	58330	A	28132	459	601	DVDRHVRGSNFHHNEIRSLAAT
27902	36330	^	20132	439	001	PRAPGTLAQ/GLTDSFPDLLGLA
		1				AED
27963	58331	A	28133	112	331	LGLGDLP\WEINPLSSCSLLHEK
2/903	36331	^	20133	1112	331	DPPTTSGPOTDOPKKRLTNFKS
	1	1			1	ATPRAPGTLAQGSLTDSFPDLL
	1	1				GLAAED
27964	58332	A	28134	1	579	GLAKED
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	Ā	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	В	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	A	28145	1	573	
2/9/0	126344	١^	28140	L*	313	L

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	' '	
		_				
27977	58345	Α	28147	163	593	GFLEVQTPHPPNLDGPRRANRN
			1			TFLWTCHVGIPDLPALPAPASFL
l	1	l				GTQLTLKKASDGPRTEKVTQD
1		ļ.			l .	LAQPFWTTGRQLRFVLHLSLQQ
1						KDLSKCWRGAEVVLGPTRLFL*
1	i					GYSEGVKENGTGGVNK*AFSM
						CDSKWFNPCLTF
27978	58346	Α	28148	159	405	PRLRVKYTQLCIL*S/CWRERKK
ŀ		l				FHLGKRVELRQGTTLGRVGWP
					1	KRRLSQGSAGCFPAGLAHSPPH
1		1		İ		LAEAPGSGFCTALFLWL
27979	58347	В	28149	123	1561	
27980	58348	Α	28150	1	1771	
27981	58349	Α	28151	68	698	
27982	58350	Α	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	Α	28154	1	245	
27985	58353	Α	28155	5	422	
27986	58354	Α	28156	3	1372	
27987	58355	Α	28157	1	1653	
27988	58356	Α	28158	586	867	
27989	58357	Α	28159	1	1410	
27990	58358	Α	28160	1	1441	MDIKKGITDISASLRVESGWEA
						RTRKEKTHINTVIIGHVDSGKST
	1	1	l .			TTGHLIYKCGGVDKRTIEKFEK
i		1		l		EAAEMGKCSFKYAWVLDKLK
		1				AEREHGITIDISLW\KFETSKYY
		1				VTIIGAPGHRDFIKN\MITG\TSO
	1	ı				A\D\CAVLIVAAGVGEFESWYSP
	ŀ					RNGQTREHALL\AYTLGC*NKL
1		1				IVGV\NKMDST\EPPYS\QKRYE
1						EIVKEGSTYIKK\IGYNPSTVAF
1		i				VP\ISGW\NG*QHCLEAKWLTCP
		l				WFOGDGKVTP*GLAIASWEPRL
						LWRALALQSYPPTRPTDQAPLR
1						PASPRMSYQKLGGIVNVATEV
					1	
Į.						KSVEMHHEALSEVLPGDN/VGA
						FNVKNVSVKDVRRGNVAGDSK
1		1			1	NDPPMEAAGFTAQVIILNHPGQ
1		1	1		1	ISAGYAPVLDCHTAHIACKFAE
1	1	1	1		1	LKEKIDRRSGKKLEDGPKFLKS
		1			1	GDAAIVDMVPGKPMCVESFSD
					1	YPPLGRFAVRDMRQT\VAVGVI
		_				K\AVDKK\AAGAGKVTK\SAQK
27991	58359	Α	28161	125	370	
27992	58360	Α	28162	156	547	
27993	58361	Α	28163	108	919	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
27994	58362	A	28164	I	712	LNSEGNSGSGDSISYDAPAGNS FLEDCELSROJGAQLKLLPMND QIRELQTIIRDKTASRGDFMFSA DRLITLVVEEGLNQLPYKECMV TYPTOYKYEGVKFFEGNCGVSI MRSGEAMEQGLRDCCRSIRIGK LLQSGGETHRAQVYYAQFPPDI LYRKVLLMYPILQTGNTEFEA VKVL†DHGVHPSVIJQLSPFLP HGGQSIJGRFFFFIP*PTEVHPV APTHFGQKYGTD
27995	58363	A	28165	1	606	GIRSAMQNTQNLLQMPYGCGE (OMMULAPNYGLDELINETQ) LTPEIKSKAIGYLNTGYQRQLN YKHYDGSYSTFGERYGRNQGN TWLTAFVLKTFAQARAYIFIDE AHITQALIWLSQRQKDNGCFRS SGGLLNNAIKVNISGASFDLSI MISARMRIGSDNVKNSKGKPQ RKIKRGWHQKRGDRTKV DCDT LSYRDGYG
27996	58364	A	28166	1	4626	
27997	58365	Α	28167	15	4479	
27998	58366	Α	28168	256	852	
27999	58367	Α	28169	319	405	
28000	58368	Α	28170	606	896	
28001	58369	Α	28171		372	FRRVACVGSAGD\TAGAEP\RG ACATAWVCEMAADISESSGAD CKGDPRNSAKLDADYPLRVLY CGEYCEYMPDVAKCRQWLEK NFPNEFAKLTVENSPKQEAGISE GQGTAGEEEEKKKQKRGKT
28002	58370	A	28172	1	731	LSRGSAAGGRALGRPWGARRV ACVGSAGDITAGAEPRGACAT AWVCEMAADISESSGADCKGD PRNSAKLDADYPLRVLYCGVC SLPTEYCEYMPDVAKCRQWLE KNFPNEFAKLTVENSPKQEAGI SEGQGTAGEEEKKKQKRGGR GQIKQKKKTVPQKVTIAKIPRA KKKYVTRVCGLATFEIDLKEAQ RFFAQKTSCGASVTGEDEIIIQG DFTDAIINDVIQEKWPEVG**QPL EDLGRK
28003	58371	Α	28173	335	2297	
28004	58372	Α	28174	23	416	
28005	58373	Α	28175	1	681	
28006	58374	Α	28176	1	1668	
28007	58375	Α	28177	1	1587	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28008	58376	A	28178	250	687	AATSLPFRASTIASANSILRVGV MTSIHHFVFSKRVCCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQQTQIKSVRPDYLLVE PPHHMGPSFFASSGLHYDQ*PH HRLHLYWFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	С	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	С	28181	151	351	
28012	58380	A	28182	2	355	
28013	58381	Α	28183	19	428	
28014	58382	В	28184	61	2118	
28015	58383	A	28185	I	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEGE MYELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSYPDSSG9 ERLISIANDIETIGEILKKIIPTLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIIQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD FVPECKILLDLISESPIKGRVAQP VDPNFYGWKPMDYGGFTMMF DDRRGRPVGFPMKGRGFDRM PGRGGRSPNGFRRSPYDFPMKGGSFSARNLPL PPPPPRGGGRAGSSARNLPL PPPPPRGGRSGSSARNLPL SPSEWMAYEPQGGSTDYSY AGGRSSYDDLMAYDRRGRAD RYDGMVGFSADETWDSAIDTW SPSEWMAYEPQGGSGYDYSY GLAGGSGYDYSY DLAGSIIGKGGQRIKGIRHESGA SIKIDEPLEGSEDRITTITGTOQQI QNAQYLLQNSVKQYSGKFF

SEQ ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28017	58385	A	28187	221	1634	KNMETEOPEETFPNTETNGEFG
28017	30363	l^_	20107	221	1054	KRPAEDMEEEQAFKRSRNTDE
ļ.		1				MVELRILLOSKNAGAVIGKGG
		1				KNIKALRTDYNASVSVPDSSGP
!		1		1		ERILSISADIETIGEILKKIIPTLEE
1	l			1		GLOLPSPTATSOLPLESDAVECL
		1		1		NYOHYKGSDFDCELRLLIHOSL
	1	1		1		AGGIIGVKGAKIKELRENTQTTI
	i i	1		l		KLFQECCPHSTDRVVLIGGKPD
		1		1		RVVECIKIILDLISESPIKGRAOP
1		1		I		
1	l .	l		i		YDPNFYDETYDYGGFTMMFDD
l						RRGRPVGFPMRGRGGFDRMPP
				1		GRGGRPMPPSRRDYDDMSPRR
	i	1		1		GPPPPPGRGG\RGGSRARNLPL
		i		1		PPPPPPRGGDLMAYDRRGRPGD
		1				RYDGMVGFSADETWDSAIDTW
l		1		}		SP\SEWQMAYEPQGG\SG\YDYS
		1				Y/AQGGRGSYGDLGGPIITTQVI
		1		1		IPKDLAG/SLFIGKGGQR\IKQIR
				1		HESGS/SSIKIDEPL\EGSEDRIITI
		_				TG\TQDQIQ\NAQYLLQ\NSVKQ
28018	58386	Α	28188	218	497	
28019	58387	С	28189	183	254	
28020	58388	Α	28190	1	1056	
28021	58389	Α	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYAEIG
1	1					NR*GRNLGLTEVTGAVCEALR
		┺				QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	
28024	58392	Α	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN
						FSSFPFLVENGDAFYLAATLRA
						PGTVAQGSLTPSQIFSA*WRHPS
		1_				ISPFS
28025	58393	Α	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ
		<b>⊥</b> _				SPWNSGPRLSD*LLPRSSGLSG
28026	58394	Α	28196	372	782	LRSADLPWEINPLSSCSLLHEKE
						PPTSSGPQTDQPKEHLTNFKSE
1						KKETRFIRGPKTPAPVMD*GRQ
						PSLGV*PLQGCLSDYSPRFQRC
1						QTTQGHLPWSFTLSSKSHFSGG
1						RGKSLLQVPEIWPPGQGMPAA
					L	QDSS
28027	58395	Α	28197	189	380	SLCIFSSASALQQQWQHEGWC
1		1				GQLLPRGHGPNRKLQQQRQWI
1 1				1		LL*VPEILPLGQGMPAAQDSS
28028	58396	A	28198	33	302	FRICALSTKLFCLSTPWCQTHIL
1	1	1		I		SYPOYLPLLPIYSVLDLRHAFFT
1		1	1	1		IALHPSSQPLFAFT*TDPDTH*A
		1	1	1		OOITWAALPOGFTDSPHYVO
						1,

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X-{inknown, *=Stop codon, /~possible nucleotide deletion, \~possible nucleotide insertion)
28029	58397	A	28199	I	532	MRVRNREEGNVGKWGERQVD QRDAVMRVRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTEGA GGAESISVRLPRRSGSVSLQLLS REDLGRSGSEI,GPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA-QLKTD AASPRKRPDTYTECSPGSFSCTH SSVESHNYHCSRPGLQSGLPHY SFYHTPS*LHSLHLTFTPFPHI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRVPLVENQILTG ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFSLSPCCLHCQGKRLCG HHEEARRKNVSIPRKEAGIIHC KGHQKIASDPIAQDNAYADKL AKKAASVPTSVPHGISQAPPPLP THQARYWQIDFTHMPRVRKLK YLLVWVDTFTGWVEAFPTGSK KATAVISSLLSDIPQFSLPTSIHS DSRLAFISQITQAVSQALGIK
28032	58400	A	28202	3	518	KRPHPYLPLLTLFSDSAHLHPO EINNHVAHTRPVWSLHTDVH EIWCRDSDRGTSLGRSIPCPPVL CSVRKIHLQPQVLRPTSPRNISPI LNQVSGLFLLSSPTSLTVPQPLS PFNLGATLQS/APFS*FQFLSFSG RDKGDTFYPWSQNSGACHRLG KAAFPWCLIIAGTPL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
28033	58401	Α	28203	3	1626	SEGEAKGSITLTVCTALYLKLT
						LFHKTGVFGPLRFPVVNTLNPS
					1	PFHDGTRELGASEAIGQCQSSA
		ŀ		1		AKLRRSGKESESLGPEFQGLWK
Ì		1			1	WLPGSSQCFARESLEEKLSLCF
						RPSDPGAEPPRTAVRPITERSLL
1						QGDEYCCALGQGVPNPWSTDR
						YWNWATLQEIGPSSCRKTSSGI
		1	1			PLILRYGHVRDLHGSSSHHRPG
		1		1		GPKRNKWFRELGLGSACCMRP
ļ		1				RDLVPCVPAAPAVAERGESTA
		1		1		QAVASEGASPKPWQLPGGVGP
				i		VGAQKSRIEVWEPLPIFRRMYG
						KACMSRQKFAAGAGFSWYVP
						AVVGAKVHDVNLHMLSFPSK
						WKLHTCMKFGAVTQIVTSLGR
		1				SSCSLLLEKDPPMVLRPTSPRNI
						SPISNLTKETRFIRGPKTPAPVT
		İ				DWEGSLPLVFNHCRDASLIIHP
1	l					GFRGVRPRRDACLSPSPLANLIN
						LTFKVYNNRKKLQFLAFTVRQ
						TSAMSPAHKNFQ\SLNLSGQAF
						LQNLLPQELATSARNPATRPRN
						ACSPGFLLSHVPSVRDPTGNWT
		_				VQLTWHPLPEPLELWPKAL
28034	58402 58403	A	28204 28205	921	1009	
28036	58404	A	28206	<del> </del>	2706	
28037	58405	A	28207	1336	1490	
28038	58406	A	28208	466	560	
28039	58407	A	28209	863	1672	
28040	58408	A	28210	1	876	
28041	58409	A	28211	133	746	SVKMVRYSLDPEN\PMKSCK/S
20041	30407	ľ.	10211	1,22	7.0	ORGSNLRVPFKDHS*KLPOAHO
						RVCHIRKSPTKY\LKDVHLTRN
		ŀ				OCVPIPDRYNG*OLGOVCRRPK
		ļ.		İ		QMGPGTTKGR\WPQKGVLKFL
		1				PAHALKTAEM*C*TLRVLDVD
						LVIEHI\QVNKAP\KM\RRRTYR
		1	1		1	AHGRINPYMSSPCH\IEM\ILTEK
		ļ				EQIVPKPEEEVAQKKKIS\QKKL
						KETPTLWHGE
28042	58410	Α	28212	3	466	
28043	58411	Α	28213	1	2772	
28044	58412	Α	28214	1	1353	
28045	58413	Α	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR
					L	S*DY*CWR

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nuclcotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28046	58414	А	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEK ASSQATLPNQPVEKAI IMOLGTLLTH-HELVPTALSCS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQXIWNSW*SC LULI*PPCVILSFLVYQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
28047	58415	Α	28217	2383	2651	
28048	58416	Α	28218	125	1396	
28049	58417	Α	28219	466	643	
28050	58418	Α	28220	73	150	
28051	58419	C	28221	1	240	
28052	58420	Α	28222	2	499	
28053	58421	Α	28223	192	351	
28054	58422	В	28224	1	2103	
28055	58423	Α	28225	247	400	
28056	58424	Α	28226	288	589	WCSRRRGWYLLLGFHNYWRSS TFLVRCTPSCPGGCCPRYGIYPV RSCPRLPGGVSRYGSIHSG/RWC SWSPSWSPWLTSVTPRLYVAL M*AVVCPVVGKQP
28057	58425	Α	28227	319	398	
28058	58426	Α	28228	1299	1506	
28059	58427	Α	28229	1250	1907	
28060	58428	A	28230	547	638	EKRKSNCPCLQMT*LYI*KTPSS QPKISLS

SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or pepude sequence	detetion, (=possible nucleotide insertion)
		_		<u> </u>		
28061	58429	Α	28231	488	2358	RLSLGHWAAGKQGASDSCEKF
		1	l			TQPPSGVLESTTP/CAAPSPPNR
	1		İ		DSGPCPASSPGLSRPLLSGTAW	
	1				APPPAPPWARVRPPREVWRAD	
		1				LLTPQGGGPATGVSGGEECDSI
		1	l			VGGNPGIWKAWGHRRTRVAG
		l				GRRGGPGEADKQPLLVILRQTO
	i	l				SGVDLQQTPTDLQLRVLTVRR
		l				NTNKRKGHPHQNPICTSPSSKT
		1		i		EGRSMRQKVNKDIQELNSALH
	İ					QVDLIDIYRTLHPKSTEYTFFSA
		1		1		PHHTYSNIDHIVGSKALLNKCK
		1		1		RTEIVANCLSDHSAIKPELRIKK
						LTQNCSTTWKLNNLLLNDYWI
						SKRKTHSKASRRQEITKIRAELI
					1	EIETQNTLQKINESRSWFFENIN
						KIDRLLERLIKKEREKNQIDAIK
				l		NDKGDITTDPTKIQTTIREYYKI
		l				LYKNKLLNLEEMDKFLDTYTL
						PRLNQEEIESLNRPITGYEIEAII
						NSLPTKKSPGSDGFTAEFYQRY
						KQELVTFLLKLFQSTEKEGILP
						SFHEASIILIPKPGRDTTKKENFI
						PISLMNIDAKILNKILANQIQQH
		į				KKLIHHDQLGFIPGMQGLFSTC
						KSINVIHHINKTKDKNHMIISID
						AEMASDKIQQPFMLKTLNKLG
						DGMYLKIIRAIYDKPTANIILNO
28062	58430	В	28232	1	2664	
28063	58431	Α	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK
						NPLQTSKC*EILSPP\ACPKRAPE
						GSTKHGKEQPVPATAKTGQIV
28064	58432	Α	28234	804	920	RDIYSNKCPQEKPEKI*NGHPNI
						TIKRIREARAKTFKS
28065	58433	A	28235	786	935	
28066	58434	В	28236	3	1555	
28067	58435	Α	28237	895	1389	GELLEVVMTLAWSWGLFLARI
						QTQVFKAFNLFVLILRSSWAFC
			l		1	WTHGDELWALVSRKPK*HPGF
					1	CDHAPSTFPPPGLCP/EPTPPPGA
				l .		VSQYPCPPPSCPWPRWLVLPLP
				Į.	1	VLAGTSSPWKGFSYPPCCFSPF
		1	l			HLPARFLHRGNCLSTFDLVVLP
		1	l	1	1	PLEMPVLALS
28068	58436	Α	28238	704	799	EKRKSNCLCLQMT*LCI*KTPS
						QPKISLGW
28069	58437	С	28239	178	1287	
28070	58438	В	28240	1	1028	
28071	58439	Α	2824I	476	678	
28072	58440	В	28242	I	1059	
28073	58441	В	28243	1	924	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first coden for peptide sequence	codon for last amino acid of peptide sequence	deletion, \=possible nucleotide insertion)
28074	58442	A	28244	39	200	LPLFLIECPLFPSPA*LPWPGLPT LC*IGVVREGIPVLCPFSKGMLP VFAHSV
28075	58443	A	28245	225	314	
28076	58444	Α	28246	243	311	
28077	58445	A	28247	21	1593	RKRTAPAGPRRHPKHCECPNCC SGGGRPSCGTIPPPGKLKSSP *SRKAENSKNQSAFSPPKDHSSS PVMEQSWMENDFDELTEVGFF SSAETQQQKEKFRPISLMNID VKILMKILANFIQQHIKKLIHHDI VGIJSKNGQWFNICKSINVIH HINRTNDKNHMIISIDAEKAFD KIQOPPHLKTLKKLLGIDGTY LIKOPTRQGCPLSPLLFNIALEVI LKDRTRQGCPLSPLLFNIALEVI SLFAEDMIVYLENPIVSAPPLKE LYINNRQRESQIMNEPPFTIARRR IKYLGIQLTRDWKGDLFENNKPU YINNRQRESQIMNEPPFTIARRR IKYLGIQLTRDWKGDLFENNKPU KLKEIKEDTTNKWKNMPCSWIG RINIMKMAILAKVIYRNAIPIK RINTHERETTLEFIENDOK
28078	58446	A	28248	129	239	FFLTMSMECSSICLCPPLFR*AV VCRSP*RGPSHPL
28079	58447	A	28249	3	254	GTAWAPPPAPPWARVRPP\EKC GAPTCSHPREEAPRLASPAGKN VTVPWGETQGSGRLGVTGEPE LLGLGGAGALARLISSLCW
28080	58448	A	28250	80	517	GHFLGQQPRPQLHSPAPDIPPAP TPTDABGLPQQQQLPQLEPQPE CQGPVEAEARQLKSCMKPVRR RPAEEELKTKNMDDNTFAMAE HPDVQESVGPLVAPTPLRPWPQ MTLQVCWSLLEFHSRPCLPGY HQQRLQNSKDCCLFLP
28081	58449	Α	28251	1	670	
28082	58450	A	28252	1450	1650	QWISRQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKSS
28083	58451	Α	28253	1010	1294	QRFSWQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKS\PE GSAKHGKEQPIPTTAKTCQIVK TIQA
28084	58452	Α	28254	41	812	
28085	58453	В	28255	1	2957	
28086	58454	В	28256	650	3212	
28087	58455	A	28257	1	556	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
				sequence		
28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA
20000	30430	ľ	20230	15,70		SRDSS*AVSHLCGTPLEIGWSNL
						PGSHSQSPWNSGPRLSD
28089	58457	A	28259	1	253	T GOTTO GOT WITHOUT RESS
28090	58458	A	28260	409	884	
28091	58459	A	28261	1	2256	
28092	58460	A	28262	118	302	
28093	58461	A	28263	558	659	
28094	58462	A	28264	1	400	
28095	58463	Λ	28265	308	433	
28096	58464	A	28266	1	711	
28097	58465	A	28267	559	657	
28098	58466	A	28268	1	400	
28099	58467	В	28269	232	498	
28100	58468	A	28270	1	2978	
28101	58469	В	28271	128	290	
28102	58470	Α	28272	3	193	DVNIFIRYGLWCFLSPFGLL*QF
	1	ļ			WRLEVQYQDAADSMSGGDPLS	
ł						HS
28103	58471	В	28273	125	197	
28104	58472	Α	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGNKNGGEASM
				1	VRGCLERAET*GCPNGMPQGE	
l						RLSRFGLRTETTGTVTFRLHCL
						QQSR
28106	58474	Α	28276	3	334	
28107	58475	Α	28277	2	1698	
28108	58476	В	28278	1	1281	
28109	58477	Α	28279	198	532	NSLFLLCLCQALVSG*CWPHK
		1				MS*GGFPLFLLTGIVS/GRNGTS
		1		1		SSLYLW*NSAVNPSGPGLFLVS
		1			Į.	RLLTIASISEPVIGLFRDSTSSWF
	1	1		1		SLGRVYVSRNLSISSRFSSLFA
28110	58478	Α	28280	3	610	TDFCFCFWLPGLSVLFLSFFLSF
l		1		i		FLSFFLSFFLSLSFSFSLSLFLFLS
		1		i		VSLSFLPSFLFLSLSLSLFLSLFS
		1				LL/YCLSFLSLFSFFLFLLSFSLSS
		1				SLLFSSLLFSSLLFLLLLL
	1	1	1			LSLSLLFFLSFLFSESVLWEGSV
						AGLQTPALSSALNRAVLPVSCS
		İ				MIDQLCDPGKYFISLCLFLHLR
		İ		1		VRTCGVWFSVLVIVC
28111	58479	Α	28281	203	470	QAKSVWKKILSFRI*LHRMSDG
		1		1		IFWLCFYISMHLCWLVLYWAV
	1	1		1		WFKLQTTRLSRWLTDSLPVSY
	1			1		GYCQGMNEGCSSQFKTVFPTLF
		1		1		SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK
	1			1		EISKG/LTKTPRLLVMSPSSCSR
	1			1		RGIWPNPDTCPLLLL

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28114	58482	Α	28284	179	445	QLSGLASGMRESRDVLGLRFTP
	1					LLLWIVHSRAWALVESAVMST
	l .					WECWVGDERGTGVKLAGAHT
						ELPTGPGV*YSPPCVHVFSLFNS
				Į.		HL
28115	58483	A	28285	128	381	
28116	58484	Α	28286	1	1392	
28117	58485	c	28287	1	3169	
28118	58486	A	28288	1905	2449	AQLPTPAPLPFLGRRWGTWGFP
	1					GHAFHSWFWYST\GEGAMGSF
1						LALLSFPPLGMKLAILEDFFGIS
						GTAAPLGSSFGSSLRSSLSVTEA
						LLARSL/HFLLILLPLLFLLLFLIA
		l	ŀ			FORTLLVGQCPAKSPLGNALEC
İ						NLGAAGSRAHGGEHATGGLQL
	Į.					LALFEAGOSLOPLTACVPGPRP
						LTCL
28119	58487	Λ	28289	693	905	EESIS*KWPYCPSFHNLHPQAY
	i	1				KAIPHPASLGKT*YNQDNNNAG
						KLFKANRNPALGCQQPVCSKT
	1	ŀ				DGFRF
28120	58488	Α	28290	3	427	
28121	58489	Α	28291	1	1195	
28122	58490	Α	28292	158	779	
28123	58491	A	28293	227	378	
28124	58492	A	28294	1	621	
28125	58493	A	28295	J	351	
28126	58494	Α	28296	1	507	
28127	58495	Α	28297	1	543	
28128	58496	Α	28298	343	428	
28129	58497	Α	28299	785	1178	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28130	58498	A	28300	842	2592	IREEVESLKRPITSSDIEAVINSL
28130	30470	<u>۱</u> ^	28300	042	2372	SIKKKVOYOTDSOPNSTRGENL
1		l				GNTIQDTGMGKDFITKTPKAM
l		l			1	ATKAKIDKWDLIKLKSFCTAKE
		l				TIIRVNROPTEWEKIFEIYPSNK
		l				
		l			l	GLISRIYKELKQIYKKKTNDPIK
İ		1		•		KWAKDMNRHFSKEDIYAAKK
		1				H/DEKMLIITGTWMKLETIILSK
		1			l	LTQEQKTKHRMFSLLIPDDGNS
		ł				LTRRMLLIGISVKTPVGTGAIPG
		ł				PVGGTTAAGAYGRKEKALSNC
		l				DSILALALAKMSENQMSMESFF
		l				EKGKDPMRRQQKTLTLTKKKN
		l				AFKRKYQESYLNYGFIATVRAS
1		l			l .	FLVANCIVKAKKPFTIGEELILP
		1				AAKDICYELLGEAAVQKVPHV
	1	l				PLPVSTITRPIDEIAEDIEAQFLE
ļ		l			1	RINESLWYTIQIDKSTIADNKAT
]						MLVFVQYIFQEDVHEDVFFQES
1		l			ŀ	LRATSQPLKTPQTGKEWVHDPF
						VDKPSESTLSMLEEDQLLEIAN
		l				DGSLKSMFEKTSNLHIVCIKVK
		l				AEYPEIATKALRRLLAFPWVAA
		l			į	VDRECQWGSRDVEMRRLLDPK
1		ł			,	AGFSLLGVGNCHCLRTLEFVGL
1					ł	SMSSLCGAMLLCGLRAAPYISL
						RDHKGQGTLL
28131	58499	Α	2830I	I	1662	
28132	58500	Α	28302	2	406	CWWDCKLVQPLWKSVWRFLR
		1	l			DLELEIPFDPAILLLGIYPKDYKS
		l	l		i	CCYKDICT/RVCVPAALFTIANT
	1					WNQPKCTSMIDWVKKMWHIY
		l				TMEYY\AAIKKDEFMSFAGT*M
		1	İ	l .	l	KLETIILSKLTQEQKTKHRMFSL
		1		į.		YWKS
28133	58501	Α	28303	1	1404	
28134	58502	Α	28304	68	2269	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28135	58503	A	28305	189	1890	MKMASSLAFLLINFHYSLLLV QLLITECSAQFSVLGPSOPILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDROGAPYRGTSILROGITAG KAALRIHNVTASDSGKYLCYFQ DGDFYEKALVELKVAALGSNL HVEVKGYEDGGIHLECRSTGW YPOPQIGWSNAKGENIPAVEAP VVADGVGLYEVAASVIRNGGS GEGVSCIIRNSLLGLEKTASISIA DPFFRSAQPWIAALAGTLPILL LLAGASYPLWRQOKEITLALSSEI ESEQEMKEMGYAATEREISLRE RKKIQVLTPDVILVPOMANALL USSEDQRSVORAEEPHDLPDNP ERFEWRYCVLGCESFMSERHY WEVEVGDRSEWHIGVSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTERTINLE/EPPR KVGVILDVETGHISFYNATDGS HYTFLHASSSEPL.PYFRILTLE PTALTVCPIPK/GRFFPFTLVP DHSLEIPLTPGLANESGEPQAEV TSLLIPAQPGAKGLTLHNSQSE PYSYSHTLKHETDIHSIP

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide Idention of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino aeid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequenee		,
28136	58504	A	28306	172	1905	I MKMASSLAFLLLNFHVSLFLVO
20150	20301	ľ	20300	1.72	1.703	LLTPCSAQFSVLGPSGPILAMV
					1	GEDADLPCHLFPTMSAETMELF
						WVSSSLRQVVNVYADGKEVED
		i				RQSAPYRGRTSILRDGITAGKA
						ALRIHNVTASDSGKYLCYFQDC
		ı		1		DFYEKALVELKVAALGSDLHIE
				ľ		VKGYEDGGIHLECRSTGWYPQ
						PQIKWSDTKGENIPAVEAPVVA
						DGVGLYAVAASVIMRGSSGGG
						VSCIIRNSLLGLEKTASISIADPF
	1	1				FRSAQPWIAALAGTLPISLLLLA
1		1				GASYFLWRQQKEKIALSRETER
						EREMKEMGYAATEQEISLREKL
		1				QEELKWRKIQYMARGEKSLAY
						HEWKMALFKPADVILDPDTAN
1						AILLVSEDQRSVQRAEEPRDLP
1						DNPERFEWRYCVLGCENFTSGR
		1				HYWEVEVGDRKEWHIGVCSK
1		1				NVERKKGWVKMTPENGYWTM
1						GLTDGNKYRALTEPRTNLKLPE
						PPRKVGIFLDYETGEISFYNATD
					İ	GSHIYTFPHASFSEPLYPVFRILT
1		1				LEPTALTICPIPKEVRRVPPI/AD
1		1				LVPDHSLETPLDPGA*LMKVGE
1						POAGK*HLCFSLPTLGAEGLPF
28137	58505	A	28307	1	2220	TOTAL TIDOLOGIA TECHNOLIT
28138	58506	Α	28308	134	509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAORSP
i						AEKMGETPGAAVSRIRLGGRV
		ĺ				ALRRHVRGEPLRAPDCPLGPDA
						WVPTRGSHFPGFFPREOSLS/W
						GATPPSYRSSEVRSGAESGRPAF
ľ						DSVGSGVQAH
28140	58508	Α	28310	1	1066	20100014:11
28141	58509	Α	28311	77	273	
28142	58510	Α	28312	1	415	
28143	58511	Α	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	A	28315	2	671	PGEFTRAPRVRRRAMGISRDN
						WHKRRKTGGIRKPYHKKRKYE
1						LGRPAANTKIGPRRIHTVRVRG
		1	1			GNKK\YRALRLDVGNFSWGSO
		1		1		CCTRKTRIIDVVYNASNNELVR
1		1	1			TKTLVKNCIVLIDSTPYRQWYE
		i				SHYALPLGRKKGAKLTPEEEEI
1		1	I			
						LNKKRSKKIQKKYDERKKNAK
1						ISSLLEEQFQQGKLLACIASRPG
	-04.	ļ				QCGRADGYVLEGKELEFYLRKI
28146	58514	A	28316	3	1259	
28147	58515	A	28317	1745	2681	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28148	58516	Ā	28318	1	2502	
28149	58517	Α	28319	1097	1417	
28150	58518	Α	28320	I	398	MTAEERDKFPTDQQAIPSMDPH
				1	1	WDPDSDHGDWSHKHLLTCVLE
		l		İ		GLRRIRKKPMNYSMMSTITQG
		l		1		KEENPSAFLKWLREALRKYTPL
						SPNSLRGQLILKDTFITQSAADI
	ŀ					RRKLQKQALGPEQNLEALLNQ
		1				ATSVFYNRDQEEQAQKEKRLSS
		ł				RSVTIRGILGQSVTRPEAHKGL
				1		QDIVKHLKAQGLVRKCSSDCN
		ŀ				TPILGVQKLNGQWRLVQDLGLI
		l				NKAIIPLYPVVPNPYTLLSQISEE
		l				AEWFTVLDLKDAFFCIPLHSDS
						QFLFACEDPTDHTSQLTQT1LPH
						GFRDSPYLFGQALAQDLGHFSS
ŀ		1				SGTLALQYVDDLPLATSLEASC
ŀ		1				OQATLDLLNFLANQGYKASRS
ŀ		1				KAQLCLQQRDGQTTLYSNQGA
l		l				PEGKYSSSRMRPRVRNSLQNLK
		l				AGPSTTPALSLPTGQNLSLYVT
						ETAGIALGVLTQAHGMNPQPV
		ĺ				AYLSKKIDVVAKGWPHCLRVV
		ŀ				VAVAILVSEAIKIIQGKDLTVWT
1		1				THDVNGILGAKGSLWLSDNCL
				1		LRYQALLLEGPVLQIPMCAALN
		1				PATFLPEDGEPIS**PLTLRWPLP
ł		!			l	QLPLNSEASLLLLHQFSYLGMP
ļ		l				LVGGSSHEPA
28151	58519	Α	28321	318	363	
28152	58520	Α	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP
		1				PLPARWPIH
28153	58521	Α	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD
	1	l				TSEHLKEQTADTSSLRTVTLTA
					1	RVCGFILEVSETKNSPEGTNSG
l					I	HILTSQMGLSPIAKRRETSASAA
		1	1			ALVSATIPICRVQGPLRVLGQE
		1	1		l	VFLLLLRLPTAPLPINDKPP/PN/
			1		1	TPLPRRKQAKKSPKDHKNPWAI
		l	1			GYVPFKQ*GEGNLA*PGYMSPS

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /**possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
28154	58522	Α	28324	350	1563	FLYIQLYPTPITCSLKYQRKQNG
20134	36322	<u>۱</u> ^	20324	330	1303	SLFWTSRMPSSVFPCTLTPSFSL
1		1				PLRIP/PDHTSQLTWTVLPPGFR
		1				DSPPLFGQALAQDLGHFSSPGT
		1				LVLOYVDDLLLATSSEASCOOA
	1	l	ŀ			TLDLLNFLANQGYKVSRSKAQ
		1				LCLOOVKYLGLILAKGTRALIK
	İ					ERIQPILAYPCPKTLKQLRGFLG
		l				ITGFCQLWIPGYSEIARPLYTLIK
		l				DTQRANTHLVEWESEAETAFK
		l				TLKQALVQAPGLSLPTGQNFSL
	1	l				YVTERAGIALGVLTQTRGTTPO
	ŀ	1				PVAHLSKETDVVAKGWPHCLR
	ŀ	1				VVAAVAVLVSEAIKIIQGKDLIV
		l				
		1	l			WTTHEVNGILGEKEVYGYQTN AYLDTRRSALRDWCFKYARPV
	İ	l				
	ł		İ	1		AAILLLLAFGPCIFNLPVKFVSS
		l			1	RIEAIKLQMVLQMDPQISSTNN FYRGPLD
20155	50500	١.	20225	020	1143	FYRGPLD
28155 28156	58523 58524	A	28325	234	510	PWQSLP*VAQKVPKDHRSLPLE
28156	38324	Α.	28326	234	210	P*TRSLNNS*QHWWLCPPARAP
		1				STCSTSCPARDGPPPPSPAPHGP
						RNTSVPG\HSRPGSPPP\PPRTPP
	l	1	l			VS
28157	58525	A	28327	2	816	V 3
28158	58526	A	28328	1	1311	
28159	58527	Ā	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	<del></del>	484	
28162	58530	A	28332	72	299	
28163	58531	A	28333	737	847	
28164	58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	Â	28339	65	244	
28170	58538	A	28340	2	584	GKSRRMFPAQEEADRTVFVGN
28170	30330	Ι^	20340	ľ	364	LEARVREEILYELFLQFLI\AGPL
		l				TKVTICKDREGKPKSFGFVCFK
		1	l	I		HPESVSYAIALLNGIRLYGRPIN
1		1	l	1		VOYRFGSSRSSEPANQSFESCV
1	1	l		I		
1		1	l	1		KINSHNYRNEEMVVGRSSFPM
1		1	l	1		QYFPINNTSLPQEYFLFQKMQR
1	1		l	I		HVYNPVLQLPYYEMTAPLPNS
L			l	l		ASVSSSLNHVPDLEAGPSS

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \= possible nucleotide insertion)
				sequence		
28171	58539	A	28341	2	367	MTMHYEIPVRTRRSKGTT*LPQ
					\	NA/SVNNMPH*TGAI*ADISMTN
ļ				ı		YARIERNHLGRGNSNSKDPKLR
	1			1		ESSEHLRKLKTRVVNEQTRLGL
				l		IMETFVGRGGEAPFYFQCDKHL
				1		SRSFQGLGLICL
28172	58540	Α	28342	98	387	RKQPPKVLQWLLLAF*SHRSW
						LSSPWPSDLWRPWAGGACARL
						LLQQPRDSASLKERQQPQSGAY
1				1		R*NSHLPGTEHLGEGVAVCAAS
				1		ADLNVTACWL
28173	58541	Α	28344	1	269	
28174	58542	Α	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	Α	28347	59	310	
28177	58545	Α	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQL
						LDSLIF*RVFCVSISFSSALILVIS
						CLLLAFECVCSCFSSSFNCDVR
		-		1		VSILDLSCFLL*AFSAINFPLHTA
						LNASQRFWYVVSLFSLVSKNIFI
		ł				SAFISLCTQ*SFRSRLFSFHVVER
		1			i	L*VRF/CNPEF*FDCTVV/WRDS
		1		i		LL*FLFFYIC*GELYFQLCGQFW
1		l		ı		NRCGVVLKKMYILLIWGGEFC
		ļ.,				RCLLGLLGAELSSIPGYSC
28178	58546	Α	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQL
l						LDSLIF*RVFCVSISFSSALILVIS
				ı		CLLLAFECVCSCFSSSFNCDVR
		1	1	i		VSISDLSCFPLWAFSAINFPLHT
		1		I		ALSASQRFWYVVSLFSLVSKNI FISAFISLCTO*SFRSRLFSFHVV
		1	l	ı		ERL*VRF/CNPEF*FDCTVV\WR
		1		i		*FVIISVLLHLLRRALLPTMWSI
	1	1		1		LE*VWCGAEKNVYSVDLGWR
		1				VL*MSIRSAWCRAEFNSWVSLL
1		1	ĺ	1		TFCLVDLSFSLAALNIFSFISTLV
1		ı				NLTIMCLGVALLEEYLCGVLCI
28179	58547	В	28350	1	3135	THE TIME DO VALLEE TECHNECI
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNOL
20.00	2 3340	١,	1-333.	1	1	LDSLIF*RVFCVSISFSSALILVIS
1		1		i .		CLLLAFECVCSCFSSSFNCDVR
1		1		1		VSILDLSCFLL*AFSAINFPLHTA
1		ı		1	1	LNASORFWYVVSLFSLVSKNIFI
1		1		1		SAFISLCTO*SFRSRLFSFHVVER
1		1		1		L*VRF/CNPEF*FDCTVV/WRDS
l		İ		1		LL*FLFFYIC*GELYFOVCGOFW
		İ		1		NRCGVVLKKMYILLIWGGEFC
1		1		i		RCLLGLLGAELSSIPGYPC
	1	_	L	1	1	THE DESCRIPTION OF THE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
l	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28181	58549	Α	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL
						LDSLIF*RVFCVSISFSSALILVIS
	į.					CLLLAFECVCSCFSSSFNCDVR
				i		VSILDLSCFLL*AFSAINFPLHTA
						LNASQRFWYVVSLFSLVSKNIFI
	1					SAFISLCTQ*SFRSRLFSFHVVER
						L*VRF/CNPEF*FDCTVV/WRDS
						LL*FLFFYIC*GELYFPVCGQFW
	Ì					NRCGVVLKKMYILLIWGGEFC
		İ				RCLLGLLGAELSSIPGYPC
28182	58550	A	28353	i	3531	
28183	58551	A	28354	1	3126	
28184	58552	Α	28355	2357	3083	FFSLFFFIILASGLSILLIPSKNQL
				1		LDSLIF*RVFCVSISFSSALILVIS
		l				CLLLAFECVCSCFSSSFNCDVR
		l			ŀ	VSILDLSCFLLWAFSAINFPLHT
1		l				ALNASQIFWYVVSLFSLVSKNIF
						ISAFISLCTO*SFRSRLFSFHVVE
	Į.					RF*VRF/CNPEF*FDCTVV/WRD
	į			i		SLL*FLFFYIC*GELYFOVCGOF
	l .					WNRCGVVLKKMYILLIWSGEF
						CRCLLGLLGAELSSIPGYPC*FF
1						VLLICLMLTVGC
			000 # 5	6412	7092	
28185	58553	Α	28356	0412	7092	FFSLFFFISLASGLSILLILSKNQL
						LDSLSF*RVFCVSISFSSALILVIS
	1	l				CLLLAFECVCSCFSSSFNCDVR
						VSILDLSCFLLWAFSAINFPLHT
1						ALNVSQRFWYVVSLFSLVSKNI
İ						FISAFISLCTQ*TFRSRLFSFHVV
1						ERL*VRF/CNPEF*FDCTVV/WR
						DSLL*FVFFYIC*GELYFQLCGQ
1						FWNRCGVVLKKMYILLIWGGE
1				į.		FCRCLLGLLGAELSSIPGYPC
28186	58554	Α	28357	1	2019	
28187	58555	Α	28358	1	1263	
28188	58556	Α	28359	77	304	
28189	58557	Α	28360	1	756	
28190	58558	Α	28361	1	369	QQRTLLASNEAFKSQAKSASQP
		1				ASKYMKENDQLKKG\AAVDGG
1				l		KLDVGNAEVKLEEENRSLKAD
		1	1			LQKLKDELASTKQKLEKAENQ
		1	1	l	1	VLAMRKQ/SPEGLTKEYDRLLE
1				I	1	EHAKLQAAVDGPMDKKEE
28191	58559	A	28362	879	1156	, , , , , , , , , , , , , , , , , , , ,
28192	58560	Ā	28363	54	407	
20.72	10.00	-	1	I- ·		

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28193	58561	Α	28364	620	1246	GSTWHGWDGSRCRSQNRWSC
		1	ļ			MTKRSSQPSSLS*SRSRRRWMS SSPNW*KTGPESSMSRMSSAG*
	l					SAASSRSCATRWTRRRPAAWR
						G*GVTPVAWWPPWTCSWSRPR
						EPGSGWPKPSVCWNSSEMRTT
						MSSSGSSTPWPPVSRRRPWTER
						RLGSVRGDRLRERSRPAVNRTP
						RMSRVPSGAPRGTPSRRWWM
		_				MKCWDHQMRGLVEEEVG
28194	58562	Α	28365	86	402	KGWWCRKKGWNWKRSWFLT
						FLQGLLEGPHPPSPTPAPRRTT*
						SLYSAPSRMVQVLLDDLHKWF
	ł	1				LYSCLVSAISIGIKFPLKIHISPGS
		L.				GVLEARETMSHFKEAAL
28195	58563	Α	28366	54	353	
28196	58564	Α	28367	66	352	
28197	58565	Α	28368	442	700	HWNKVPAENPHLPWVRCSPPT
						PLGKPKPCSSWNRRSGTDVSGT
	l	1				GLSESGSSWPSGSCNGVTGTDA
						YGP\GYVKSGSFPGPRVRGTV
28198	58566	Α	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR
						SKDATPDPPRGLGKFPPRLPQA
						PRLLGSQRLLSTLCSTLSGRGG
		1				KNTSRLSFSPSGSVKGRVRDVK
	ł	1				EPGPIRAHRTAFFPNASS\GSEG
	1	1				R*SPSVVAWRGFR/CVGVWRFP
	i	1				TVGVWHAPPRCTR*SPITGSAP
		L.				LSVWSPPACTGSPTCTAGA
28199	58567	В	28370	163	387	
28200	58568	В	28371	112	419	
28201	58569	A	28372	1	1902	MSRIAWKLLWKLIQGYLGQPA
						GTARRHPGIGIFKSPPGDFTCNG
						LIAVIKNQSDNQRGMSPGSWSP
						GRENNPTLVEVLEGVVRLPETV
	i					HTAVRYTSIELVGEMSEVVDRN
1	1	1		I		PQFLDPVLGYLMKGLCEKPLAS
		I				AAAKAIHNICSVCRDHMAQHF
		I				NGLLEIARSLDSFLLSPEAAVGL
	1	1		I		LKGTALVLARLPLDKITECLSEL
		I				CSVQVMALKKVFVGATSRRVA
	1	I				KLFREGLKAHGNSFETSGEAER
1		1		I		CCTWRPKEMTCVE
28202	58570	Α	28373	1	2019	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28203	58571	A	28374	12	1455	SAAVAARSPQPQRPSATLGPGP
		1			\	QRRPPSAAPTPAWAAAAAPGS
	l	l			1	RRRRPLPARPLWAPARGAAAA
		l				GPAEAPMLARRKPVRAALTINP
		ı				\TIAEGPSP\TSEGASEANLG\DL
		1				QKKLEELE\LDEQ\QKKRLEAFL
		1				TOKA/RRVGELKDDDFERISE\L
						GAGNG\GVVTKSPAQDPSGLIM
		1				\ARKLIH\LEIQAGASGNQIIPR/D
						LQVLHDGTWPTMGG\FYGAFY
		1				SDGE\ISICIEHMDGGSL\DQVLK
		ı				E\AKRIPEEI\LGKVSHRSFSGGL
		1				AYLREKHQIMH\RDVKPS\NILV
		1			1	\NSRGEIKLCDFGVSGQLIDSM\
						ANSFVG\TRCYM\APERLQG\TH
						YSVQSDI\WSMGLSLVELAVGR
l						V\PIPPRDAEELEAIFGRPVVDG
	ł					EEGEPHSISPRPRPPGRPVSGHG
		1				MDSRPAMAIFELLDYIVNEPP\P
	1	1			1	KLPNGVFTPDFQE\FVNKCLIKN
1		1				P\AERADLKMLTNHTFIKRSEG\
i		1				EEVDFAGWLCKTPAG*TKPGTP
1						TRTAV
28204	58572	A	28375	229	257	VSLSASPLVSLAGRSPSRPLGRG
28204	36372	Ι^	203/3	229	237	COSLDGYGVGWOAOSPGADE
		1				GNRSFT*PELADKNVPNLHVM
		1				KAMOSLKSRGYVKERLPSSAP
l		1				GDCACHPTP
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP
20203	36373	Ι^	20370	ľ	377	KQQK*PGGTEDS/YDASGPPPKF
i	1					LIKEIKLG VPRFFPIRGV*NPGPG
Į.						KNFGGPFKKT*FCWARVPKM*
	1	1				FFKGGPSSSSPAVSLFNAKESSPI
	1	1				LLRWMTTSTTKSAYKLEFGC
28206	58574	A	28377	1	367	EERWINI IST TROATREET GE
28207	58575	A	28378	i -	1001	MSWEMEQDEVYKEMSINHKN
20207	30373	1,	20370	ľ	1.00.	EGTRVEKPNRYRIIHIOPDAINH
i		1				VSRKKDVPSASGAGHSRSSTGS
		1	İ			RPGVRRLWPLLLRSAPSGPLNN
	1	1				AVPAPGKGPGRWGGSPSLSRSG
		1	İ			GKASTRVAPGLSAHSQAASGV
	1	1				PEPAEPQHQRTKASGSRRRSLR
	1	1				VVPEAPKPRTRTAREGKGAGA
		1				GHTGGAQEQRRRRRWACRGLR
		1			1	GRPGAVSPGGAEAINOLASEHC
	1	1			1	GNPAAALHRCIASLPRNLLVW
	1	1			1	AGRMLMPKKNRIAIYELLFKEE
	1	1	1		1	VTVVKKDVHMPKHLELADKNS
1	1	1	1		1	RGYYVKEQFAWRHVYWYLTN
	1	1			1	ED/MPVSP*LPSSAPGDCACHPT
		1			1	
	1	1	l .	l		PQPSRDWQASV

SEQ 1D	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	locatiun of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG
Lower						ADEGNHGDTGYPHW*GTSRNV
						SRQTVQTRSLGT
28210	58578	A	28381	168	378	
28211	58579	A	28382	1	900	GTRDATAEENRVLLAMVNPTV
						FFDIAVDGEPLGRVSFEVRGLD
l		1				TKK*LLI*SIKLC*QIGGSSIFITS
1		l				D*KNSCLPLIVQQCLLFLRILP\L
1						FADKVPKTAENFRALST\GEKG
						FGL*GVPCFHRIIPGFMCQGGDI
						TRHNGT\GGK\$I\YGEKFEDENF
		1				LKHTG\PG\ILSMAKCWDPTQN
1						GSQFFNLALAKTEWLGWASHV
						GVLAK*KKGMNIVEAMERFGS
		1				RNGKTSKMITTADCGQLRIKFD
		1				LVFYLNHQDHSFWKPQGEHPS
		ı				NPFARRILRILWLSLAVPFWVPC
						FPCSLPCLAGLQS
28212	58580	Α	28383	393	683	HAKDGMEQRGNNECPKVGKQ
		ł		1		VTLQHSDPEDRKTSTRCGENLY
	1	1	1			MSSDPTSWSSAIQSWYDEILDF
	ł				Į.	VYGVGPKSPNIVLLVII*IIERIPR
		_				TNKEHLVPV
28213	58581	A	28384	119	193 567	
28214 28215	58582 58583	A	28385	957	1145	EQNLLIYLVSIVQDCMDKGCII*
28213	28283	l <sup>A</sup>	20300	937	1143	LRHTSGNCMYVSDKFDFKEOC
		i				FSPRSSQKSLSGNDLQK
28216	58584	A	28387	153	2257	I SI KSSQKSESGNDEQK
28217	58585	IA.	28388	369	539	KKPARRRHLFTLLCCVFSPKLC
20217	50505	ľ.	20200	1		TAGGPMRRTFKSYDEAGTGLL
		1				SVADFRTVLRQYSINLSEEEFFH
	1	1				ILEYYDKTLSSKISYNDFLRAFL
		1				Q*TPKL
28218	58586	A	28389	3	1364	
28219	58587	Α	28390	1	996	
28220	58588	Α	28391	296	549	ETSSSVTVSDP\EMENKGGQTL\
		1				NNSSLMAEAPGTMCRFTLAPH
		1				V\LAVQGTITDLPDHLLSYDGSF
		<u>L</u>				NLSRFWYDFTLENSVLCDS
28221	58589	Α	28392	1	1065	
28222	58590	Α	28393	412	428	WILPISEPPSNRIFACWGKPAWT
1		ı		1		ACCNSLRARR*RAISCCPSHW*
		1				KEKPPWRPIRKPPLPARWPDSL
		<del>  _</del>				MQLARQVSRLESGQ
28223	58591	A	28394 28395	3	505 1201	
28224 28225	58592 58593	A B	28395	518	1606	
28225	58593	A	28396	11	798	
28226	58594	A	28397	737	3067	
28221	כעכאכן	ĮA.	46378	1/3/	12007	I

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleatide insertion)
28228	58596	В	28399	133	239	
28229	58597	Α	28400	3	376	
28230	58598	Α	28401	1	1194	
28231	58599	Λ	28402	405	611	
28232	58600	Α	28403	204	4198	
28233	58601	Α	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMFTFITQLLLVVEV KDSLERLAVEVVFILQKAMYE
		1	ł			KOAHIYMKSLCPOMVLMLRFI
		1				QWVQIMPMLKLENLQHLMAR
		1	İ			WNETVKEKK*DTLLFSMHERN
28235	58603	A	28406	359	517	
28236	58604	Ā	28407	68	487	
28237	58605	A	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQTQEPSWLHPVDP
20250	30000	ľ.	20.05	ľ	257	APGLQVELPASHAPCARTPQPL
		1	l	1		GGRWDWAPWSRGWCSLGRLG
		1				PHRSPWSGWEAQA*QWIPHQG
	l	1	l			CRWSCLPVTRRVLALLSPWVV
		1	İ			DGTGRRGAGGGARWGGSGRT
		1			i	GAHGVGGRLRHSRLOVPSPAL
		ł				LFKYYYCDIFK
28239	58607	A	28410	1	609	MVFSNLKGHWLOPIRLDSGSR
20239	38007	ļ^	20410	l'	003	NTAIGCDNOYKPTGVKLOTFA
		1	l			VSVTALKAARLGLFVPPGGLV
1		1	l	ł		VSLGSGVKLOIFASQVVCFDRA
		1				LIGAFTIPELDTKVLHVPIRLVR
ł		1				YRVWTORFSKAPPDSGAOLASP
ł		l				SESHTRAAGGAACOSOCRAPA
l		l				LLSPWVVDGTGRRGAGGGAHR
ļ		1				GGSGCTGTHGVGGRLRHSGLO
		1				
		l				VPSSA*VSHPLRGFL/LQPEPPR*
						APPPAPRRPVPSTTQGLRSAGA
		1	ŀ			RHWDWQAAPPAALVWDSLGE
		1				ASWAPESGGALENLCVHTLYL
		l	·			TNLMGTWRTFVSSSGIVNAPIS
				l		ALSKQTTWLAKICSFTPEPRETT
			1			SPPGGTNNPRRAALRAVTLTAK
			1	l		VCSFTPVGLYWLSQPMAVLRE
						PESNLIGWSQWPFRLLKT
28240	58608	Α	28411	548	753	TLLWE*SRLRKKSHLMMTLNH
l				l		STHSITFGLDKHCASYLMGFLYI
l	1			l		VELLIAQCGSPGATLIQWRMAS
	I	l	l	l		MD

SEQ ID	lero in vo.	134.4	SEQ ID NO:	[Nonlantida	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0.	sequence	"""	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	, , , , , , , , , , , , , , , , , , , ,			sequence		
28241	58609	Α	28412	1	903	MAKKIQLTYKCVQNWWVLGL
		1			1	TDFKNEAADPRRVKLQTFVVS
			ł		i	VTALKAARLELFIPPGGFVVSL
	i		l			ASGVKLOTFAVSVTAHKGSVD
		l	l			PKTRHKGSPSPHOTOEPSWLHP
		l		ŀ		VDPAPGLOVELPASPAPCARTP
						QPLGGQWDWVPWSRGRCSSG
1						RLGPRSSPRWGAGSGMAGCRS
					l	RALPHGEAAKAQRKVTAAAGP
			l			GAKHLTAWGWQGQLATPSVG
						PAEPTHTQNSHWPASAVCSPSS
						RLRLSLHTYPQAEGAGSGLGQP
		1				RKGLPQCSSRLKGSSSAAKVGA
				1		QAEEVPRASEACEG*RAPQVLP
		1				KWEPRORRCRERARPARAAST
202.40	50(10	١.	20412	1170	1400	LSPLISI
28242	58610	A	28413	1178	1480	CRHLIQSHSICLHQWDCHTQHL
1						YHPQ**WNQQQQLHHRCLLQG
			l			SIHLVFGPQWDPRRRRPLRGTR
						SAMARMDILRISREYITQEITEA
						ATKRKVLSVPKE
28243	58611	A	28414	126	407	WIPHRGCRWSCLPVPCRALALL
					i	SPWVVDGTGRRGAGGGARQG
		1				GWGSTGAHGVGRRLRHGGLQ
						VPSPAPRESS*GPARNRSQRRRS
	_					DSSLRERK
28244	58612	Α	28415	27 .	363	
28245	58613	Α	28416	1	576	
28246	58614	Α	28417	813	923	YSLIHAAPQQRS*SLSGPHQTY
		١.				DISSYTCQCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVP
						TRLRSPASFTQWIPHWGCRWSC
						LPVPRRVPALLSPWVVDGTGG
	l	1			Į.	CGAGGGAHRGGWGCTGAHGG
				:		GGRLRHGGLQVASPAPREGS*G
				į.		PARN*AQSRWAGTAGGPSTPSA
		1				AAGPGAKPLIAPGROGNEPCH
				1		WCGAROAHAHPELOLATSASW
		l		l	I	TRAFRECVSPAWPSCLGAACFH
						CLLIGPFPFSFSSQHLSTSLGHLV
						LLSWHLTSLSVSFRILTRLLRVF
		ŀ				TGSWGGGAA
28248	58616	A	28419	1	616	
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28252	58620	A	28424	1300	1648	
			28424	1300	599	
28254	58622	Α	20423	μ	399	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
ŀ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
28255	58623	A	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK
20233	30023	ľ	120.20	[~	100	YVGLWDFKSRTDEELSFRAGD
ļ						VFHVARKEEOWWWATLLDEA
						GGAVAQGYVPHNYLAERETVE
1						SEP\RDTOAVRHYKIWRRAGGR
1						LHLNEAVSFLSLPELVNYHRAQ
						SLSHGLR
28256	58624	Α	28427	3	438	
28257	58625	Α	28428	37	403	
28258	58626	В	28429	1	1176	
28259	58627	Α	28430	2	2150	
28260	58628	Α	28431	1593	3025	
28261	58629	Α	28432	322	2168	
28262	58630	Α	28433	183	591	
28263	58631	A	28434	2	258	
28264	58632	С	28435	52	363	
28265	58633	Α	28436	1	3363	
28266	58634	Α	28437	1	918	
28267	58635	Α	28438	1	1422	
28268	58636	Α	28439	3	10899	
28269	58637	Α	28440	277	586	
28270	58638	A	28441	3	3364	
28271	58639	Α	28442	1	1851	
28272	58640	A	28444	3	253	CGIEDNNFSLALNPDTDILLS/HS
		1				GGRGAEAPTMCLKLTVSKRAC
		l				FEGLE\WQFNLWRNKK**C*DK
						KHKTAGCSIS*VMRSVYR
28273	58641	A	28445	1	950	MGSSAVQSQLAALAPRVLTGG
		l				LADVTALLRAPATPGRLVAGA
		l				RGGWGYVQSCRGAGAAAVKP
		l				LGSAETAVPIARLGCRRFSRSRC
l		l			1	CRRRGRGSLLSFSAAKPIVFKEK
		l				LTMKTDSLMEEKLECSLWCCL
l		l				SDPSTPGRCCVLERRIVPWMQQ
		i		1		LLANIKQAEKHEKNHPEVTVA
		l				MALTDIDLQLQFSMSQPE/GPPS
		1				PGSRPS*PPPAAALLWTPAGQA
	1					CPGPGGAEAADPSRNSTEWLRP
		l				PHHSSDCLRGLAHIVSQWVSEC
		l				LLCSPGSPPRSPLWALCWEHWE
			1	l		TWPALPEGNQPSPEGLPPCSRS
						QWPQTPPASDPQ
28274	58642	Α	28446	3	213	LTQHCWTHLVRSSHSRTGSSRL
			1	I		HNHQLHQPCA*S*LCQKEHASR
1	1		1	I		GWSEQFNLWRNKK**C*DKKH
		l				KTAG
						GWSEQFNLWRNKK**C*I

SEO ID	Tero in vo	155.4	SEQ ID NO:	Terror action	Internal de la continue de la contin	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	liou	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28275	58643	IA	28447	1142	1772	LVNVDVDADLVGLCVSHRHTV
20213	30043	l^	20447	172	l'' <sup>2</sup>	EEOYSTLALLNHGPOVALKYV
						HMDEVPMPACCLEGOGCLPAL
		1				CGECKLOGSFILSAPGROGSOR
						VGPREAQGHIVIGRKLFSTALM
						LIGGORLEESAAIESGCMEATP
	1	1			1	QGMAGSPQVGQAKSPSVPNKE
		1				PIGDF*GGSQDYRGGIQKPID*Q
	ľ	1				CGPVL/SROSELWCGGRSHSVE
		1				FLLGSAASAPPGPGQA
28276	58644	A	28448	1	1935	EEGOATSATTOTOGA
28277	58645	A	28449	2	1571	
28278	58646	A	28450	2	301	PRPFYSKNFYKILSLYSSEFNNS
20210		1	20100	1		FVDA\LGSD\ODSGNEDVFDME
ĺ	1	1				YTEAEAEELKRNAEVIVFIPEYS
	1					WSNSVSLFPLCPGAKGPTFSVH
						CRVHFGPFSSH
28279	58647	IA	28451	1	1329	
28280	58648	A	28452	240	503	
28281	58649	Α	28453	1039	1896	
28282	58650	Α	28454	1	2397	
28283	58651	Α	28455	1	4011	
28284	58652	Α	28456	3	1088	
28285	58653	Α	28457	1	4878	
28286	58654	Α	28458	1	174	
28287	58655	Α	28459	3	161	
28288	58656	Α	28460	992	1102	
28289	58657	Α	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV
	1	1				GFPQGCQLVHIW*M/PLDAGPE
1	1	1				HNSLKGFLVPLFPLAATPRAPG
						TPAQGSLTDSFPDLLGLAAED
28290	58658	A	28462	3	278	HEAAMSMLRLQKRLASSVLRC
		1				GKKKVWVRPL*TNEIANANSR
	1	1				QQIRKLIKDGLI\IRTPVTAHSWP
	1					SCRTNTLSRRMGHS*SLRTLLD
	1					PVNM*GLLNASWITKC*LLDPV
						NM
28291	58659	Α	28463	1	1043	
28292	58660	Α	28464	185	804	VTSGCGKKKVWLDPNET\NEI\
						ANANS\RQQIPEASSKMGLIIRK
						P\VTV\HSRA\RCPVKTPLARRG
						RGRATWGIR*GGKGYKPNARN
		1	1			AQRKFTW\MRENGGL*TRGCL
					1	RKIPVNPKKDRIANMY\HSLLPE
					1	G*RGNVFKNKADFSWEHIHKL
					1	EGRQRPRKKAPWLTQA*GPAG
		1			I	S*DPRKPRKRR*RAPPRPKKEEI
					l	HQRLFSKE\EETKK
28293	58661	Α	28465	221	350	GPSSFRLPTLSSLHVSHGREET*
		L				HSLET*RDAVSLRIFKSLSV

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop eodon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28294	58662	A	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PPLQGELQTTAQGNKRGYKQME EHSMLMGRKNQYREMGHTAQ GNLQHHAIPIKLPMTFFTELEKT TSKFIWNQKRARITKSILSQNKK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYPYLIFDKPEKNKQWGKD SLFNKWCWFSWWLAICRKLD, PHLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMA TROKIDIS WDLIKLK SFCTAKETTIRVNRQPKWEKI FATYSSNGGLISRIYNELRQIYK KKTNPIKKWAKDNNRHFSKE QIKTTMRYHLTPVRMAIIQKSG NNRCWRGCGEIGTLLHCWWD CKLYPHILTHRWELNNEITWTQ EGEYHTLGTVVGWGEGGGIAL GDIPMAR
20205	60662	<del>  -</del>	20467	1	1863	ODIFINAK
28295	58663	Α	28467	1		
28296	58664	Α	28468	2	1308	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
28297	58665	I <sub>A</sub>	28469	1	1901	I IMPESPTPLLGRDILAKAGAIIHL
2027	30003	1	20407	ľ	1.70.	NIGEGTPVCCPLLKEGINPEVW
						ATEGOYGRAKNAHPVOVKLK
		1				DSASFPYOROYPLRPEAOOGLO
						KIVKDLKVQGLVKTCNSPCDTP
						ILGVQKPNGQWRLVQDLRIIDE
						AIVPLYPAVPNPYTLLSQIPEEA
ĺ	1	1				ELFTVLDLKDAFFCIPVHPESQF
	l	1				
		1				LFAFEDPSIPMSQLTWTVLPQG
						FRDSPHLFHHTLAQDLSQFSYL
						DTLVLCLPLRNQQECHQATQV
		ı				LLNVLATCGYKVSKQKAQLCS
İ						QQVKYLGVKLSKGTRALNNEE
						QIEHNCQQVIAQTYATRGDLLE
		1				VPLTDPNLSLYTDGSSFVEKGL
		1				QKGGYAVVSDNGILERNPLTPG
	ļ	1				TSAQLVELIALPRALELGEGKR
ļ		1				GSSESICFLSFLVPPMTIYTEQDL
ı		1				YNHVVPKPRNKRVPILTFVVGA
		ĺ				GGLGGLGTGIGGITTSTQFYYK
		1				LSQELNGDMEWVADSLVTLQD
		1				QLNSLVAVVLQNRRALDLLTA
1		1				KRGGTCLFLGEECCYYVNQSGI
		1			l	VTEKVKEIRDQIQRRAEEI.QNT
		1				GPWGLVSQWMPWILPFLGPLA
				i		AIILLFLFGPCIFNLLVKFVSSKI
	1					EAVKLQIILQMEPQMQSMT/KI
1						YHGPLDQPASPCSDVNDIKGTP
		<u> </u>		Ļ		PEEISTAQHLLCPNSAGSS
28298 28299	58666 58667	A	28470 28471	I	432 4314	
28300	58668	A	28472	1	330	
28301	58669	A	28473	1	1425	
28302	58670	A	28474	3	1110	NEEOIEHNCOOVIAOTYATRGD
28302	38070	Ι^	28474	ľ	11110	LLEVPLTDPNLSLYTDGSSFVE
						KGLQKGGYAVVSDNGILERNP
		1				
					1	LTPGTSAQLVELIALPRALELGE
		1				GKRGSSESICFLSFLVPPMTIYT
		1			1	EQDLYNHVVPKPRNKRVPILTF
	1	1			1	VVGAGGLGGLGTGIGGITTSTQ
	1				1	FYYKLSQELNGDMEWVADSLV
	1	1				TLQDQLNSLVAVVLQNRRALD
		1				LLTAKRGGTCLFLGEECCYYV
		1				NQSGIVTEKVKEIRDQIQRRAEE
		1				LQNTGPWGLVSQWMPWILPFL
		1				GPLAAIILLFLFGPCIFNLLVKFV
		1			1	SSKIEAVKLQIILQMEPQMQSM
		1			1	TKIYRGSLDQPASPCSDVNDIEG
		1				TPPEEISNAQPLLCPN*AGSSWS
		1			I	SRRPTSPTALGFSC
28303	58671	В	28475	1	1989	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28304	58672	A	28476	l	1280	MGNITADNSSMSCTIDHTIHOT
28304	38072	^	20470	'	1200	LAPVVYVTVLVVGFPANCLSL
						YFGYLOIKARNELGVYLCNLTV
		1				ADLFYICSLPFWLQYVLQHDN
		1			ŀ	WSHGDLSCQVCGILLYENIYIS
		1				VGFLCCISVDRYLAVAHPFRFH
		1				QFRTLKAAVGVSVVIWAKELL
		1			ŀ	TSIYFLMHEEVIEDENQHRVCF
		1				EHYPIQAWQRAINYYRFLVGFL
	1					FPICLLLASYQGILRAVRRSHGT
i						QKSRKDQIQRLVLSTVVIFLACE
					ł	LPYHVLLLVRRYWEASCDFAK
	ı	1			1	GVFNAYHFSLLLTSFNCVADPV
	i		i			LYCFVSETTHRDLARLRGACLA
	1					FLTCSRTGRAREAYPLGAPEAS
		1				GKSGAQEEEVTKFEGGRNGHT
	1					AKKSPCNSVQDFTGIKAVKLQI
	1					VLQMEPQMQS\KLKIYSRPLDR
		<u> </u>				PASPCSDVNDIEGTPPEEISTAQ
28305	58673	A	28477	1	717	
28306	58674	Α	28478	2	409	
28307	58675	A	28479	1	675	
28308	58676	A	28480	332	399 436	
28309	58677 58678	A	28481	980	1399	
28310		A	28482	132	218	RINLMHFRN*TSQQALSLSYNL
28311	58679	A	28483	132	218	FLMQRH
28312	58680	Α	28484	1	34	
28313	58681	Α	28485	985	1170	
28314	58682	A	28486	1	1203	
28315	58683	Α	28487	505	716	REPCPVSQREVWRPGCLD/HCP
		1				RQSGSLGETLRGTAE\QPWPHS
			ŀ			QVLSNLRVLQLPLISLPSLRRRA
		_				LFPAA
28316	58684	A	28488	1	998	
28317	58685	Α	28489	477	955	TPIHNGFKENKIPRNPTYKGCE
l						GPLQGELQTTAEGNKRGYKQM
						EEHSMLMGRKNQYRENGHTA
						QGNLQVQCHPHQATNDFLHRI
		1		ľ		GKNYFKVHMEPKKSPHRQVNP
		1				KPKEQSWRHHTT*LQ/YYTTRL
		1				Q*PK*HGTGTKTEI*INGTEQSP
		↓_				QK*CRISTTI
28318	58686	A	28490	37	430	
28319	58687	A	28491	507	829 945	CALL HEL BOHCVOURVESTER
28320	58688	Α	28492	643	945	CALLHSLPQHCVQHPYRSYTHR
		1			1	MASCRWKWGHCHSGIKMYSIP
		1				WYSTPMEGKALGDAHPQIAHS H*GAAFL*ALY*EKS*SMANRL
1		1	1		1	WYSRL*PLAGDGRRE
28321	58689	A	28493	1092	1346	W I SKL PLAUDURKE
20321	130009	IA.	20473	1072	11340	<u> </u>

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown,  *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28322	58690	Α	28494	173	527	
28323	58691	Α	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSVPSPALPCSLKYPFYD HRTKFTLTTQPFSHTLAQKENQ SPLKHMGKKRLQNIFLPIRP*DQ TPWLERS
28325	58693	Α	28498	921	1008	
28326	58694	В	28499	I	2169	
28327	58695	A	28500	455	523	YPLYHFLLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVYSEIQLLPGLVL GGCMCRGIYPFLLDFLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLLRVFSMKSC *ILSKAFSASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFASILLRIFTS MFIRDIGLKFSFFVVSLPGFGIK MMLAS
28330	58698	Α	28503	1	957	
28331	58699	Α	28504	41	412	IALIILRYIPSIPSLLRVFSMKGC* ILSEAISASIEIIMWFLSLVLFI*W ITFIDLHVLNKPCIPGMKPS*SW WISFLMCCWIWFASILLRIFASM FIRDIGLKFSFFVVSLPGFGIRM MLAS

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28332	58700	Α	28505	1	1699	MDEFLDTYTLPRUNQEEIESLN
	İ					RPITSSEIEAVINSLPTKKCPGPD
	1					GFTAEFYQRYKEELVPILLKLIQ
						TIEKEGLLPNSFYEATNILIPKPG
	1	ı				RDTTKKENFRPISLMNINAKILN
		1				EILATESSIKKLIHHDQDSFIPGM
						QGWFNICKSINVIHHINRINNKN
i	1					HMIISVNAEKAFDKIRHLFMLK
						TLIKLGIDETSLKTVRAIYDKPT
	į.					ANIILNGQKLEAFPLKTGIRQGC
	l	1				LLSSLLFNIVLEVLARAIRQEKE
l						KDIQIGREEVKLSLFADDMIVY
		1				FKNPIVSAONLLKLIGNFSKVSG
	l					YKINVQKLQAFLYTNNRQTESQ
						IVSELPFTIAAKRIKYLGIOLTRO
		1				VKYLFKENYKPLHKEIIEDTNK
						WKNIPCSWIGRINIMKMAILPK
1	İ					VIYRFNASPIKLLLNFFTELEKN
	1					CLNFIWNOKRAHIAKTILSKKN
						KAGGITLPDFKLYYKSTVTKTT
	l	1				WYWYONRYIDOWNRTEASEIT
	1					PHIYNHLIFDESDKNNOWGKDS
						LHNKWYWENWLAICRKLKLD
		1				SFLTHYTKINSRWIKDLNAGSKI
						QY\HADRTKSRERRAIASSYVSS
28333	58701	Α	28506	2	1689	WRAWGRGATRRSSCHRQSAPS
						LSRVGRSSQIRSALSAASGLWR
ĺ						RKPASAKFGRPRTGSLHLPVK*
				l		KAFVSLQESSA*MNLRQ*PE*D
						WISWIN*QNFGN/CQGSTLKIPV
						VERKILDLYALSKEHSFSPATEQ
				ŀ		SWTENDFDELREEGFRRSDFSE
					'	LKEEVRTHRKEAKNLVKRLDK
						WLNRITSVEKSLNDLMELKTM
ŀ						AREQLRDECTSFSSQFDHLEER
						KYKLPSENKHLYANKLENLEE
						MDKFLETYTLPRLNQEEVESLN
				1		RPITGSEIEAIINSLPTKNSPGPD
		l				RFTAKFYQMYKEELVPFFLKLF
		1				QSIEQEGILPNSFYEASIILIPKPG
					1	RDPTKKENFRPISLMNIDAKIFN
		1				KILANQIQQHIKKLIHHDQMGFI
		1				PGMODWFNIRKSINVIOHINRT
		1		l		KDKNHTIISIDAEKAFDKIQQCF
		1		l		MLKTLNKLGIDGTYVKIIRAIY
		1		l		DKPTANIILDGQKLEAFPLKTST
	1	1	l	l		IOGCPLSPLLFNIVLEVLARAVR
				i		QEKEIKGIQSGKEEVKLSLFAD
		l l				DMTVYLENPIISAQNLLKLKSN
		1	l	l		FSKVSGYKINVQKSQAFLYTNN
28334	58702	A	28507	Г	1428	( )

SEO ID	Tero in vo.	134.4	SEQ ID NO:	Tatana di da	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
1.01	sequence		09/540,217	codon for peptide	of peptide sequence	delction. \-possible nucleotide insertion)
				sequence		
28335	58703	Α	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC
						WIMFIDLRMLNOPCTPGMKPT*
	1	1	i			SWWISFLMCCWIRFASILLRIFA
1						SMFIRDIGLKFSFFVVSLPGFGIR
					1	MMLTS
28336	58704	A	28509	765	950	LLPOFONLLLVYSEIOLLPGLVL
	1	1		l		GGCMCPGIYPFLLDFLVYLHRG
i						VYSIL*W*FVFLWDQW
28337	58705	A	28510	778	981	SOKEWYOLLFVPLVEFGCESIW
28337	38703	n	20310	//*	261	SWAFFGWOAINYCLNFRTCHW
l	1	1			i	SIQRFNFFLV*SWEGVCVQEFIH
1	Į.	1	į .		l	FF
20000	40006	١.	20511	1001	1841	
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI*
		<del>  -</del>				TLK
28339	58707	Α	28512	1	1641	
28340	58708	Α	28513	1	2307	
28341	58709	Α	28514	1	3793	
28342	58710	Α	28515	178	674	ERPRIMDLAGLLKSQFLCHLVF
		1		ľ		CYVFIASGLIINTIQLFTLLLWPI
		1				NKQLFRKINCRLSYCISSQLVM
	1	1		1	1	LLEWWSGTECTIFTDPRAY\SS
		1	1	1		MGKENAIVVLNHKFGN/IDFLC
	1	1		1		GWSLSERFGLLGVSQKCIPPCL
		1				THFFGSAPPLVFLLLVIQNLQKN
		1				QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCGLFFGSI*
		1				TLKYFFPIL
28344	58712	A	28517	1	2167	
28345	58713	В	28518	65	2652	
28346	58714	Ā	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	A	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	i	669	
28351	58719	A	28524	li	1089	***
28352	58720	Ā	28525	91	507	AGTASASPAPNRSLSGSEPTSSS
20332	36720	l^	20323	P'	507	VTQENGADVQGHERVPWKAR
ł	1				}	SRRFCPMEGTFRKVPSHGSHVP
	1		l			EVSMLWKACSGSFRPVEGHSV
						RCALTPASGCSP*AGTASASPAP
		1				NRSLSGSEPTSSSVTQENGADV
						QGHERVPWKARSRRFCPMEGT
1	1	1	l		i	FRKVPSHGSHVPEVSMLWKAC
1		1	l			SGSFRPVEGHSVRCALTPASGC
						SPSKSKATVGCRCSDFCTVEEF
	1	1				LQKIFLQVESLDRRPRCLPLT
28353	58721	Α	28526	1	1213	
28354	58722	A	28527	130	211	KPHYAAHGQPFTAE*RPGTDNR
1						ADNRQ
		_				

28355 S8723 A 28528 793 I382 NTTAAGRVIR YDVLDRLIGE HIDLTGKLIRS DEADRLIHRI DERGWLTDIS RYDEKGRLTHRI GERGWLTDIS RYDEKGRLTH ALLWCHETRI CIPPSLPAVEF MKLGDTPLV ASPADGSTAL GAGEPLYTIC RLPGRHETRR PGNAAQLERP	uselbie nucleotide e nucleotide e nucleotide inscriion)  LTSENGSHTTFR TGFDGRTQRYH EDEGLVTHWHY EDEGLVTHWHY ERQTVHHPQTE HAYNAQGLANR VLTYGSGYLAG **ERPAR**ASDG A**DQTCVQRA A*DQTCVQRA
28355 S8723 A 28528 793 I382 NTTAAGRVIR YDVLDRLIGE HIDLTGKLIRS DEADRLIHRI DERGWLTDIS RYDEKGRLTHRI GERGWLTDIS RYDEKGRLTH ALLWCHETRI CIPPSLPAVEF MKLGDTPLV ASPADGSTAL GAGEPLYTIC RLPGRHETRR PGNAAQLERP	LTSENGSHTTFR TGFDGRTQRYH TVKGETAERWQY HISEGHRVAVHY SERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG AA*DQTCVQRA PARRGMADLRQ
28355 58723 A 28528 793 1382 NTTAAGRVIR YDVLDRLIQE HDLTOKLIRS DEADRLTHRI DERGWLTDIS RYDEKGRLT ALLWQHETR CIPDSLPAVE MKLGDTPLV ASPADGSTAL GAGEPLYTG RLPGRHETR PGNAAQLEPI PGNAAQLEPI	TGFDGRTQRYH EDEGLVTHWHY IVKGETAERWQY HISEGHRVAVHY GERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG AA*DQTCVQRA QPARRGMADLRQ
YDVLDRLIQE HDLTGKLIRS DEADRLTHRI DERGWLTDIS RYDEKGRLTC ALLWQHETRI CIPDSLPAVE MKLGDTPLV ASPADGSTAL GAGEFLYTG RLPGHETRR PGNAAQLERP	TGFDGRTQRYH EDEGLVTHWHY IVKGETAERWQY HISEGHRVAVHY GERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG AA*DQTCVQRA QPARRGMADLRQ
YDVLDRLIQE HDLTGKLIRS DEADRLTHRI DERGWLTDIS RYDEKGRLTC ALLWQHETRI CIPDSLPAVE MKLGDTPLV' ASPADGSTAL GAGEFLYTG RLPGRHETRR PGNAAQLEPL	TGFDGRTQRYH EDEGLVTHWHY IVKGETAERWQY HISEGHRVAVHY GERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG AA*DQTCVQRA QPARRGMADLRQ
HDLTOKLIRS DEADRLTHRI DERGWLTDIS RYDEKGRLTC ALLWOHETRI CIPDSLPAVEV MKLGDTPLV' ASPADGSTAL GAGEPLYTOG RLPGRHETRR PCNAAQLERP	EDEGLVTHWHY IVKGETAERWQY HISEGHRVAVHY GERQTVHHPQTE HAYNAQGLANG VLTYGSGYLAG **ERPADR**ASDG AA*DQTCVQRA QPARRGMADLRQ
DEADRLTHRI DERGWLTDIS RYDEKGRLT. ALLWQHETRI CIPDSLPAVEV MKLGDTPLVY ASPADGSTAL GAGEPLYTG RLPGRHETRR PGNAAQLERPL	IVKGETAERWQY HISEGHRVAVHY GERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG .AA*DQTCVQRA QPARRGMADLRQ
DERGWLTDIS RYDEKGRLTC ALLWQHETRI CIPDSLPAVE MKLGDTPLV ASPADGSTAL GAGEFLYTG RLPGRHETRR PGNAAQLEPL	HISEGHRVAVHY GERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG AA*DQTCVQRA QPARRGMADLRQ
RYDERGRLTC ALLWQHETRI CIPDSLPAVEF MKLGDTPLV' ASPADGSTAL GAGEPLYTCC RLPORMETRR PCNAAQLERPL	GERQTVHHPQTE HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG .AA*DQTCVQRA QPARRGMADLRQ
ALLWQHETRI CIPDSLPAVEN MKLGDTPLY: ASPADGSTAL GAGEPLYTG RLPGRHETRR PGNAAQLRPL	HAYNAQGLANR WLTYGSGYLAG **ERPADR*ASDG .AA*DQTCVQRA QPARRGMADLRQ
CIPDSIPAVE' MKUGDTPLV' ASPADGSTAL GAGEPLYTG RLPGHETRR PGNAAQURPL	WLTYGSGYLAG **ERPADR*ASDG .AA*DQTCVQRA QPARRGMADLRQ
MKLGDTPLV' ASPADSTAL GAGEPLYTG RLPGRHETRR PGNAAQLRPL	**ERPADR*ASDG .AA*DQTCVQRA )PARRGMADLRQ
ASPADGSTAL GAGEPLYTG RLPGRHETRR PGNAAQLRPI	.AA*DQTCVQRA QPARRGMADLRQ
GAGEPLYTGG RLPGRHETRR PGNAAQLRPL	PARRGMADLRQ
RLPGRHETRR PGNAAQLRPL	
PGNAAQLRPL	
	HTAGGVHPRPPA
	,
28356 58724 A 28529 1039 1689	
28357 58725 A 28530 I 2406	
28358 58726 A 28531 I 2928	
28359 58727 A 28532 2 1271	
28360 58728 A 28533 250 929	
28361 58729 A 28534 3 273 GKLIAVIGDE	DTVTGF\LLGGIG
ELNKNRHPNI	LVVEKDTTINEIE
DTFRQFLNRD	DIGAFRLLGLCW
	PPLPLPCAVTQCH
28362 58730 A 28535 2 415	
28363   58731   A   28536   1	
28364 58732 A 28537 2551 2651	
28365 58733 A 28538 2 295	
	VSRLR*CQEAAG
MADSCPRSGO	GAILAFKSAPEVI
RRALSAQSLR	ATSSSSASGAGA
FCLSPSKYFPI	TSASSSATARYV
LGWAASSGLI	TSSQKMG
28367   58735   A   28540   1   400	
28368 58736 A 28541 257 516	
	QRVVFKNISPAD
	RGHKTVTYLTLQ
GNDQDDMFP	ALCEVLRHPECN
LRYLGLVSCS	ATTQQWADLSL
ALEVNQSLTC	VNLSDNELLG*G
C*VAVHN/S*I	OTPSAFLQRVVV
GKTGHLTEAN	NLQGTLLLCWVF
SRELTHLCLA	KNPIVNTGVKYL
CEGLRYPECK	LQTLVLWNCDIT
28370 58738 A 28543 I 2633	
28371 58739 A 28545 127 2030	
28372 58740 A 28546 I 3066	
28373 58741 A 28547 259 3222	
28374 58742 B 28548 1 2640	

SEQ ID NO:			SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADORLIF AKSWPRASRYQGHODIFILRS DLPSQVVQTQNISSCRNSC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QKSBGTLQEHDGIGEHVAKY AEIFGLTSAEPRIFTOFRISET EITNPYAMRLYESLQYKKPDG SGIVSLKIDWIIERYQLPQSYQR TSPCCCHMKKDVFASPSTMISS SRVSNNTSKTTIIKNQCQKDDS KRSLLVNNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGGVR RCLQQCEQTVRILHAKVAQK SYGNEKRLIRFTIRVGFWSQTN NQTDDTSGTVVQSSYQTDDTS GTVVRTNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	В	28551	1	1954	

NO: of pepide sequence of pepide	SEQ ID	SEO ID NO-	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
28378   58746   A   28552   1424   3807   HPLWKWLEGDMNMNIKKIVK QATVLTETTA/LLAGGATQAFA KENNQKAYKETYGVSHITRIE MLQIPKQQQNEKYQVPQFDOS HIKNIESAKGLDWDSWPLQN ADGTVAEYNGYHVVFALAGSI KOADDTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDPIL KOATVAEYNGYHVVFALAGSI KOADDTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDPIL KOATVAEYNGYHVVFALAGSI KOADDTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDPIL KOATVAEYNGYHVVFALAGSI KOADDTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDPIL KOATVAEYNGYHVVFALAGSI KOADDTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDPIL KOATVAEYNGYHVVFALAGSI KOADDTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDPIL KOATVAEYNGYHVVFALAGSI KOADTSIYMFYQKVGDNSID WKNAGKVFKDSDKFDANDFIL KOATVAEYNGYHVVFALAGSI KTAQVN SKSDDTLKINGVEDHKTIFDGG GKTYQNVQGFDEGHYTGDFL EAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDORMMLLYF DQIRKSDGTLQEHDGIGEHVA KYAEIFGLTSAASKDIRQALK FAGKEVVFYRPEDAGDEKG GSPFWFIKKAHSPSGCLYSVHIP PYLIPFFIGLQNFFTQFTLSTK ITNPYAMRLYESLCQYRKPDG GGVSLKIDWILERYQLPQSYQKI PYLIPFFIGLQNFTQFTLSTK ITNPYAMRLYESLCQYRKPDG GGVSLKIDWILERYQLPQSYQKI PYLIPFFIGLQNFTQFTLSTK TITNPYAMRLYESLCQYRKPDG GGVSLKIDWILERYQLPQSYQKT PYLIPFFIGLQNFTQFTLSTK TITNPYAMRLYESLCQXFR QPPQSYQKMPDFRRFFLQSFTQ QPPQSYQKMPDFRRFFLQSFTQ QPPQSYQKMPDFRRFFLQSFTQ QPPQSYQKMPDFRRFFLQSFTQ QPPGSYQKMPDFRSFTQ QPPGSYGKMPTALLFAVHLA GAVAVNSSDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AQVNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AQVNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AQVNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYQNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYQNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYQNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYQNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYQNVSSDDTLKINGVEDIK TITDGDGKTYQNVQGFIDEGN TISGDNHTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYQNVSSDDTLKINGVEDIK TITDGDGKTYQNV QGFIDEGN TISGDNHTLRDPHYVEDKGHK							
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DQIRKSDGTLQEHDGICEHTVA			1				
KYAEIFGLTSAÉASKDIRQALK   FAGKEVVFYRPEEDAGDEKGY   ESFPWFIKRAHSPSRGLYSVHII   PYLIPFFIGLQNRFTQFRLSETK   TINPYAMRLYSSLQYYKPDG   GIVSLKIDWILERYQL PQSYQKI   PDFRRFLQVCVNEINGAVIGII   CVSIRKPDGSIVSIKIAWILERN   QPPQSYQRMPDFRRFLQSRP/CMHDWLCAEALAWSIQTASY)   VTMQVNLTSLSSDTDRDLSVV   NSGWYSSGSLYRAFNIKTSSGE   KRTVPRILPDPDDPRSAIAEAPS   EMPGHEVPVEEHPFAGTNSG   PQGARKGDESMTKADDSSPS   SSGRPKPVRGAAPGSQTGKKQQ   TALQASTLAPANLJFKAVHLA   PAGASTLAPANLJFKAVHLAPANLJFKAVHLA   PAGASTLAPANLJFKAVHLAPANLJFKAVHLA   PAGASTLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLAPANLJFKAVHLA			l		l		
### FAGKEVYPYRPEDAGDEKOY ### ESPWFIKRAHSPSRGLYS VHIR ### PYLIPFFIGLONETOFRIS.ESTK ### TITNPYAMRLYESLCOYKRPDG GIVSLKIDWILERYQLOPSYNGN PDFRRFLQVCVNEINGAVIGII CVSIRKPDGSGIVSIKIAWIIERN QPPQSYQRMPDFRRFLQSRPY CMHDWLCAEALAWSIGTASYI VTMQVNLTSLSSDTDRLSVV NSGWVSSGSLVRFNTIKTSSGE KKTVPRILPDPDDPRSAIAEAPS EMPGIEVPVEEHPPEAGTNSG PQGARKGDESMTKASDSSSPSS SSGPRVPKGAAPGSQTGKKQQ TALQASTLAPANLI.PKAVHLA  28379 \$8747 A 28553 2372 3570 EALLPGDODSQSGKGVAREW WFLPSSRAPVLERLVSNHHVG DNSIDSWKNAGRVFKDSDKFI ANDPILKDTQFWSGSASATFTSI GKIRLPYTDYSGKHYGQSLT. AQVNVSKSDDTLKINGVEDIK TIFEDGOKTYQNVQQFIBEGNI TISGDNHTLRDPHYVEDKGHKN LVFEANTGTENGVQGESLFNI AYYGGGTNFFRESOKLQQSA KKRDAELANGALGIIELNNDY LKKVMKPLITSNTVTDEI  28380 \$8748 B 28555 1 2232  28381 \$8749 B 28555 1 1 2232  28382 \$8750 B 28555 1 1 2169 28383 \$8751 A 28555 1 2259 28383 \$8753 A 28555 1 2259 28385 \$8753 A 28555 1 2418			l				
ESFPWFIKRAHSPSGGLYSVHIR   PYLIPFFIGLQNRFTQFRLSTK   ITINPYAMRLYESLQYKKPDG  GIVSLKIDWIIERYQLPQSYQRIPDG  GIVSLKIDWIIERYQLPQSYQRIPDG  GIVSLKIDWIIERYQLPQSYQRIPDG  GIVSLKIDWIIERYQLPQSYQRIPDG  GIVSLKIDWIIERYQLPQSYQRIPDG  PPFRRFLQSRP/CMHDWLCAEALAWSIQTASY  VTMQVNLTSLSSDTDRDLSVV NSGWYSSGSLVRFNTIKTSSGE KRTVPRILIPDPDDPRSA1AEAPS EMPGHEVPVEEHFPEAGTNSG  PQGARKGDESMTKASDSSPSS  SSGRPVPKGAAPGSQTGKKQQ  TALQASTLAPANLJPKAVHLA  PKAVHLASTLAPANLJPKAVHLA  PKAVHLASTLAPANLJPKAVHLA  PKAVHLASTLAPANLJ			l				
PYLIPETIGLONETTORILSETK   ITNPYAMRLYESLCQYRKPDG   GIVSLKIDWILERYQLPGSYQRI   GIVSLKIDWILERYQLPGSYQRI   PPFRRRFLQVCVNENGAVIGI   CVSIRKPDGSGIVSIKIAWILERY   QPPGSYQRMPDFRRFFLQSRP/CMHDWLGAEALAWSIOTASY)   VTMQVNLTSLSSDTDRDLSVV   NSGWYSSGSLVRFNTIKTSSGE   KRTYPRILPPDPDPRSA1EAPS   EMPGHEVPVEEHPPEAGTNSG   POGARKGDESMTKASDSSSSS   SSGRPVPKGAAPGSQTGKKQQ   TALQASTLAPANLLPKAVHLA   EALLPGDQDSGGKQVAAREW   WFLPSSFAPVLLRLVGNHHVG   DINSIDSWKNAGRYFKDSDKFT   ANDPILKDQTGEWSGSATFTSI   GKIRLFYTDYSGKHYQGSLT   AQVNVSKSDDTLKINGVEDIKK   TIPEDGDKTYQNVQQFIDEGN   TITEDGDGKTYQNVQQFIDEGN   TITEDGDGKTYQNVQQFIDEGN   TITEDGDGKTYQNVQQFIDEGN   TITEDGDGKTYQNVQQFIDEGN   AYYGGGTNFFRESGKLQQSA   KKRDA ELANGALGILEINNDY   LKKVMKPLITSNTVTDEI   LKVMKPLITSNTVTDEI   LKVMKPLITSNTVTDEI   LKVMKPLITSNTVTDEI   LKVMKPLITSNTVTDEI   LKVMKPLITSNTVTDEI   LKVMKPLITSNTVTDEI   LSSSS   SSSSS   SSSSS   1 2259   28385   SSTS			l		l		
ITINPYAMRLYESLOQYKRPDG   GIVSLKIDWIERYQLPQSYQRI   PDFRRRRLQVCVNEINGAVIGII   CVSIRKPDGSGIVSIKIAWIIERY   QPPQSYQRMPPGRFLQSRP-   QPPQSYQRMPPGRFLQSRP-   QPPQSYQRMPPGRFLQSRP-   QPPQSYQRMPDFRRFLQSRP-   QPPQSYQRMPDFRRFLQSRP-   QPPQSYQRMPDFRSFLQSRP-   KRTVPRILPDPDDPRSAIAEAPS   EMPGIEVPVEEHPPEAGTING-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PQGARKGDESMTKASDSSPSG-   PPSSFAPVLLRLYGMTHYG-   DNSIDSWKNAGRVFKDSDKFI-   ANDPILKDQTQEWSGSATFTSI-   GKIRLYTDYSGKHYGKQSLT-   AQVNVSKSDDTLKINGVEDHK   TIFDGDGKTYQNVQFIDEGN-   TSGDNHTLRDPHYVEDKGHK-   LVFEANTGTENGVQGESLFNI-   AVYGGGTNFFRESOKLQQSA-   KKRDAELANGALGIIELNNDY-   LKKVMKPLITSNTVTDEI   LKKVMKPL			1				l .
GIVSLKIDWILERYQLPQSYQKT			ı		l		
PPFRRRLQVCVNEINGA VIGIL			1				
CVSIRKPDGSGIVSIKIAWIIER   QPPQSYQRMPDFRRFLQSRP/   CMHDWLCAEALAWSIQTASY    VTMQVNLTSLSSDTDRDLSVV   NSGWYSSGSLVRFNTIKTSSGE   KRTVPRILPDPDDPRSA1AEAPS   EMPGHEVPVEEHPPEAGTNSG    PQGARKGDESMTKASDSSSPS    SSGRVPKGAAPGSQTGKKQQ   TALQASTLAPANLJEKAVHLA    28379   58747   A   28553   2372   3570   EALLPGDDSQSGKGVAAREV   WELPSSPAVLLRLVGNHHVG   DNSIDSWKNAGRVFKDSDKFI    ANDPILKDQTTQEWSGSATFTSI   GKIRLFYTDYSGKHYGGSQLTI   AQVNVSKSDDTLKINGVEDHK   TITEDGDGKTYQNVQQFIDEGNI   TSGDSHTLRDPHYVEDKGHKS    LVFEANTGTENGYQGESLFNI   AYYGGGTNFFRESQKLQQSA    KKRDA ELANGALGIIELNNDY    LKKVMKPLITSNTVTDEI     28380   58748   B   28556   1   2232     28381   58750   B   28556   1   3198     28383   58751   A   28557   1   2169     28384   S8753   A   28558   1   2259     28385   58753   A   28559   1   2418			1		l		
QPPQSYQRMPDFRRRELQSRP/ CMHDWLCAEALAWSIQTASYI VTMQVNLTSLSSDTDRLSVV NSGWYSSGSLVRPNTIKTSSGE KRTVPRILPPDPDPRSA1AEAPS EMPGHEVPVEEHFPEAGTNSG PQGARKGDESMTKASDSSSPS SSGRPVRGAGAFOSJTGKKQQ TALQASTLAPANLLPKAVHLA   28379   58747   A   28553   2372   3570   EALLPGDQSQSGKQVAREV WFLPSSRAPVLRLVGNHHVG DNSIDSWKNAGRVFKDSDKFI ANDPILKDQTQEWSGSATFTSI GRIRLFYTDYSGKHYGQSLT- AQVNVSKSDDTLKINGVEDI-K TIFEGDGKTYQNQGFIBEGNI TSGDMTTLRDPHYVEDKGHK LVFEANTGTENGYQGESLFNI AYYGGGTNFFRKESQKLQQSA KKRDAELANGALGIIELNNDY- LKKVMKPLITSNTVTDEI   28380   58748   B   28555   1   2232     28381   58750   B   28555   1   2169     28384   58751   A   28557   1   2169     28385   58753   A   28559   1   2418							
CMHDWLCAEALAWSIOTASY/ VTMQVNLTSLSSDTDRDLSVV NSGWVSSGSLVRFNTIKTSSGE KRTVPRILPDPDDPRSAIAEAP EMPGIEVPVEEHPPEAGTNSG POGARKGDESMTK ASDSSSPSS SSGPRVPKGAAPGSQTGKKQQ TALQASTLAPANI.IPKAVHLA   28379   58747   A   28553   2372   3570   EALLPGDDSQSGKGVAREV WFLPSSFAPVLLRLVGNHHVQ DNSIDSWKNAGRVFKDSDKFI ANDPILKDQTQEWSGSATFTSI GKIRLFYTDYSGKHYGKQSLT AQVNVSKSDDTLKINGVEDHK TIFDGDGKTYQNVQFIDEGNI TSGDNHTLRDPHYVEDKGHKX LVFEANTGTENGVQGESLFNI AYYGGGTNFFRESGKLQQSA KKRDAELANGALGIIELNNDY LKKVMKPLITSNTVTDEI   28380   58748   B   28555   200   2602   28381   58749   B   28555   10   2169   28384   58751   A   28557   1   2169   28385   38753   A   28558   1   2259   28385   58753   A   28558   1   2259   28386   28753   A   28558   1   2189   2418							
VTMQVNLTSLSSDTDRDLSVV					}		
NSGWYSSGSLVRFNTIKTSSGE							
KRTVPRILPDPDPRSA1 EAPS					i		
EMPGHEVPVEEHFPEAGTNSG:					Ī		
POGARKGDESMTKASDSSSPSK   SSGRVPKGAPGSQTGKKQQ   TALQASTLAPANILIPKAVHLA							
SSGPRVPKGAAPGSOTGKKQQ   TALQASTLAPANLIPKAVHLA					ĺ		
TALQASTLAPANLI_PKA_VHLA    28379   58747							
28379   58747							
WFLPSSFAPVLRLVGMHHVG			Ļ.				
DNSIDSWKNAGRAFKDSDKFI	28379	58747	Α	28553	2372	3570	
ANDPILKDOTOEWSGS ATFTST GKIRLFYTDYSGKHYGKQSLT AQVNVSKSDDTLKINGVEDIEK TIFEDGDGKTYQNVQQFIDEGNI TISGDDHTLRDPHYVEDKGHKS. LVFEANTGTENGYQGESLFNI AYYGGGTNFFRKESQKLQQSA KKRDA ELANGALGIIELNNDY LKKVMKPLITSNTVTDEI  28380 \$8748 B 28554 1 2232  28381 \$8749 B 28555 200 2602 28381 \$8749 B 28556 1 3198 28382 \$8750 B 28556 1 3198 28383 \$8751 A 28558 1 2259 28384 \$8752 A 28558 1 2259 28385 \$8753 A 28558 1 2259					ĺ		
GKIRLFYTDYSGKHYGKQSLT			1				
AQVNVSKSDDTLKINGVEDHK TIFDDGGKTYQNVQQFIDEGN TSGDNHTLRDPHYVEDKGHK\)   LVFEANTGTENGVQGESLFNI AYYGGGTNFFREKSQKLQQSA   KRDA ELANGALGIIELNNDY-   LKKVMKPLITSNTVTDEI   28380   58748   B   28554   1   2232         28381   58759   B   28555   200   2602       28382   58750   B   28555   10   3198       28383   58751   A   28557   1   2169       28384   58752   A   28558   1   2259       28385   38753   A   28559   1   2418							
TIFDGDGKTYQNVQQFIDEGN  TSGDNHTRDPHYVEDKGHK) LVFEANTGTENGYQGESLIFN  AYYGGGTNFFRKESQKLQQSA KKRDA ELANGALGIIELNNDY* LKKVMKPLITSNTVTDEI    28380   58748   B   28554   1   2232     28381   58749   B   28555   2000   2602     28382   58750   B   28556   I   3198     28383   58751   A   28557   I   2169     28384   58752   A   28558   I   2259     28385   58753   A   28559   I   2418	1				İ		
TSGDNHTLRDPHYVEDKGHK							
Lyfeantottonyoggesleni   Ayygggtnffrkesoklogsa   Kkrdaellangalelinndy    28380   58748   B   28554   1   2232							
AYYGGGTNFFRKESQKLQQSA   KKRDAELANGALGIIELNNDY**   28380   58748   B   28554   1   2232	1		1		l		TSGDNHTLRDPHYVEDKGHKY
KKRDAELANGALGHELNDDY   LKKVMKPLITSNTVTDEI     2232     28381   88749   B   28555   200   2602     28382   88750   B   28556   I   3198     28383   88751   A   28557   I   2169   23384   88752   A   28558   I   2259   23385   38753   A   28559   I   2418     2418	1		1		I	l	LVFEANTGTENGYQGEESLFNK
LKKVMKPLITSNTVTDEI			1		l		AYYGGGTNFFRKESQKLQQSA
28380     58748     B     28554     1     2232       28381     58749     B     28555     200     2602       28382     28750     B     28556     I     3198       28383     38751     A     28557     I     2169       28384     58752     A     28558     I     2259       28385     38753     A     28559     I     2418	İ		1		l		KKRDAELANGALGIIELNNDYT
28381     58749     B     28555     200     2602       28382     58750     B     28556     1     3198       28383     58751     A     28557     1     2169       28384     58752     A     28558     1     2259       28385     58753     A     28559     1     2418			L				LKKVMKPLITSNTVTDEI
28382     58750     B     28556     I     3198       28383     58751     A     28557     I     2169       28384     58752     A     28558     I     2259       28385     58733     A     28559     I     2418					· I		
28383     58751     A     28557     I     2169       28384     58752     A     28558     I     2259       28385     58753     A     28559     I     2418	28381	58749	В	28555	200	2602	
28384 58752 A 28558 I 2259 28385 58753 A 28559 I 2418			В		I		
28385 58753 A 28559 I 2418	28383	5875 I	Α	28557	I	2169	
	28384	58752	Α	28558	1	2259	
28386   58754   B   28560   I   1974	28385	58753	Α	28559	1		
	28386	58754	В	28560		1974	

SEQ ID		Met	SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28387	58755	A	28561	3	2077	
28388	58756	Α	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGO
				i		AIQAFAKENNHKAYKETYGVS
						HITRHDMLQIPKQQQNEKYQVI
		l				QFDQSTIKNIESAKGLDVWDSW
						PLQNADGTVAEYNGYHVVFAL
i				1		AGSPKDADDTSIYMFYQKVGD
		İ				NSIDSWKNAGRVFKDSDKFDA
						NDPILKDOTOEWSGSATFTSDG
						KIRLFYTDYSGKHYGKQSLTTA
			ŀ		1	QVNVSKSDDTLKINGVEDHKTI
					1	FDGDGKTYQNVQQFIDEGNEGI
	1					LPISEPPIKODFRLLG
28389	58757	Ã	28563	610	2303	SLPNLDNAAICSSSSSPTRTR*SL
		1				SEGATQ\AFAKEKYPHKHTKKR
		l				SGVFHITRHDMLQIPKQQQNEK
	ļ				1	YQVPQFDQSTIKNIESAKALDV
						WDSWPLONADGTVAEYNGYH
		1				VVFALAGSPKDADDTSIYMFY
		l			l .	QKVGDNSIDSWKNAGRVFKDS
l		l				DKFDANDPILKDQTQEWSGSA
I	ľ	l				TFTSDGKIRLFYTDYSGKHYGK
		l	1		l .	QSLTTAQVNVSKSDDTLKINGV
		1	l			EDHKTIFDGDGKTYQNVQQFID
ł		1	l			EGNYTSGDNHTLRDPHYVEDK
l		1				GHKYRGPLESPSTHQAEFNPTS
		1				CVSSLGTLQGFPAPAWLALAHF
	l	1				VHPLKHKSGGSNRLSAAIWGIK
					l	RKPARVCPGTGIHASSQIQGEW
		1				RTECAVGPKAKAKATAGWRR
		1				GNNQHISSTYDINRADTQVRRA
		1				VNNYDIIVMSNSFNGQSEHQTY
		1				ESIVIDSAPNLGIGTINVVCAAD
	1	l	İ			VLIVPTPAELFDYTSALQFFDM
	1	1				LRDLLKNVDLKGFEPDVRILLT
		l		l		KYSNSNGSQSPWMEEQIRDAW
1		l		I		GSMVLKNVVRETDEVGKGQIR
		l				MRTVFEQAIDQRSSTGAWRNA
		l		1		LSIWEPVCNEIFDRLIKPRWEIR
28390	58758	Α	28564	I	2079	
28391	58759	Α	28565	1	774	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
28392	58760	Α	28566	J	2124	MNMNIKKIVKQATVLTFTTALL
		l				AGGATQAFAKENNQKANKETY
						GVSHITRHDMLQIPKQQQNEKY
		1				QVPQFDQSTIKNIESAKGLDVW
		1				DSWPLQNADGTVAEYNGYHV
		ł				VFALAGSPKDADDTSIYMFFKR
		l				GAIFRVHKHAVNPMSPKCRRPG
		1				GRQAYPLVNWEDRNGRSQKTV
						HTEGDMNMNIKKIVKQATVLT
		l				FTTALLAGGATQAFAKENNQK
						AYKET/YPKQQQNEKYQVPQF
	1					DQSTIKNIESAKG\LDVWDSWP
		1				LQNADGTVAEYNGYHVVSALA
	1					GSPKDADDTSIYMFYQKVGDN
						SIDSWKNAGRVFKDSDKFDAN
						DPILKDQTQEWSGSATFTSDGR
		1				RSLESTTTAARPIWRKDVGGDQ
	1					TQEWSGSAPFTSDGKIRLFYTD
						YSGKHYGKQSLTTAQVNVSKS
		1				DDTLKINGVEDHKTIFDGDGKT
						YQNVQQFIDEGNYTSGDNHTL
						RDPHYVEDKGHKYLVFEANTG
		1				TENGYQGEESLFNKAYYGGGT
		1				NFFRKESQKLQQSAKKRDAEL
						ANGALGIIELNNDYTLKKVMKP
						LITSNTVTDEIERANVFKMNGK
						WYLFTDSRGSKMTIDGINSNDI
		1				YMLGYVSNSLTGPYKPLNTTG
l		1		l	1	LVLQMGLDPNDVTWASLEPHE
						SFQWVRGLASSGVKLQTSVVL
		1		l		QLIKAMWTQRVSSSKVYCKEQ
				1		MNNASTMSKRTSAGCHCWQG
28393	58761	A	28567	1	3987	

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	i i	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL
						AGGATOAFAKENNOKAYKETY
						GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFYQ
i	1				ł	KVGDNSIDSWKNAGRVFKDSD
		i				KFDANDPILKDQTQEWSGSATF
		}		ļ		TSDGKIRLFYTGSLNSSKTEKY
		1				QVPHIDQSTIKNIESAKGLDVW
						DSWPLONADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFYQ
				1		KVGDNSIDSWKNAGRVFKDSD
	1			1		KFDANDPILKDQTQEWSGSATF
		1				TSDGKIRLFYTDYSGKHYGKQS
						LTTAQVNVSKSDDTLKINGVED
				1		HKTIFDGDGKTYONVOOFIDEG
	1	İ				NYTSGDNHTLRDPHYVEDKGH
						KYL/VFEANTGTEEHPQPQ\ERP
						RTQSFTSAFAERRECIPNVPADT
	l	1				KLSKIKTLRLATSYIAYLMDLL
	l	1				AKDDQNGEAEAFKAEIKKTDV
		1				KEEKRKKELASKCLDLEQLGAS
		1				VEPTGNLRTKITKEKPRHTGPPE
	1	1				VVVPGCCPHRSRAYKSDKYAH
		1				TLTVTASQHAPPPPTHMEGFEL
		1		1		FHLPDLCSPSQDAQTTGRTQMK
		1				PDHSPRPSHRVPQAKGNNVVIT
	İ	i		1		SYMTNRGFFEDKKATFAPSFLM
						NIKGNKTSVVKNSILEQGQLTV
28395	58763	A	28569	2	1778	
28396	58764	Α	28570	1099	2224	DGQQLIALHRLALRELQQAVH
		1				AGLPQQAKILFDGGSE/TRQNPL
28397	58765	В	28571	1	1938	QQLVHMGLPRPLDKKNFQEP
28398	58766	A	28572	li -	2367	
28399	58767	A	28573	4659	13369	TVFRPFHVGVHVLLIVDSCSKL
20533	50707	1	20370	1.00		EOHSTLSRAILLIYKGFCRFRNH
		I				HOTGFSPAGANORGPLAATLSG
		l				PGGEGQSAVARLTGEKKNHPG
						AQYANRLSPRVGRFINAAGTTG
						FPTGKRAVSATQLMDFADFGT
						TIKODFRILIGOTSVDRLLQLSQ
				1		GQAVKGNQLLPVSLVKRKTTL
						APNTQTASPRALADSLMQLAR
						QVSRLESGQGGEDSPNRFFDGG
		1		1		RKKQIRTVRQFIDEGNNTPADT
						QTLRDPHYVEDKGHKY
28400	58768	Α	28574	6803	8521	
28401	58769	В	28575	2010	17745	
28402	58770	Α	28576	1	1060	

SEQ ID	SEQ ID NO:	Mct	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28403	58771	IA	28577	1	3585	
28404	58772	A	28578	44	317	LKALLLTOSLFGGLLTOTRMKF
						GAVTRIG\DLPWEINPLSSCSLL
						HEKDPPTTSGPQTHQPKEHLTN
ļ					i	FKSGCSSPCRAKSOFFLSLCSST
28405	58773	A	28579	98	617	KALLLTOSLFGGLFTRTRMKFG
		1				AVTOIG\DLPWEINPLSSCSLLR
l		1				EKDPPTTSGPQTHQPKEHLTNF
ļ	ŀ					KSARFKKIKACYHSPATAWPFK
						AYKLSLQFPHFTCPKTRQALQV
				i		SSGSVPYQPNCFAYPPHGAKPI
				1		YSPILNTSLHNPLFCSGSOTCFL
İ					i	YYSFAPFIPASLRFHLD
28406	58774	A	28580	ī	1500	
28407	58775	A	28581	42	257	
28408	58776	A	28582	3	425	KTGKYD/AVIALGTVIRGGTAH
						FEYVAGGAS/NTLAHVA/QDSEI
		1				PGAFGVLTLKA*TNDERAGTKL
						HGGWGGKCLTACRSALWADL
		1				QIRPYDHKNRGSNVHNRVPAS
		1				GAAAMAIHCLECGWAPLAAGD
	1					NVGKVCVPDAGLLPA
28409	58777	Α	28583	327	1512	SYWTIHIQVSLEINHSYLPGG\IS
		1				SLKKMAGRNSERKTVLVKSSF
l		1				QEVNRGTEALALWENGDFEAP
1		ŀ				VLTFTTALLPEGATQAFGKENT
		ł				QKASKERYGSLNITRNNMLQIL
١.						NKQQTEKYQVPQFDQSTIKNIE
Ι΄		1				SAKGLDVWDSWPLQNADGTV
		1				AEYNGYHVVFALAGSPKDADD
}		1				TSIYMFYQKVGDNSIDSWKNA
l						GRVFKDSDKFDANDPILKDQTQ
		1		İ		EWSGSATFTSDGKIRLFYTDYS
	ŀ	1				GKHYGKQSLTTAQVNVSKSDD
		1				TLKINGVEDHKTIFDGDGKTYQ
	i					NVQQFIDEGNYTSGDNHTLRDF
1						HYVEDKGHKYLVFEANTGTEN
		1	1		1	GYQGGVNADVGDVVVRLPVW
		1	1			HRRGGEAVFMQVSRLQILRHLP
		1	1			HGVVAVDRDHHIAHDRRRHVA
						GDRSGSVRL
28410	58778	Α	28584	845	966	
28411	58779	Α	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL
	1	1				QTVLQNRQPGGAIARCTGHIDP
						VTRFRPRAR*GSSHRNKAVDTQ
L	L	L				RH
28412	58780	Α	28586	464	847	

SEO ID	SEQ ID NO:	Mar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletiun, \=possible nucleotide insertion)
28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ GIKRPDALPGPLLHA*PDNLRCS CPRSGTAAGSIHQDARLRYSVW RWGLLDRLAAVICRQSTHSRCR
						RKORRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	A	28589	404	733	
28416	58784	Α	28590	2	246	
28417	58785	A	28591	466	861	
28418	58786	Α	28592	122	926	
28419	58787	Α	28593	171	733	
28420	58788	A	28594	1	774	
28421	58789	Α	28595	i i	1575	
28422	58790	A	28596	1	105	SVKLGWNGVSTYVPFCLTICSV SFFQENLHLTTCRA*PSIPPPAA RRSPKKCSP*KLRLP*LSGKSSS YNL
28423	58791	Α	28597	237	461	
28424	58792	Α	28598	1	1341	
28425	58793	Α	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGFLPRKRSSRHRGKVKSFP KDDPSKPVHLTAFLGYKAGMT HIVREVDRPGSKVNKKEVVEA VTIVETPPMVVVGIVGYVETPR GLRTFKTVFAEHISDE/CRLLPL RQKKAHLMEIHVNGGTVAEKL DWARERLEQQVPVNPVFGQDE
28427	58795	Α	28601	1	1251	
28428	58796	A	28602	37	1307	EFOFDOVMSIIRKFSAPRHGSLG FLPRRKSSRIRGKVSSFPKDDP SKPVHLTAFLGYKAGMTHIVRE VDRIVGHRCNIKKERWWRAVT HCIRPPBWVVGGHLVGYVETP RGURITKITVFAEHISDECKRIF KNIWHKAKKAFITKYCKKRO DEDGKKQLEKDFSSMKK'YCQ VIRVIAHTQMRLLPLROKKKR DEDGKKQLEKDFSSMKK'YCQ VIRVIAHTQMRLLPLROKKNO REKLEOQVIPVN\QVFGQDEMI DVIGGDQRAKGFKGVTRS\WPT N*LPFKAHLGUSRVACFGAW HPARVAFSVARAGQKGYHHRT EINKKIYKIGGYYLIKDGKLIKN NASTDYDLSDKSINPLGGFWHY GEVTINDFVMLKGCVVGTKKR VLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFGTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	Α	28603	1	2133	
28430	58798	Α	28604	3	245	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28431	58799	A	28605	1	11824	
28432	58800	A	28606	1	1035	
28433	58801	A	28607	1	496	
28434	58802	A	28608	1568	1793	<u> </u>
28435	58803	A	28609	1308	1392	
28435	58804	A	28610	1	1389	
28437	58805	C	28611	104	253	
		A		114	469	VCD DTV 4 V VPTTEVT 4 DOV VCD
28438	58806	A	28612	114	469	VSRPTYAKVFTTSKTAPQKVFP
İ	i					TAWCSA/TGHETALSATQVPIQ
ŀ	ļ	İ				WIATAPNSPAPPSDPRRQSWVS
						QIPSSATSPNFTM*EPRTQEVTE
1	1					PHDSRPAIPSPAVPRRESCTGRP
						HLPATTP
28439	58807	A	28613	3	2196	
28440	58808	A	28614	237	348	NPVN*SQTT*TSE
28441	58809	Α	28615	950	1094	
28442	58810	A	28616	146	822	LGFLLRLSEMPRKQGVYRTRIW
		1	İ			KFEDGLSNVLVI/PIEQINHMRD
		1				VFGSGSERATCLARGRGYINSL
		i		1		ARCQNLVNRDLDHLSLPQDSTL
		ı				VHYIDDIVLHGFSEEEKGQVAQ
						SADLDEGLLKIPGDTFGPEADK
	ŀ	l				DFLHKDLSTEIVGOSYNTHHM
1						AODSIPWNPSGQEPOVREHEAC
1						
						HHLGSGSPPSWELCEQGPPVTE
						SFQVLVTSGLDKENMAYMHCG
28443	58811	A	28617	1	1791	IICSNKKG
28444	58812	A	28618	244	416	
28445	58813	A	28619	244	1520	
	58814		28620	95	421	PVTSTSTKRTPTOKPHPKVISLK
28446	58814	A	28020	93	421	
			i			DQIHHVDKSMMMRKNQCKNV
	l					EKSKNQNSSSPHDHNSSP\SARA
	ļ		1		1	ENWTEYESDKLTEVGFRGWVI
		L_				NSSELKEHVLTHCKEAQNLHN
28447	58815	С	28621	46	174	
28448	58816	A	28622	425	1291	
28449	58817	Α	28623	1	1410	
28450	58818	A	28624	14	348	GLFPNKIPFSVLEIRTWAHLSGR
		1				HHSAHCTSCA WPQVACLPLAT
		1				HPSCTCTFCSLQAPGRPGQSPLS
1				l	l	PRRACGPEDLPPPPYV*DLAPSL
						GPSLGPLMSQSQPRRTPPLRG
28451	58819	Α	28625	96	295	PWKPHPAWRQRWELCHPPFP/I
						RPLTAALREQPGLLGRSTTVFT
1	1	1			1	LMAREPPQPAAADSCLCIVQME
1	1	1			1	A
		_	L	L	1	r

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletiun, \-possible nucleotide insertion)
28452	58820	۸	28626	105	389	CQFAHGTASSPRVCLRHRCRS WQKAWAVVCCTFCSLQAPGRI GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQPRRT PPLAWGS
28453	58821	A	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	A	28629	301	987	
28456	58824	A	28630	239	384	VLPAGAQAAARSSDTRP*PEPH FS\ESVFPRWIFSAFQSLNNFFQA RF
28457	58825	Α	28631	1	1054	
28458	58826	C	28632	243	392	
28459	58827	Α	28633	1	1104	
28460	58828	Α	28634	194	863	YLLFVKNMSSLEISSSCFSLETK LELPSPLVEDSAFEPSRKDMDE VEEKSKDVINFTAEKLSVDEVS QUVISPLOGAIS/LNWKGLTENT FEGKKVISLEYEAYLPMAENE VRKICSDIRQKWPVKHIAVFFHR LGL/PVPSEAKP*SFAVSNAHRA AISLKLLSYC/AFDTFKRPKYPI WKKEIVEESSTWKGNKECFW WKNEIVEESSTWAGNECFW
28461	58829	A	28635	3	338	SSPPTAPAKLRIVPLVGGLPAR WCLSVCASQCPDTRVHVFLHW WCSSLCPAPVCLSLCRGL*GHF PPDSEDQSSPNCSGYTLEEYKL LRSQTIPSCNGKFPCPPRRAYDG
28462	58830	Α	28636	405	800	
28463	58831	Α	28637	265	539	
28464	58832	A	28638	3	1116	
28465	58833	А	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	Α	28641	563	594	
28467	58835	Α	28642	245	580	
28468	58836	В	28643	1	435	
28469	58837	A	28644	673	1012	QPQVSFSSEYAIHIMRCPHSKIS SLYYFNCFRY*DCYCH\TFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLNTGA WVRAWKATSTSVVHLTKWVL
28470	58838	A	28645	1171	1328	MVIGGTKNERKHIDSDEPLFPSP NSSARGRAISSTS*ALVPGVRGF LSSIPLSLTTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGSAVDLSHGLHLGLHL KNDL*FYSFNSGIDKPEIAKLSG CSFGGTFLIWG
28472	58840	c	28647	199	309	

SEO ID	ICEO IN NO.	Mat	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLSLPKLK
20113	500	1	20010			L*SYKSFFKWSPRCSP
28474	58842	В	28649	107	264	
28475	58843	Α	28650	301	470	EIQLVLSLSGGGYSHAVLMIVS
				l		SHKI**FYKGLFPTFALHFSLLLP
						CEEGCICFPF
28476	58844	Α	28651	2	263	WEKKDTEWRKKVILSSV*LRL
				l		VIF*PFSLM\LFSHPVWR*ARSH
					l	ESHLAITHLWALYF*PPCQICFL
		_				*DRGHQATDGLTNGTPSELN
28477	58845	A	28652	63	191	DLPWTPGPAC*PMLQC**GGAN
	ļ	<u> </u>			L	IYARRQGADAAGDQGSSCRL
28478	58846	Α	28653	1	554	MPTYCPGASLLILTYKTPKELLS
Ì		1		l		IYVSTIRKSRCRERRNRRLGAR
		1	1			NFRSEEQIYDQWRLDQVGKFFP
						FPRPRENYHFGSEHVGSFSLDK
						CCNEKLYEVIDLHLKKKFLNTE TLSLVKCEVSRCWVTLNLLLPY
						H/VLFQI*LSWRERQNQSCKTTN
		ı		1		GSSNGAPDAVHN*NLLWSLGP
			1			AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWLPALPEN
28479	30047	<u>۱</u> ^	20034	ľ	317	GYMKOFCVSGLGVLFHGCVFL
		1				CWHHCCFVL*VWSLGSPRSRG
		1				LHLVKAFFLCYPRSNCFLLNWG
	1	1				IVGVVQLRFPQEGCLWCH
28480	58848	В	28655	1	400	1701122121222
28481	58849	В	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTLALPVSSQPFSLHTA
		1				EVQGCAVGILTQGPGPCPVAFL
		ı				SKQLDLTVLGSPSCLHAVASAA
		1				LILLEALKITNYAQLTLYSSHNF
		ı				QNLFSFSHLTHILSAPRLLQLYS
		ı				LFVESPTITILPGPDFNLASHIILD
		1		1		TTPDPDDCMSLIYLTFTPFPHISF
		ı				FSVPHVDHIWFTDGSSTRPDRH
		1				SPAKAGYAIESSTSIIEATALPPS
		ı			i	TTSQQAELIALTRAFTLAKGLH
ĺ		1				VNIYTDSKYAFHILHHHAVIWA
		ı	l			ERGFLT/IARVLHH*CLFNKNSS
		ı				QGCFTSKGSWSHTLQGPPKGV
		┖				RSHYSRKCLC
28483	58851	Α	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	A	28661	1	704	
28487	58855	A	28662	41	275	
28488 28489	58856 58857	A	28663 28664	159 275	1504 552	
28489	58858	A	28665	178	619	
28490	58859	A	28666	3	369	
28491	28839	IA.	∠0000	l <sub>2</sub>	1202	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
28492	58860	A	28667	li	340	
28493	58861	A	28668	516	734	WTGDWRRTCDRENOHVSGAA
20	50001			1		RTAFIPTNGAISPGINYSPGH*Y
						DCHLPQA*P*LCRAAGONRCH
						VARTCLG
28494	58862	Α	28669	1	I163	MHTHARETCLALGKPADDATI
						TAAIEAVGLENAARVLKLYPFE
						MSGGMLQRMMIAMAVLCESP:
						HADEPTTOLDVVAQARILDLLE
		1				SIMQKQAPGMLLVTHDMDKW
						GRIIADVESOYRYOTTNPKIFAC
		1				GDAVRGADLVVTAMAEGRHA
		1				AQGIIDWLGLDVDKLGALEERI
		1				KVLQVKTENLQAERNSRSKSIG
				1		QAKARGEDIEPLRLEVNKLGEE
	i	1		İ		LDAAKAELDALQAEIRDIALTII
		1				NLPADEVPVGKDENDNVEVSR
		1				WGTPREFDFEVRDHVTLGEMH
						SGLDFAAAVKLTGSRFVVMKG
		ı				QIARMHRALSQFMLDLHTEQH
	ŀ	1				GYSENYVPYLVNQDTLYGVGL
						YPLGALASGW/WALASGWLPK
	Į.					RRERKD/GDTGAHGVPRGSRKF
						RIARKVRGT
28495	58863	В	28670	I	4770	
28496	58864	Α	28671	1069	1398	VIGAQPVLRIRRKQARRQINRL
		1				TLILLHYCLTTKLKNGVKPGIV
		1				AAFYFLPGAG*IHPAGCHGTQL
				]		*SFGKMRVQYTRVTLSQQASG KISAYLIDLGKPLLKLIIHCGVH
28497	58865	A	28672	4246	4453	RISAYLIDLGRPLLKLIIHCGVH
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	Α	28675	1085	1246	
28501	58869	A	28676	I	1254	
28502	58870	A	28677	1	2175	
28503	5887I	A	28678	340	994	
28504	58872	Α	28679	37	261	TITPAGRRMHCKGACMKPLLD
	i					VLMILDAVRELE*TITPAGRRM
						HCKGACMKPLLDVLMILDAVR
	1					ELEKQAIKLHEGWENELVIGVD
						DTFPFSLLAPLIEAFYQHHSVTR
28505	58873	A	28680	410	896	WAWAASAVQPRSIWQ/GAGVG
	1	1	1		l	NLTLLDFDTVSLSNLQRQTLHS
						DATVGQPKVESARDAPHIAITP
	1					VNALLDDAELAALIAEHDLVL
	1	1	1			D/WYG*RCGT*STERQQR*RG*
						RSAPAMTAHDRDAIASSSETCA
			1			RSRWSVEYASPVCAPPDSRSKR
L						RSASNSA ASHVF
28506	58874	В	28681	1	2298	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	uf peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28507	58875	A	28682	1915	5313	
	58876	A	28683	1	4221	
	58877	A	28684	1	1007	MAALQMVNGQKWVSSNQKY
2000	200	l`^		ľ		WLVYKTTDPPRLRPIFSGYOPM
						CPFNGRPFWIHKNPMGVHWAV
					i	ATGLALIPIVGIAEFGWFWFGG
	ŀ				ŀ	ETYMAAWNVSGLGTFGAIOST
						FNVTLWSFIGVESASVAAGVVK
	ŀ					NPKRNVPIATIGGVLIAAVCYV
					l	LSTTAIMGMIPNAALRVSASPF
	ŀ					GDAARMALGDTAGAIVSFCAA
		1			ł	AGCLGSLGGWTLLAGQTAKAA
		1				ADDGL\FPPIFARVNKAGTPVA
		1				GLIIVGILMTIFOLSSISPNATKE
		ł				FGLVSSVSVIFTLVPYLYTCAAL
		l				LLLGHGHFGKARPAYLAVTTIA
		1				FLYCIWAVYITHIDACVVVYIA
		l				GYRAAKLTCA
28510	58878	A	28685	867	1681	OTHER DESCRIPTION
	58879	A	28686	865	1290	RWWENRLFRKNPARAOKMVL
20311	30079	l^	20000	803	1270	PERFG*SAYPNGFAGTWRLDKL
		l		l		PIAOIHAHMIGYLAAVDMEKO
	ŀ	l				QISPAQVVVRHNRCPAIVVHLI
		l				GRARELSLKDLVVGIKNOPATV
		l				KAFIRPRTAPDVRLAKLLLQAV
		l				NRHFGNVMQMVAA
28512	58880	A	28687	1	709	
	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPOT
20010		l.,		[		AFIQVGPRVHAHLQPRAAPL*A
		l				GEVWKPRLVGRSHWASRPSPA
		l				LOKGEPGSPSWENACVPOAPH
		l				RLLHOOKAF
28514	58882	A	28689	3	227	NSODFPACGGLCHAELDRTAA
		1				GLVHOH\RHPGHTSVAAEKLCH
		l				GDVEGDGCNGPASD/PGYI*GQ
		l				AAAPAPLPDLL
28515	58883	Α	28690	1227	1719	
28516	58884	Α	28691	1	1701	
28517	58885	Α	28692	15	3298	
28518	58886	Α	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR
		l				AVWRYQTDIAANLE*RRLPSGA
		l			1	GKSDWSSGDSEKAKTAAHTIY
	I	I	ı	I	1	RDAGRRVRGYROL
1	ı	ı		1		KDAGKKYKGTKQL

SEO ID	SEO ID NO:	Met	SEQ ID NO:	INC. ST. ST.	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
110.	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	,	*
28520	58888	A	28695	1	910	MDKERIIQEFVPGKQVTLAHLI
20320	38000	^	20093	l'	1710	AHPGEELAKKIGVPDAGAIGIM
	1	ı		l		TLTPGETAMIAGDLALKAADV
						HIGFLDRFSGALVIYGSGNYTL
				ļ	1	ARKTQAVEFNDKGDIDTPGEYF
		ı				NHPRWYHALITTLQDVDMLSP
	l	1				LIWGFRNYKDVQVIKATPHKIV
						ILMGILLSPSVFATDINVEFTAT
						VKATTCNITLTGNNVTNDGNN
	1					NYTLRIPKMGLDKIANKTTESQ
	ł					ADFKLVA\MGAAVASVGLIPL*
	1					
						PEMHHQAHLSLLYRSLVIHLRR
				i i		QVISVWVSKNGLLMMPLSLNL
20721	50000	١.	20000	105	2021	TVRKRYAGAQTRCSPIRVLK
28521	58889	A	28696	605	2021	CIV.CCA.D.DIA.D.EDC.VI.ECX*D.CV
28522	58890	Α	28697	2256	2330	CIKCCARRIAREPGYLFS**RCK YPG
20.522	50001	١.	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN
28523	58891	A	28698	1802	4488	
		1				V*SWIKSS/MQMGQKMGVKISD EOLDOAIANIAKONNMTLDOM
1		ł			i	
		Į.				RSRLAYDGLNYNTYRNQIRKE
1						MIISEVRNNEVRRRITILPQEVES
		1				LAQQVGNQNDASTELNLSHILI
						PLPENPTSDQVNEAESQARAIV
						DQARNGADFGKLAIAHSADQQ
1						ALNGGQMGWGRIHASLPGIFA
1						QALSTAKKGDIVGPISSGGRFD
						GTVEVKDGHLIVNGKKIRVTAE
1		1				RDPANLKWDEVGVDVVAEAT
	1	1				GLFLTDETARKHITADTPAALR
	i					WLEENQLEDGHECLLRRVISSD
		1				GRSRGFINGTAVPLSQLRETSTT
		1				TGARRVIRAIRRINSSDASTIPTL
		1				MAITISNNTVSDMHSSMTMMS
		1		i		TRIRTLITTIYNGDLRMIRQRKL
		1				CKTAIARTYGNDDTFHPGMRH
	1	1				QRMHRVFKNAPHLDQPVVTLN
		1				IYPKADESSSLKASRGTRGAAY
						RPARQNLYSASSGKKDENPVIE
						FKNVSKHFGPTQVLHNIDLNIA
						QGEVVVIIGPSGSGKSTLLRCIN
						KLEEITSGDLIVDGLKVNDPKV
1						DERLIRQEAGMVFQQFYLFPHL
1	1	1				TALENVMFGPLRVRGANKEEA
	1	1				EKLARELLAKVGLAERAHHYP
1	1	1				SELSGGQQQRVAIARTLAVKH
1		1				KMMLFDETTFDFDPELVHEVL
1		1				KVIHEFAEKGITNDSLTENPAKT
						QGEGGCLQSQERGPQREPTPRH
28524	58892	A	28699	1	2307	
28525	58893	A	28700	3	976	
$\overline{}$						

SEO ID	SEO ID NO:	Mat	SEO ID NO:	Nucleotide	Nucleotide Inestion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon,/=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28526	58894	Α	28701	2	136	YLSAV*FCSPGQPPSALLVCGR
						RGYWCLWPLSSCHLTLRLCVS
28527	58895	Α	28702	1	608	
28528	58896	Α	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	A	28705	1	1184 627	
28531	58899	A	28706	478 33	1072	
28532 28533	58900 58901	A	28707	35	516	RVVEFADEGOGPAALSLWSGS
28333	38901		28708		310	SPETLKLHWPHVQN*IRFSSWK TFRIRSRDFWADRLMRTILRNF LSKWDHL*GQTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRRDGGLAGLRGN SGAQGGDA
28534	58902	A	28709	1	777	2011600011
28535	58903	A	28710	531	704	
28536	58904	A	28711	294	617	
28537	58905	A	28712	804	1020	HFLSGGRRQRPPRWTIVA*SPR*
						PRCRCWGSG*RPGTRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRRQRPPRWTIVA*SP R*PRCRCWGSG*RPGTRGALPV VRKQPGDPKTPLASCPELNQPV PEPAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSGLRRLLGR PSHEGPWLKGTSCRSGTTCRDR PWV
28539	58907	Α	28714	2	1580	
28540	58908	Α	28715	286	352	
28541	58909	Α	28716	1	531	
28542	58910	A	28717	1	1440	
28543	58911	Α	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLLQLVEVLPE ANRQLRQSGAGDGGQQAVF*F HRFLASVHQHKAASASPPYLFR IKCPVPRLRAKPALLLIDNRLYG
28544	58912	Α	28719	1	3534	
28545	58913	Α	28720	1846	2121	
28546	58914	Α	28721	176	462	TSRHSVYISDTELKPRKSSKPTF CGCDSLFSPICHFP/HGLSDVALI VQQLRQRG*PLQPARLPVHWR HQNAVVDGVLSGENGGAGWG RAWLRIRRS
28547	58915	Α	28722	225	3465	
28548	58916	Α	28723	937	1770	
28549	58917	Α	28724	142	484	

	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		_				
28550	58918	A	28725	1	1521	MIPITWPKFAELHPFCPPEQAEG
		1			\	YQQMIAQLADWLVKLTGYDA
						VCMQPNSGAQGEYAGLLAIRH
l						YHESRNEGHRDICLIPASAHGT
i						NPASAHMAGMQVVVVACDKN
						GNIDLTDLRAKAEQAGDNLSCI
						MVTYPSTHGVYEETIREVCEVV
						HQFGGQVYLDGANMNAQRRD\
						MAGKPGPLTVRKMRGSRVTVR
						AL*/ASVWIGFDDHRRNLGHTT
						ASGAIKDQISGYEGGAKSAQPA
ļ						WDAYMKAVLEGVPEQPLTPPP
ļ						GIVTVNIDRSTGQLANGGNSRE
		1				EYFIEVNEIVVNPNATLDWQLA
1		1				LRQAAGKTDLARDMLQMLLDF
						LPEVRNKVEEQLVGENPEGLV
						DLIHKLHGSCGYSGVPRMKNL
						CQLIEQQLRSGTKEEDLEPELLE
1						LLDEMDNVAREASKILGGHDN
1						GGNALLHKALPPGNVGKWAM
		1				APIPPPFPQPGKSVTICWKPASS
1		İ				ENRSNLLEIFLRELISNASDAAD
						KLRFRALSNPDLYEGDGELRVR
						VDEVLSPASVPYS
28551	58919	Α	28726	1	1279	
28552	58920	A	28727	3	762	MTQDELKKAVGWAALQYVQP
28553	58921		28728	1	1472	
1		A				
1		Å				GTIVGVGTGSTAAHFIDALGTM
		A				GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI
		A				GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW
		A				GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN
		A				GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK
		A				GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY
		A				GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLOH HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPODERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG
		A				GTIVGVGTGSTAAHFIDÅLGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL
		A				GTTVOYGTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GREGNEYSGWFDLQLKQRVYN
		A				GTIVAVGTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HYPDLNEVDSLGIYVDGADEIW QTCKAQRCQSTCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKYWEDGIGSTY YSRSGGGTASHGSPKSWAIGSL GREGREYSGWEDLQLKQRVYN ENGKRYDAVVMMDGNYGQQ
		A				GTIVOYOTGSTAAHFIDALGTM KQQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPODERRISNCSSK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG SYRSGGGTASHGSPKSWAIGSL GREGREYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNVQQ YSTGWFGDNAGGENYMQFSD
		A				CITÍVOYOTGSTAAHFIDÁLGTÍM KKQQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GREGNEYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAFEADFWVGK
		A				GTIVAVOTGSTAAHFIDALGTM KQQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPODERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GRFGNEYSGWFDLQLKQRVYVN ENGKRYDAVVMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HGAPKIEIGMLDWKTQRTDAA
		A				GTTVGYGTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYVSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG SYRSGGGTASHGSPKSWAIGSL GREGNEYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNYGQQ YSTGWEGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HGAPKIEIQMLDWKTQRTDAA AGYGLENWKVGFGKIDIALVR
		A				GTIVAVOTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSFCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIT YSRNGGGTASHGSPKSWAIGSL GREGREYSGWFDLQLKGRVYN ENGKRVDAVMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWEVGGREIDIALVR AGVGLENWEVGGREIDIALVR AGVGLENWEVGGREIDIALVR AGVGLENWEVGGREIDIALVR
		A				GTIVOYOTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPODERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSVTG SYRSGGGTASHGSPKSWAIGSL GREGREYSGWFDLQLKGRVYN ENGKRYDAVVMDGONVQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HQAPKIEIGMLDWKTQRTDAA AGVGLENWKVGPGKIDIALVR EDVDDYDRSLQNKQQINTNIID LRYKDIPLWDKATLMPRIPTQR
		A				GTTÍVGYGTGSTAAHFIDÁLGTÍM KKQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG SYRSGGGTASHGSPKSWAIGSL GREGNEYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNVGQQ YSTGWEGDMAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HAVTTKGFLPFAPEADFWVGK AGVGLENWKVGFGKIDIALVR EDVDDYDRSLQNKQQINTNTID LEYKDIPLWDKATLMPRIPTQR YGLAKA/SLEADVRY/MANAM
		A				GTIVAVOTGSTAAHFIDALGTM KQQIEGAVSSDASTEKLKSLGI HVPDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPODERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SSPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GRFGNEYSGWFDLQLKGRVYVN FONGKYDAVVMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK MYVTTKGFLPFAPEADFWVGK HGAPKIEIGMLDWKTQRTDAA AGYGLENWKVGPGKIDIALVR EDVDDYDMSLQNKQNINTNTID LRYKDIPLWDKATLMPRIPTOR YGLKAASLEADVYJMANAM GPEGVRVNAISAGQITETLAAPG
		A				GTTÍVGYGTGSTAAHFIDÁLGTÍM KKQIEGAVSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG SYRSGGGTASHGSPKSWAIGSL GREGNEYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNVGQQ YSTGWEGDMAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HAVTTKGFLPFAPEADFWVGK AGVGLENWKVGFGKIDIALVR EDVDDYDRSLQNKQQINTNTID LEYKDIPLWDKATLMPRIPTQR YGLAKA/SLEADVRY/MANAM
		A				GTIVAVGTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HVPDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRPPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SYBMILADESSEKVENDEIGESVT YSRSGGTASHGSPKSWAIGSL GREGREYSGWFDLQLKQRVYN WYDTKGFLEYPAPEADFWVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWEVGPGKIDIALVR EDVDDYDRSLONKQUINTNTID LRYKDIPLWDKATLMPRIPTOR YGLAKA/SLEADVRYMANAM GPEGVRVNAISAGQTRTLAAPG IKIDAKSKMILAHCEPVTPIRRTYT IKIDSKKMILAHCEPVTPIRRTYT IKIDSKKMILAHCEPVTPIRRTYT IKIDSKKMILAHCEPVTPIRRTYT
		A				GTIVOYOTGSTAAHFIDALGTM KGQIEGAVSSDASTEKLKSLGI HVPDLNEVDSLGIYVDGADEIW QTCKAQRCOSPCSKTLGAOPEN PDLSQISRFPODERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG SYRSGGGTASHGSPKSWAIGSL GREGREYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HGAPKIEIGHULDWKTQRTDAA AGVGLENWKVGPGKIDIALVR EDVDDYDRSLONKQQINTNTID LUTKYDIPLWDKATLMFRIPTQR YGLAKA/SLEAD/NZYMANAM GPEGVRVNAISAGQTTLAAPG IKUDSRKMILAHCEPVTPIRRTVT

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.01	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
						L
28554	58922	Α	28729	2	419	RPRPRPRHMLQGTHRQRHLHA
	1					GPGVARRRWGGMARRAARGR
	l					PRLRLCIFSRSROLGLRLRFLSST
	1					VNEGDQVKTVA\RSGHFCGGLS
	1					SFSFSSSFSSGKKRPSNSPGSMR
	1					LGSPPSGAGRAGGIVTVAC*AR
	1			ł		
20.555	50000	١.	20520	70.5	2004	LSTCNTKQ
28555	58923 58924	A	28730 28731	725 661	2804	DVREGDRDPFMIKVHSCVFVDF
28330	38924	A	28/31	001	1218	
		1				AKTMHDGA/SVSLRGNLISHKG
						EDRY/VFRDKSGEINVVIPAA/V
		1				FDGREVQPDQMINISGIADKLP
		1				VIAPTNATSKLKLASQPEDDSEI
						YDGCNGAQPGDYWFAAFVSG
		1				MFSRWLAKTILSRHILSVTIRSC
		1				KNGEWLAVGGAENGAYSDSR
		1				VAVMLLLSAWGLFDF
28557	58925	A	28732	1	624	
28558	58926	Α	28733	1	1281	
28559	58927	Α	28734	114	266	
28560	58928	Α	28735	1487	1570	
28561	58929	Α	28736	1	3402	
28562	58930	Α	28737	1	2466	
28563	58931	Α	28738	372	647	SGWSWNTKFPTGGFRWPAQPG
		ı				TELESSQPR*LVMPATTSPFRAL
						DVCEYLPACVAVISGCHPSRFA
		1	ł			RSYVSAPD*QNVQLTYPHIVLN
		1				RHL
28564	58932	Α	28739	1	2235	
28565	58933	Α	28740	3	293	
28566	58934	Α	28741	737	963	
28567	58935	Α	28742	3	282	RRLRASGCIDKLPSG**YARPAR
						*DPAPGFR*STPVRKCDQTRSPA
		1				MKVIAAADRKLWCGAICPLSA
			İ			KPPAGRAPNAPAAPASPNRPMT
				ĺ		PSL
28568	58936	A	28743	2	289	
28569	58937	A	28744	1	1662	
28570	58938	A	28745	421	2634	
28571	58939	Α	28746	134	954	
28572	58940	Α	28747	1036	1383	
28573	58941	Α	28748	2	589	
28574	58942	Α	28749	1	801	
28575	58943	В	28750	14	499	
28576	58944	Α	28751	3	916	
28577	58945	A	28752	3	589	
28578	58946	Α	28753	1	1675	
28579	58947	Α	28754	1	522	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		i i		sequence		[, F
28580	58948	Α	28755	1229	1660	LMVSGFLTSPKDHERIIVAKPEQ
					1	FWKLRQVMFMAIVISLPTIGER
		1				FSPFLLKSPLIRPSRCGTTDFISG
		l			1	LTARPEFSOSRMVLIAASTITSL
		l				MCAGSFLPIRPLASICSLNATTS
		ı				**LPFSSGRDSSRKRRTQAITCSF
		1				RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF
		1		ľ		NSIWSCASAILGNLGILTGSPPL
	i	1				ALCRTLCLTYPI*CPRDAKALR
		1				RPRECVIRHD
28582	58950	A	28757	h	850	MPVMFLASLSGKHQGHHFPKG
20002	30730	١,	20151	ľ	1000	ERGKFKIKERGTVATEDRRSGD
		1		l		STFYAIQPTRRQKRVYGLALLL
		1		ĺ		
		1				QLHRRRQNLNIDSVSSVGLAAL
		1				VTAFIGVDFFANGEQTYSQPLW
		ı				TWMSVGDFNIGFNLVLDGLSL1
		i				MLSVVTEGYSR*EHRPTPSQPR
		l				YISSRLSASTRTTM/PGDEQVGV
			ĺ			SEEARVALSDHREHGQRQAVQ
		1				HQVKTDVKVAYRHPRPQRLAV
			i			CLLAVSEEINADKGGYQRRQA
						HRAY
28583	58951	Α	28758	20	282	
28584	58952	Α	28759	38	966	RDGLESRGRVCSLRTAFQRSSS
						EAFTSDLQAAELQNRASNRPAR
						IGHAHLVIFPVQSSWM*RKLAS
						PRNNLVIPQEKALKEYIKIGNLV
	1					MSLAAAPLNR*GLL/IEWNDND
1		l				GGCKGACDRVPHONVTALNLR
		l				DOCINGECYDEVLFHGLEEYIN
1		ı				NLOGDGVIVLHTIGSHGPTYYN
						RYPPOFRKFTPTCDTNEIQTCTK
1		1				EOLVNTYDNTLVYVDYIVDKAI
1						
		1				NLLKEHQDKFTTSLVYLSDHGE
ł		1				SLGENGIYLHGLPYAIAPDSQK
		l				QVPMLLWLSEDYQKRYQVDQ
		L				NCLQKQAQTQKDCVLLIFAKQ
28585	58953	A_	28760	1120	1335	
28586	58954	Α	28761	846	1245	TVRKRGTRHPHGSRRTLSLPLR
						HSSDRCNRTRSADRSTGPRL/A
		1	l	l		QPRYISSRLSASTRTTMPVTTES
	Ī	1	l			MVSDRPSSTRLKPMLKSPTDIH
			ĺ	l		VHSGWLYVCSPVAKKSTPMKA
		1	l			GTTAGRPTEPTPTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	A	28763	188	322	
-0000	1-0/00	1	-0700	1		

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop eodon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28589	58957	A	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE TITNRPRKVKIRHPVASFFHLFR VSAIIVCLLCELSSSFITCMSKK WLAVVIVGVVLQGANLYGYLR CKGQEVRETFAEPSLQATQMK KRRAILADDINEKIAQRFOPM ELVEKNILPVDSSVKEAIIGKTL KIYYLGAPAEAATKEDERTTSG PGHHATNYHFLKFFDFYLL HFVHKDAILSGHPLVRLLSTRV LRGPMOVFHGYSSVOSVLAIFV LAEPMOSLSASLEN
28590	58958	<u> </u>	28765	1	3219	LAEPMOSLSASLEN
28590	58959	A	28766	3	245	
28592	58960	A	28767	2	1193	CANQLRDCLVIPTITGLVRLVV AGANGDRLGQPVTGADVRLSR CREVMPSSSYEMGLVPSSSVIV TVLPLIGFVLLAFSRGRWSENV SAIVGVGSVGLAALVTAFIGVU FFANGEQTYSQPLWTWMSVGD FPNIGFNLVLDGLSLTMLSVVTIG OFGLIHMY ASWYMRGEEGYSR FFAYTNLFIASMVVLVLADNLL LMYLGWEGVGLCSYLLIGFYY DPKNGAAAMKAFVVTRVGD VFLAFALFILYNELGTLNFREM VELAPAHFADONNMLMWAT MULAGFALFILYNELGTLNFREM AMAGPTPVSALHAATMVTAG AMAGPTPVSALHAATMVTAG VYLJARTHGLFLMTFEVLHLVG IVGAVTLLLAGFAAL*0*K*HP RHPKHRNAG**TRVLQRGAGC AGARVTDHFRG
28593	58961	Α	28768	3	2191	
28594	58962	В	28769	1	2263	
28595	58963	Α	28770	1089	4965	
28596	58964	Α	28771	41	249	
28597	58965	А	28772	533	709	VSFLIVSSSLIALWSERQFVIISV LLHLLRSALLPTMWSILE*VWC GAEKNVYSVDLG
28598	58966	Α	28773	2714	3599	LGSQWH*IYKLPWAVWSFSQY
28599	58967	Α	28774	45	188	GKVQCHRGLIHVNWLPPVKKF *LRQKGKPTSSSQETPKTEPGRL LKP
28600	58968	Α	28775	722	856	GNDLCPKTIRTGDAWCVPGTT RKSAWK*GKISGSLSFLPVRDG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*-Stop codon, /-possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
28601	58969	Α	28776	474	1338	PANQKKPRTRWIHSRILPEVRR
20001	36707	^	20770	7/7	1,550	GAGTIPSETIPNNRKGGNPP*LIL
						*GOHHPDTKTWORHNKK*KFO
				l		ANIPDEH*CENPQ*NNGKPNP\E
	1			i		HSKKLIHHNQVGFISGMQGWF
						NICKSINIIHHINRTNDKNHMIISI
		l				DAEKAFDKIOHPFMLKALNKL
1	1	l				GIDGTHLKIIRAIFDKPTANIILN
	j	l				GOKLEAFLLKTDTROGCPLSPL
1		l		i .		LFNVVLEVLARAIRQEKEITGIQ
1	l	l		ŀ		
	İ	l				IGKEEAPQKQQRLFCRYYHGK
						RAPQLLITHLEEDDEWDIIRYY
		_				NVMSEEEIKRMKEIVKPKII
28602	58970	Α	28777	2289	3225	LTNQNKSRTRWIHSRILPEVQR
1						GAGTVSSETIPNNRKRWTPP*LI
						L*GQHHPDTKTWHRHNKKRKF
						QANIPDERQCKNPQ*NTSKPNP
						AAHQKAYP**PSQLHPWDARL
1						VQHMQTNKHNPSHKQN\HDKN
						HMIISRDAEKSFNKIQQPFMLKT
1						LNKLGISGTYLKIVKMHTMSSS
1						HLFYLALCLLTFTSSATAGPETL
						CGAELVDALQFVCGDRGFYFM
						EQCTMAVSIRGRELLGPSEQEM
1		1		l		LHKESGKQRQKANTIPVTSKIV
						HLALYATLLLFVMEQFLGESHK
						SREIFSFEQQISELGKESMKFSEE
		_				KEKE
28603	58971	Α	28778	1177	1272	
28604	58972	Α	28779	480	766	SSEIQHWFQGQPRWSRCRVSGR
				l		RHEASTVLPLCFLLPQNSSSMQ
	l	1	1			LG*NRSMP/HVSESSRTLVL*EV
1	l	1		l		TKHQVSSNFKMRDKDRSGRAS
		1				SLRKHRRE
28605	58973	Α	28780	1	1344	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28606	58974	A	28781	971	2314	PTNOKKSRTRWIHSRILPEVOG
						GAGTIPSETIPINRKRRNPL*LIL*
						GQHHPDTKAWQRHNKKEEL*T
						NSPDEH*CKNPQ*NTGKPNP\EH
	l					IKKLIHHDOVGFIPGMOGWFNI
						HKSINVIOHINRTKDKNHMIISI
		-				DAEKAFDKIQQPFMLKTLNKL
	İ					GIDGTYLKIIRAIYDKPTASIILN
	i			ł		GOKLEAFPLKTGTROGCSLSLF
						LFNVVLEVLARAVROEKEIEGI
	1					QLGKDEVKLSLFADNMIVYVE
	1					NPIISAONLLKLISNFSKVSGYKI
		1				NVOKSOAFLYTNNROTKSOIM
						SELPFTIASKRIKYLGIOLTRDV
		ı				KDLFKENYKPLLNEIKEDTNK
		l				WKNIPCSWIGRINIVKMAILPKV
	ŀ	l		ļ		IYRFNAIPIKLPMTFFTELEKTTL
		l				KFIWNOKRARIAKTILSOKNKT
	i	l				GGIMLPDFKLYYKPTVTKTKW
	l	l				YWYONRDIDOWNRIEPPEIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHHP*
2000	00370	``				GSIPSRSLLVATTPTRGVTAALE
28608	58976	A	28783	1	1938	
28609	58977	Α	28784	1389	1499	
28610	58978	Α	28785	I	351	
2861 I	58979	Α	28786	I	329	KNLDEKLLPASSSSCRIWATSP
	l					VHHLWQVLKKILF/GLEPYEIST
ŀ	l					LFEQRQAM/LQSIKEGVVAVDD
i	l	ļ		ŀ		RGEVTLINDAAQELLNYHNFIR
	1					SRSLPVFVLASACGSGTRRRRA
28612	58980	Α	28787	1	419	VRPGHLLDIDDTDMPSLRYSDP
		1				EAQRIGQPFKGDDILKALNGEE
		1				NVAINRGFLAQALRVFTPIYDE
		l				NHKQIGVVAIGLELSRVTQQIN
		1				DSRWSIIWSVLFGMLVGLIGTCI
1						LVKVLLG/IIFG*TYKSQLFEQR
		1	1	1	1	QAMGRL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28613	58981	Α	28788	11	1795	MWIISCVMKRTAMNCVLWRK
						RRRKVCASIFTGKNRANOKRD
l						NVELFDARCRPLNDAADTVRY
						LPVLTVQLLDKQPRLTVLKKIL
		ļ				FGLEPYEISTLFEOROAMLOSIK
						EGVVAVDDRGEVTLINDAAQE
						LLNYRKSQDDEKLSTLSHSWSQ
1		1				VVDVSEVLRDGTPRRDEEITIK\
l		l				DRLLLITTVPVRSNGVIIGAISTF
		l				RDKTEVRKLMORLDGLVNYA
		1				DALRERSHEFMNKLHVILGLLH
		1				LKSYKQLEDYILKTANNYQEEI
		1				GSLLGKIKSPVI\AGFLISKINRA
						TDLGHTLILNSESOLPDSGTAA
ŀ		1				CGQSLNVLYQRIVGERKLHTGS
		1				LMSAAGKSNPLAISGLVVLTLI
		l				WSYSWIFMKQVTSYIGAFDFTA
		1				LRCIFGALVLFIVLLLRGRGMRP
	1					TPFKYTLAIALLQTCGMVGLAQ
						WALVSGGAGKVAILSYTMPFW
						VVIFAALFLGERLRRGQYFAILI
						AAFGICTATQRNRLLPCKNQPC
		l	1			KANQYQGTGDVLNQLHIDFRA
					1	FSGVMVAGSRQIFANEISSGAS
						NVGVVIFSTQDSANTFNVLNAS
				•		GGSRSVYPVMSDDMNGSSWKF
		1	İ		İ	STRMQKIDPALSVTSGQLMSHV
28614	58982	Α	28789	190	2058	
28615	58983	Α	28790	199	293	RYPPAETELS*RLCRLLR*STTV
		4				RL*LCRPL
28616	58984	Α	28791	685	1557	
28617	58985	Α	28792	1	2850	
28618	58986	Α	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR
1				I		TATTQRHCRRMHMMTIGYQFQ
				l		PGALVR*SRANHFPGRGDVNLS
						SRYSNAPGRRHQHQMRRGFVA
28619	58987	A	28794	409	1305	RSQ
20019	38987	ΙΛ.	28/94	409	1303	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop eodon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		L		L		
28620	58988	A	28795	379	1703	LKTVLVDGVVKAEKLVEGAKA
		ł				VLRQAINGDLDWKAKRQPKLE
						PLKLSKIEATMSFTIAKGMVAQ
				0.0		TAGKHYPAPITAVKTIEAAARF
						GREEALNLENKSFVPLAHTNEA
						RALVGIFLNDQYVKGKAKKLT
		1				KDVETPKQAAVLGAGIMGGGI AYQSAWKGVPVVMKDINDKSL
		1				TLGMTEAAKLLNKOLERGKID
	1	l		1		GLKLAGVISTIHPTLDYAGFDR
		1		1		VDIVVEAVVENPKVKKYPSAG
		ı		1		VFHQLYCRDVVIPMFAIYTFGP
		1			1	OIVGLLGLGVGKNAALGNVVIS
		1			1	LFFMLGCIPPMLWLNTAGRRPL
		i				LIGSFAMMTLALALLGLIPDMG
		1				IWLVVMAFAVYAFFSGGPGNG
		ı			i	FNRVKEEFDHERFLVALTNYGT
		1				AMCAFEDAARYAN/LARAVWR
						GYWSFPVDSGKIRPHGDQIKLH
		l				EKHAV*SSVESRORHHHLWRC
						SDVQILLRQCGI
28621	58989	Α	28796	713	902	CRLARPSPLKRCFQFCSTTHSCI
		l			}	PPPLAATRWPVRRRWRPSMCC
						WSRTYR\PG*AKRRYTSPA
28622	58990	В	28797	1	1521	
28623	58991	Α	28798	348	599	RHFQRSLSRSSDSNP*LDPTLFA
		1			l	SALASRQRVTESWSERHPDPLQ
			1			VRRKTEDVKTTPPFLQQSAHRS
28624	58992	Α	28799	582	732	VNIVLWIRGFSPTLLV
28625	58992	A	28800	382	1443	
28626	58994	A	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA
20020	30,,,	ļ'`	20001	1.001	1175	SGG*TGETDAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	Α	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP
		1				GLAITPGQQLFITIKLWNDDH\K
						RPREALLDSLKKLQLDYIDLYL
						MHWPVPAIDHYVEAWKGMIEL
						QKEGLIKSIGVCNFQIHHLQRLI
					İ	DETGVTPVINQIELHPLMQQRQ
						LHAWNATHKIQTESWSPLAQG
		ł				GKGVFDQKVIRDLADKYGKTP
	1	ı				AQIVIRWHLDSGLVVIPKSVTPS
	1		l		1	RIAENFDVWDFRLDKDELGEIA
	<u> </u>	L.	L			KLDQGKRLGPDPDQFGG
28629	58997	A	28804	1040	1079	O A GEWY COMPANY DE L'ACT
28630	58998	Α	28805	300	567	SAGFKKSGTRHCDVRPGACGT
	1				l	TLYQRR*VH*\WSTVH\KPETSS
			l	1		SKMHGQRGSGLLAKSLVANVI
			l	1		CSLIRNPLPIMPMPLCAFVSLKM
	1	1		1	l	IKKRPRRH

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28631	58999	A	28806	167	327	KNNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTDRRTN SPAYLSEL
28632	59000	Α	28807	1	1197	
28633	59001	Α	28808	1	4104	
28634	59002	Α	28809	1	1368	
28635	59003	Α	28810	82	1143	
28636	59004	Α	28811	72	212	
28637	59005	Α	28812	1	1078	MKDVTLVRPQDAGANTCAHIL SQLPHLQLPTLETLGLINALGY APGDMQPSDSATWGVAELQHE GGDTFMGHQEILGTRPLPPLRM
						PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQAVAIGDNL EADLGOVYNITANLSVISFDDAI
						EADLGQVYNITANLSVISEDDAI KIGRIVREQVQVGRVITEGGLLT DSQRILDAAESKEGREIGINAPR
						SGAYDNGFQVVHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ
						RVFAIFAVAIDITQVINIQYCRC QQAACGRRKDQCRNQSKENQY
						GNITQTDITIRTIAHGV\VIAAMI DNPPRIRKPTKSAS*LWWPLFY LLAVSLFTLWNRYRVFHGLSAS
						SSPLRPTPY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVDHNG YSGNACTRLHHAGGIRQ**PNF
						GYSPPASSCGQVSQNSS
28639	59007	В	28814	I	2703	
28640	59008	А	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWTITTAVCV SSCRRWKKPAALVRPLPPASAP GFITTSAKPCCASRNG*KSSFOR TLHVSRHQSRTS*SPQVDTSDN SSEIVNNQAPTARTGSGLRVAV LEQRVQEPLAANAPPQLRVSAI
		_	20214	100	200	NAAS
28641 28642	59009 59010	В	28816 28817	430	823 2667	
28642	59010	A B	28817	204	2667	
28643	59011	A A	28818	204	2659	
28644	59012	A A	28820	1	1089	
28646	59013	A	28821	1	1891	
28647	59015	A	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRDALPTEE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPYYELPERRDPV SSAGALFVSRWIVERSCADKFR
		L				VFCGASGFR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28648	59016	Α	28823	li .	1030	MMCIMYRTASSLANQYHIDSE
				[		QARRGSQNAFDVNFEAWQLEI
	i					NHVLEAASAQSQRNYQISALVF
		1				ISMIIVAAIYISSALWWTRKMIV
	ĺ	1				QPLAIIGSHFDSIAAGNLARPIA
ł		1				VYGRNEITAIFASLKTMQQALR
		ı	l			GTVSDVRKGSQEMHIGIAEIVA
	l	1		1		GNNDLSSRTEQQAASLAQTAA
	1	1				SMEOLTATVGONADNAROALG
				1		TGKNAATTAQAAAVQFIDRCQ
				1		ADFTRGAYRYRSGTYFICOYLT
						VTVSGIDAHORGOTDTORILLO
	İ					LFLVOFDTHROTLNDFDPVTGR
						ILRWKQLDRAAGDITGHRTDN
						TSTLQRQPGVTYFGGSLLHGW
ŀ						*SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	SSSEVI MIA EAETO
28650	59018	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLALWLKKHRFRLDQVQN
	1	İ		i		FYPSPLANSTTMYYTGKNPLAK
				1		IGYKSEDVFVPKGDKQRRLHK
		1		1		ALLRYHDPANWPLIRQALEAM
						GKKHLIGSRRDCLVPAPTIEEM
		1				REARRONRNTRPALTKHTPMA
						TOROTPATAKKASSTOSRPVNA
						GAKKRPKAAELQCPLVMTSGN
						LSGKPPAISNEQALADLOGIAD
İ						GFLIHNRDIVORMDDSVVRESG
						EMLRRSRGFLPTGRGLRIDYKQ
				İ		KMRGTRRAGCNFNQSGQGRPS
				1		LKRGIEQTDIKKAKKQATGLAG
					1	ESMLQDDAFYAVITHAAGPQG
					1	ALPLTPQMLMESPS\ATCSA*RR
				1	1	TPGWAGTPTSSPAKRC*LSALRI
1						TSSGSTPSCSRRHWRKRARRSD
						ACHHSRFSPTVWPVTQPKKGR
28652	59020	А	28827	1	1392	
28653	59021	A	28828	1050	1154	
28654	59022	A_	28829	]	2649	
28655	59023	A	28830	59	511	
28656	59024	Α	28831	1	2421	
28657	59025	A	28832	4594	4770	PSTSTIHAYVSGKSRISPHTREA
						MINDHSKRAWLYALRRAGR
	L	1	L			TRHRCPGRTGRQRLL
28658	59026	A	28833	1	727	
28659	59027	Α	28834	1	3069	D THE STORY OF THE STORY
28660	59028	Α	28835	1521	1841	FLPKSLGDSSGESRKHRRRRA
		1		1	1	FSPDQHPAGNYRTRLSARPFV*
		1				RCLYYSR*ARRGNYRQH*TTSP
	1			1		ALYQAASPFQ*SIAG*RAGKTR
		L.,	L		L	YRSSVYLCVDHFDHSGSW

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
28661	59029	Α	28836	1	1644	
28662	59030	Α	28837	1	1245	
28663	59031	Α	28838	1	1518	
28664	59032	Α	28839	3	491	
28665	59033	Α	28840	1092	2827	
28666	59034	Α	28841	162	1760	
28667	59035	В	28842	I	3378	
28668	59036	Α	28843	434	763	
28669	59037	A	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLENLPAADADQLAGY GGCHS\QVRSIWMIGLHAFAK ETRMYPEEPVYLPPRYRGSIVI SIAF
28671	59039	A	28846	855	1134	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAKF ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCVACNLCAVAWI VGCISLVS
28672	59040	Α	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARFINAQQ EDALVEKAKQ/VTWRLLAAGY CLLTVSSVARADSLDEGRSRY AQUKQAWDNRQMDV/VFIHAN PINTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCI ELSRRLRLHAQYQNTKRVHT QPSGYKTPEMANTAVPTISSQR RALFNPH
28674	59042	Α	28849	1	1247	
28675	59043	А	28850	533	1029	SKSINLLCRSVYSMIRRSTVAA FTLAAISVARSVALNLIIRDIGM QAMPLCRSTTGRNRWTSSAKR TILR*RQRILPLTPC*HRMFRSFI KKILSDOKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIQPAC KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	A	28851	749		SPHMPGITAGTPFSVPLAISAPS SAKSLPGKTA*AWPNIMALTPC ISLR**TEFSAITLYGSADSPECA RTT/INIGTFLAHFRHVFAHGFG NIIHRHFPG
28677	59045	А	28852	260		RQLETELSAGIAAFRTGNAPAII RFMKLAPPP*WRRKPLTGV*R\ *RGRDSVR*VAFVPTVSAIQQL DPRSLLQQDAFKKAGLDPEQPI KT/WQDLA/VLCRETESLRHEV RLRQRLAGLDPTGKL*AWNGM MPYDADAKDAPQKPLSAEPAC
28678	59046	Α	28853	776	2730	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codun for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		1	l	-		
28679	59047	A	28854	383	1367	RPTCWTSIEWVRRVRTAALRSS
						GKTWVFCCRRRIAGELMLTNR
		1				HTGGVMVTTFRASEAFAGALE
		1	l			LTGKATLVALINRCIGAVIRYM
		1	l			LIAVIPDIFORLOVVLNVWILAV
		l				ANETTVRORRVRRFKVDLVVR
		ı	ľ			VHLLLHIEVETVGVVTFIGHAR
		l				
		l	İ			HHAKLSSIETAEAIAQVFTRRA
	1			1		VETETITRFFFPLIHCLTQTFNN
		l		İ	ļ	GDTFRAKLLVVVNMLAAEQRV
						NGFVDADVTQRNRRTTVFEDF
		1	1			RNIIVSIETHATSTRYG*CVGPP
				l		AMRACSGAVQPVQWLHPGKL
		l				RQGEPSRDLVRQRPAALCLPRR
	1					HRILRGYNGNIQRRLYSTGNGL
28680	59048	Α	28855	I	1477	
28681	59049	Α	28856	I	793	
28682	59050	Α	28857	ı	1020	
28683	59051	Α	28858	i i	613	SAGDGARIEOFDRKGMVNNKF
						NYFIMSKLAEAGIPTOMERLL\S
	l					DTECLVKKLDMVPVECVVRNR
			1			AAGSLVKRLGIEEGI\ELNPPLF
						DLFLKNDAMHDPMVNE\SYCE
	1					TFGWVSKENLARMKELTYKAN
						DVLKKLFDDAGLILVDFKLEFG
		1	l			
						PVQGEVVLGDEF/SPDGSRLWA
		ĺ				QETLEKMDKDGFRQSL\GGLIG
		_				AYEAVARRLGYT
28684	59052	Α	28859	1	1002	
28685	59053	Α	28860	I	422	
28686	59054	Α	28861	625	750	RNVQALQGAHGTGGALTDPA*
						QHLGTLCADLL*NGLSPSPRD
28687	59055	A	28862	I	1449	
28688	59056	A	28863	105	297	
28689	59057	A	28864	55	423	DRPQRNRATLMQLYSRGSPGIR
						RLEHRFEKVQGKPGFEVFIPGF
			l	1		KQGKLGRPLGVKALVFGIDTGL
				[		FQLQAVKNLDGF*FDEASASQP
		l		l		GSDNILRELRVRATGRADGSGT
				1		GFTEDANSFTSYR
28690	59058	A	28865	1	2340	
28691	59059	A	28866	314	696	
230/1	27027	٠,	2000	12.4.	~~~	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28692	59060	A	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK CHGINPLRSWVGTG*VE*EEKY MMQT*PLE-EWWKPISNLHIDMSS SHSKTLGYKRLTKSNPISCQILL YKSRSKGRKNQRSTR*THCHHIB* PKIYSASAKEPWILATNLPVEIR TPKQLVNIYSKRMQIEETFROL KSPAYGLGLRHSRTSSSERFDI MLIJALMLQLTCWLAGVHAQK QGWDKHPQANTVRNRVLST MLIJALMLQLTCWLAGVHAQK QGWDKHPQANTVRNRVLST AATILTQNLFTHEEAPANSVPA AAVIRRVQALIGITGRKAHAGG SWMGTASSDNPPNIFILPQNDF MALAAAVAPPELEALLAAGKY SVKLOEPCDELISRAKVWKOE KWACVTIVGGHTNIVHIETHDG VVFTQQACVAEGEQESPLTVLS RTTLAELIKEVNEVPFAAIRFIL DSAKLNCALSQEGLSGKWGLH IGATLEKQCERGLLAKDLSSSIV IRTSAASDARPMSNSSIPSARSHILLSSSIV IRTSAASDARPMSNSSIPSARSHILLSSSIV IRTSAASDARPMSNSSIPSARSHILLSSSIV IRTSAASDARPMSNSSIPSARSHILLSSSIV IRTSAASDARPMSNSSIPSARSHILLSSSIV IRTSAASDARMGARTLAMSNS GSGNQGIGTELNYSCRPATINL
						FPVWRVAQIICAVRPFRQRIGQ LRDIFHLKGDQFTNRPAKIVAF
28693	59061	A	28868	2095	2722	LEDIFHLEGDOFINEPARIVAF
28694	59062	A	28869	789	2509	
28695	59063	A	28870	57	440	CSWDPODPHGILOGAGKEDSO
28093	39063	A	28870	37	440	AQKTTARQKRKTRKTATRQKK HEKQSEESTNEDT*ARKVEETQ HKHDAESTSGSVIQGCVQLFTQ SFTATPAASATTATRPTILCSSR ARAGYPSTTGVSRRESPL
28696	59064	А	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK KGHFVVAHPAF/P/DQFLHAAM DIKQPVISIDNLLAIHKQAEVTR FIGGDMQRADRDHPRIAVALID KRIRFGISRRFRAQSIIHRIFAQR MHIFRPVIGQHQATGNSRLSAS TQRLHHNPAFFGPFH
28697	59065	А	28872	1609	2112	HÖPVLTVVMVPVSPLIIRADNP FRDEVGFLCOPAVTVIPVKIVR VTGDTVIRPHAEGAVRVQLRV GQAVTCRVCGIRDADIQIRCGG VNAGOPAGGAVAVTFGLARAA DADEFAVVVPGVIAVRQQAVQ VLAL*LPGRGISGGEFITAEVRS VSRCRRSRVYSTRGIL
28698	59066	Α	28873	2	712	
28699	59067	Α	28874	337	383	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28700	59068	A	28875	65	436	REVWEHAKRMLGDSSLDMGM DDELTYMVAYEYIGRLGKTATI HWKVKSSPSMVWSASVWKKM ALR*LSRTLRPNQEHSLS*ASVP ELKCAASWTKRKKNSTFIASSA IRLTLTWKPKPFLSRL
28701	59069	Α	28876	206	403	
28702	59070	В	28877	1	2046	
28703	59071	Α	28878	I	1335	
28704	59072	A	28879	I	974	MEA.PPIEDVSSRDLNRRRNYGH PADLFWFYSVLRALPEVYASVLRALPEVYASVLRALPEVYASVLRALPEVYASVLRALPEVYASVLRALPEVYASVLRALPEVYASVLRALPEVYASVLRALPEVALLERGKRAMRFFFFSYTLALLLGTCGMYGLAQWALVSGGAG KVAILSYTMPFWVVIFAALFLG ERLRRGQYFAILJAAFGLFLVLQ PWQLDFSSMKSAMLALLSGVS WGASAIVAKRLYARHPRVDLLN SLTSWOMHVCROLASQLPLSH GAMPRCRRPGHSSNPDRLANVJARRVLRGMSNRQPVSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDLNTQ LWISTNAFRFGN
28706	59074	Α	28881	568	717	
28707	59075	Α	28882	1760	3092	
28708	59076	A	28883	1	1206	
28709	59077	Α	28884	1	575	MSGSYSSYMAEDDIQFDSRFLE LKCDTKLDLKRFSSQCYVEPGK YNLQVQLNKQPLAEEVDIYWY AGEDDVSKSYACLTPELVAQF GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPPSRWDDGIS GIIADYSITACTQHAKLNTEDD/ SNESTGSVWQGLWRLQDD
28710	59078	Α	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YAWRAUPSLKAKLALGEDY LNSDIFDGENIYVGGSVSTDDO MLPPNLRGYAPDISGVAHTTAK VTVSOMGRUYETQVPAGPERI QDLGDSVSGTLHIRIEEQNGQV QEYDISTASMPYLTREPGQVRVK IMMGRPQEWGHHVEGGFFSGA EASWGJANGWSLYGGALGDEN YQSAALGYGRDLSTFEA

SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
59080	Α	28887	491	681	PTGHRAQKKWNT*TRHSNSY*
					KNFAKKLI*GDIREKLOKLEGF
					AGMNATOLIEVATEVŶINCDOE
	l				AKKETEQRLRKKANLLAAALT
	1				KRKINIVKGRECSHGCGHGRGQ
	ı				VEQRAKRWLRLRGGWVKAFP
	l				VRTEKAREVTKVLLRDIIPGFGL
	l				PLTLASDNGPAFIAKIVQELTQL
	1				LKIKWKLHIAYWPQSSEKVEH
	1				MNQTLKQLLKKFCQETHLRWD
	1				QVLPMVLLRVRYTPTKQTGYS
	L .				PMRSCSANLK
59081	Ā	28888	1	963	
59082	Α	28889	123	593	KRQVLAGFLITPRRLPKNWTHC
					WCWWSM/PAQVKQVLFGETG
					VAQHLKPGTAVMVSSTIASAD
					AQEIATALAGFDLEMLDAPVSG
					GAVKAANGEMTVMASGSDIAF
					ERLAPVLEAVAGKVYRIGAEPG
	1				QVRP*KLFTSC*RAYILLPEPKR
	ļ.			-	WHLQPVR
59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPLYT
					GLPRGPHGRAAGNPVDQQFAA GDLGLSPHADAHPGGTDDVRW
	İ				CLIST*KRWDSGV*AGAGOYSG
					WRRRSLRWR
50005	B	20002	1	2110	WKKKSLKWK
	_		·		
	-				
59090		28897	ti	1188	
	c	28898	20	878	
59092	Ā	28899	1904	2281	CSAYAGLHPFWLKSTRFCTHIL
	[				APATAISPNTTIDAPPITAAGMV
	1		1	I	*ISAPNFGEKPNSMAMTAAATN
			l	1	TSVE*TLVTAITPIFSA*VVTPLP
			1		PTEPESIVARPSPTNARPIYGSIL
					RPVIPATALR
	59080  59081  59081  59082  59083  59084  59086  59086  59087  59088  59089  59090  59090	59080   A	of peptide requence         had in USSN 90/540,217           59080         A         28887           59081         A         28888           59082         A         28889           59083         A         28889           59084         A         28891           59085         B         28892           59086         A         28893           59087         A         28894           59089         A         28896           59089         A         28896           59090         C         28898           59091         C         28898           59091         C         28898	of peptide sequence         bod in INSN 90%46,217 colon for peptide sequence         location of first colon for peptide sequence           59080         A         28887         491           59081         A         28887         491           59082         A         28888         1           59083         A         28889         123           59084         A         28891         1218           59085         B         28891         1218           59086         A         28893         1084           59087         A         28894         2029           59089         A         28896         1           59089         A         28896         1           59091         C         28898         20	of peptide bequence         In USSN         location of first equence         codon for last amino acid peptide sequence           59080         A         28887         491         681           59081         A         28888         1         963           59082         A         28889         123         593           59084         A         28890         263         467           59085         B         28891         1218         1505           59086         A         28891         1218         1505           59087         A         28893         1084         8334           59088         A         28894         2029         3313           59088         A         28896         1         284           59089         A         28896         1         284           59001         C         28898         20         878

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV
26723	39093	^	28900	l''3	0220	RLCWNLISLGLWSCFSKGWVT
1		1				TPTTLSCPSPPRRGRMAPWAW
		1	1			GRSRARMCWSWSWSTRPSRPC
		l				AVRWSWSSGATGSCWRRPVST
		l				1
	1					APPRPPPWRPAAPTPAPLWART
		ŀ				RMPSHWPSTTAPAATAY*/DPD
		Ì				AGYQPTPLAAPAEPGSKYSLAS
		1				LDRGQGRGGGGGALEYVPKA
		1				VSQPRRHSRPVPSGKYVVDNSR
						PPTDLEYDPLSNYSARHLSRAS
1			i			SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSKPSCLMWAASCRN
		l				PASLLASE*TVSNA*IPAERAAC
į.		1				KMEQRANSSSVPSGERSVRRLR
1		1			l	T*SSAPRAIPIKRSEA*AISTARVI
		1				PSGDSIAASRPVLPGSRPQAFSIR
		l				RISFSISRTS
28727	59095	A	28902	1	2916	140101010
28728	59096	A	28903	1	2001	
28729	59097	Α	28904	179	324	
28730	59098	A	28905	1591	1806	
28731	59099	Α	28906	531	949	
28732	59100	Α	28907	44	477	
28733	59101	Α	28908	161	333	
28734	59102	Α	28909	1	394	MEGVAFLTFLAARAAVGNRPA
	ŀ					SPQIVRKQREGHGGILTRDPVA
						FDDVAVNFTQEEWALLDISQR
						KLYKEVMLETFKNLTSVGKSW
1						KDQNIEYEYQNPRRNFRSLIEK
	İ					KVNEIKDDSHCGETFTQVPDDR
	1	1				LNFOEKKASPEVKSCDSFVCAE
i		l				VGIGNSSFNMSIRGDTGHKAYE
1		l				YQEYGPKPYKCQQPKNKKAFR
	ŀ	l				YRPSIRTOERDHTGEKPYACKV
		1				CGKTFIFHSSIRRHMNSHWEKP
	i					YECSKCDKAFHSSSSYH
28735	59103	В	28910	1	534	T DOCTOR TO THE TOTAL THE TOTAL TO N*Q
						RRRNTSQR*LRHQPFFSSASRPG
						SRLRFAIGPLQPAEAGMVT
28737	59105	Α	28912	358	878	KLCHIACIHSVSFQCESFHVFTG
20,3/	157105	l^	23712		J***	FLSSVCPFMKSKIFDRSEGFPKL
						LTLIGVLSSVSPFMISKGSEGNK
		1				GFPTLLTLIGFLSSVRFFMYLK*
		1				LGRIKAPPTYLTFIRSLYRVHYV
1		1			1	
		I				CLCPFMNSKVLGRSEGFPTFLT
		1	1		1	CIGLLSIVCRFPTLLTLIGFLSSV
20005	50106	<u> </u>	20012	1000	1416	SPYMISKGTGMR
28738	59106	Α	28913	1382	1416	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
ŀ	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28739	59107	A	28914	li .	333	MFODPVAFDDVAVNFTOEEWA
		1				LLDISORKLYKEVMLETFRNLT
		ı				SVGKSWKDONIEYEYONPRRN
1		l				FRSLIEKKVNEIKDDSHCGETFT
		1				OVPDDRLNFOEKKASPEIKSCD
		l				SFVCGEVGLGNSSFNMNIRGDI
						GHKAYEYOEYGPKPCKCOOPK
		1				KAFRYHPSFRTPQRDHTGEKPY
		ı				ACKECGKTFISHSSIORHVVMH
ŀ		1				SGDGPYKCKFCGKAFHCLSLYL
,						IHERIHTGEKPYECKOCGKSFSY
l		1				SATLRIHERTHTGEKPYECOOC
		l				GKAFHSPRCYRRHERIHTGEKA
		l				YQCKECGKAFTCPQYVRIHERT
		l				HSRKKPYECTQCGKAL*YSLKS
						GSLMP*ALFFWLRIVLAMWAL
		1				LWFHMNFKVVFSNSVKKVIGS
		1				LMGMAWNLQITLGSMAIFMILI
						LPIHEHGMFFHLFVSSLISLSSGL
28740	59108	Α	28915	1619	2353	
28741	59109	A	28916	1	1252	MSYSVMFALLLLTPLLFSLLCF
						ACRKRRLSATRTVTVLHSLGIT
		1		į		LLLILALWVVOTAADAGEIFAA
		1				GLWLHIDGLGGLFLAILGVIGFL
l						TGIYSIGYMRHEVAHGELSPVT
		1				LCDYYGFFHLFLFTMLLVVTSN
						NLIVMWAAIEATTLSSAFLVGI
						YGORSSLEAAWKYIIICTVGVA
						FGLFGTVLVYANAASVCGTDH
				l		GGRMMRSWNGGQLISKLLAIT
				l		P\DKLVLDFGSQAEDNIAVLKA
		1				QHISIS\AETQGAKVEFTVDQLQ
		l				QSEYLQLPAFITVPPPTLWFVQR
		[				RRYFRISAPLHPPYFCQTKLAD
				l		NSTLRFRLYDLSLGGMGALLET
		1		l		AKPAELQEGMRFAQIEVNMGQ
		1		I		WGVFHFDAQLISISERKVIDGK
				1		NETIPTPRLSFRFLNVSPTVERO
		1		I		LORIIFSLEREAREKADKVRD
28742	59110	Α	28917	2	2282	
28743	59111	Α	28918	518	1046	
28744	59112	Α	28919	8	893	-
28745	59113	В	28920	1	3129	
28746	59114	Α	28921	1	1284	
20770	127117	<u></u>	29721	<u>.                                    </u>		

SEQ ID NO:	of peptide		SEQ ID NO: in USSN	location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	delction, \=possible nucleotide insertion)
28747	59115	Α	28922	3612	5412	PGLKHQNNGHRGPDAETKGVT
		ļ				RDFGPNAKPLAG/VRLN/LERLR
				1		DTHHIDVAPLVARLDQMMESV
						SQLLQLARAGQSFSSGNYQHV
						KLLEDVILPSYDELSTMLDQRQ
						QTLLLPESAADITVQGDATLLR
	1					MLLRNLVENAHRYSPQGSNIMI
						KLQEDDGAVMAVEDEGPGIDE
						SKCGELSKAFVRMDSRYGGIGL
						GLSIVSRITQLHHGQFFLQNRQE
						TSGTRAWVRLKKDQGAYPMSE
						KVVFSQLSRKFIDENDATPAEA
						QQVVYYSLAIGHHLGVIDCLEA
						ALTCPWDEYLAWIATLEAGSE
						ARRKMEGVPKYGEIVIDINHVP
		}				MLANAFDKARAAQTSQQQEW
İ						STMLLSMLHDIHQENAIYLMG
	1					VFIMLIFFPAPVASEKPLSPDCW
	İ					TTTHTLRMIGENSGLVSYMREK
İ						AVSPNCWNVIHYSGFLHLELLS
					i	SYDVDVNQIINTICEWISLIKTR
					i	GVRRPEFQTLLTGSGSEHGERFI
			}			MNRPTLFFTDLAFHVDRFTQYV
		l				HDTAQSRFTYRDFNRVFEVFYI
						QTATQTVGGTHCDAPGWWFP
		l	Í			GAVQSVPAAALIAVAAAPGLA
						SFLPFARRVPRTVVALLAQAAA
						YADGMPARADGSFNSP
28748	59116	Α	28923	1	2910	
28749	59117	Α	28924	470	723	PGFGDARKLISLNFFIWV*TA*I
					ŀ	M*P/LAGSDFVYRNS*RNVFIAQ
	1					TLQLRSRQPVTMHHATRAFQT
		_				EHNLILRFECCEYSRYLFT
28750	59118	Α	28925	599	1117	av av a a a a a a a a a a a a a a a a a
28751	59119	Α	28926	279	455	SLSHSSGRCSRGGISFWVVWEF
		l				GPVACLAASVV*L*VSVVWLW
20000	50.120		20027		2012	LSPSGQGCLGCRVWL
28752 28753	59120 59121	A	28927 28928	I	2913 2328	
28754	59121	B	28929	55	327	
28755	59123	A	28930	9	107	
28756	59124	A	28931	1	2106	
28757	59125	A	28932	1	1123	
28758	59126	A	28933	260	709	
28759	59127	Α	28934	467	631	LEVIEAPQPNWS*SVQQSACST
1					1	WPGCWVDLEDPQVWVWYEW
1						TTKRASLLPIFQD*LKALRKAQ
1				1		VWAFAS*STWPGCWVDLEDPQ
						VWVWYEWTTKRASLLPIFQD
28760	59128	A	28935	989	3010	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	Α	28937	1	1006	
28763	59131	A	28938	185	384	
28764	59132	Α	28939	2	615	WAFRVIRFIVTANWSLAAVWM RRILIVVAALLT.RTYPMRQLNR LLLITPSLSRIMVSTGPATSCVN RGFLSPTVYSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGEE QISLGWRNTSPDVPYLIQSWVM TPDNIKKSADHITPPVFVLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRAVPSTTKRKEGNTLKIAHK RMITN
28765	59133	A_	28940	1	1686	
28766	59134	Α	28941	76	981	
28767	59135	Α	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPAHRQWSASYWRSA *SSSFRLNKKCHTQNHSNCIKM ARE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28 769	59137	A	28944		2539	MPIEEPALRSWORPFLKWAGG KYSLLPELDKLIPAGKRLIEPFV GGGSVFLNSDKHERFLLADVSA DLINLYQMLAVVPDSVIYEAM KAFRHLNDAENYTLIREAFNAG KLDAVERAAAFLYLNRICENG LIRYNLDVFENVGFGGKHKQMT NNESKGPFEGLLVIDMTHYLNG PROTOLLCNMGARVIKVEPPCH GDDTRTFGFYYDGGSLYYSFIN HOKESVULDLKNDHDKSFGHT GPLKDAPAYDTIIQAMSGIMME TGYPDAPPVRVGTSLADLCGG VYLFSGIVSALVGREKSQRGAH VDIAMFDATLSFLEHGLMAYIA TGKSPORLGINRHPYMAPFDVF NTQDKPITCCGNDKLFSALCQ ALELTELVNDPRESSNILRVQN QAILKQYIERTLKTQAAEVWFT PFSNKYNGHRIAETDKASMPTY FSSKYNGHRIAETDKASMPTY FSSKYNGHRIAETDKASMPTY TSSLFFGFTTASKLPGFSFIRSPK MTGSVLLPGPFTRRQAQAFTT TYSNTLEDDQGSHFRLVKDG EGRMASVQTRPADREAFTIHGL LPEHTLYPHPAAAGAFTIHGL PHYPDEGRIBOFWOYFGAIPOW
						LLLEPHIFAWMDRFCEGYSGGI WSFYTLSNGGAFMSPEPDNDET WRLFNCLNATMPPYRMTCGTV
28770	59138	A	28945	907	1917	
28771	59139	Α	28946	1	3033	MVWGFTCSTTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQTDHLTGMMTSTLFSSPSV HNVMETVTQETAPPDEMTTSFP SSVTNTLMMTSKTITMTTSTDS SSVTNTLMMTSKTITMTTSTDS SITAGQEGQSRTTSWRTSIQDTS ASSQNHWTRSTQTTESGTSTL THRTTSTPSFSPSVHNVTGTVSQ KTSPSGETATSSLCSVTNTSMM TSEKITVTTSTGSTLGNPGETSS VPVTGSLMP
28772	59140		28947	636	725	
28773	59141	Α	28948	1	1123	
28774	59142	Α	28949	2345	3644	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Anino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28775	59143	Α	28950	34	437	CGRLLQKSGFVVSVGIDGIERL NTRRARGLPNGTACGQQFSSFR GAFCTQVAHIVFCTEGDTDQ/D ARKRERFPLRG*SPAEIQSPPAG RCCRVHDHRLFRYAGSFFQYPE HPERYRFSADAQRPHHRERRLP
28776	59144	Α	28951	1	457	
28777	59145	Α	28952	176	757	KPMKSTAAAADAALLSAERQ VIDDAAAHLSEVAQGDVDAI EQAIKNVDKQTQDFAARRMDQ SVRRADRSDLIETFDHVCTVIFI ROGITSAEVETADTARGNVDVI RTGEVGAVCGTEETKSILQYLQ YAITKDIFATLCVLLQDGKNNV LLTHTSQVFQPHIFAESDQLRN RRIFGDRFDSPVSIRMMFGI
28778	59146	Α	28953	1	1503	
28779	59147	Α	28954	425	619	AGWSFLPSPAEQNRWRFPLSRF CQIPAPLQVRS*LACRFFAAYSP PLLRKSPAASMAYTTSRLH
28780	59148	A	28955	55	476	SYHALANVFYQRRMAITQVAG RQAQVFKAHLRDDVHHHIDG VTATESVMEGNRHAVL*TRAT NRFFQVGAQFAIARFFSLVGLL WRVLESGKIAFSATIPGRYPFLS LRLFNFLRHFGLILRGCRKVL HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	В	28957	12	271	
28783	59151	A	28958	309	1238	GSGCYSALVKRKWSARSLRA DRNGARRGAYVGRFGFFGFG LAGFFSAHASNLCRSDSRAPAH YHQLLNFADPVDMMQ*KRGM VFLLLMDQRQQRVDDWRRLPS WSFQGATVFQALAEDLRRNLQI VVATVAFGMGINKPNVRFVVH FD/IPRNIESYYQETGRAGNDGL PAEAMLFYDPADMA/WLRRCL EEKPQGQLQD/IERHKLNAMGA FAEAQT/KCRI.VLLNYFGGGRQ EP/CGNCDICLDPFKQYDG/STD AQIALSTIGRVNQR/FGMGYVV EVIRVAAFLEPDYSHRP
28784	59152	В	28959	I	2123	
28785	59153	A	28960	1	2834	
28786	59154	Α	28961	1	2505	
28787	59155	В	28962	145	494	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *-Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
28788	59156	A	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHA F*PLLGDFGCRNGVIQGRENAH LMNGGGRRVTALHFQQYRFHH LFNILTARHHLIDNANHAQIDR* RFAFMRLAGGTATHQ
28789	59157	Α	28964	1	1423	
28790	59158	A	28965	1	863	
28791	59159	Α	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	Α	28968	1	1215	
28794	59162	A	28969	1	1678	
28795	59163	A	28970	1	4674	
28796	59164	Α	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFGHQLIAGDHFF HHFQAHLVGFGDFFOLFNLG EGQLVVSIFTPVRLAVHGVKIE TVFVGFSSLIHGSGTVLVSSASG ASVASTRGKCTIVTSGISG/VIA KND/GLFRVHGATAPSCASQFL VFAAPTPRPDRHG*RTDDSTPQ RLSSPAVEKAPTASSASGNSRN DKFLREHTLITSDRYPPDAAVSP TGFWPLTIPFHRCRRMSSLPGIPI RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSGRRAPGGR*FHW RFHGHGFPGAGGGSPAKPVNR RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	
28800	59168	A	28975	904	1473	
28801	59169	Α	28976	738	893	
28802	59170	A	28977	I	1108	MADTRYFGMHMSQETPASTTE AQIKNERRISPFWLLPFIALMIA SWLIWDSYQDRGNTVTIDFMS ADGIVPGRTPVRYQGYEGTV QDISLSDDLRKIEVKVSIKSDMK DALRETGFWLVTPKASLAGV SGLDALVGGNYIGMMFGKGKE QDHFVALDTQPKYRLDNGDLM HILQAPDLGSLNSGSLVYFRKIP VGKVYDYAINPNKQGVIIDVLI ERFFTDLVKKGSFFWNYSGVD ANVSISGAKVKLESLAA
28803	59171	A	28978	1	861	
28804	59172	Α	28979	5	337	
28805	59173	Α	28980	1	612	
28806	59174	Α	28981	128	1742	
28807	59175	Α	28982	1	2688	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28808	59176	Α	28983	361	738	FLQPFPFKREINKFIRDIANNMK
28808	33170	1	20703	501	756	TDFFSAVTLFTDCVTVMLWII*F
						FORKFFLKGFI*PPLGSFYRE*IIT
						SLFLYLLCNIFLATHRISCDDFSF
						NIQHVKKFWDSCNLIRFLIRLDL
						SDDQTVHC .
28809	59177	В	28984	l	1263	SDDQ1VIIC .
28810	59178	A	28985	363	569	KGYSRRSGKHRQGCCNVLRLR
20010	39178	^	20903	303	309	FPDHOTAPRPMPLKROTRAPGO
						SPPGLPADPHPGOF*LPLLRGRF
						AR
28811	59179	ļ.	28986	1	1035	AK
28811	591/9	Α	28986	275	721	LMVSGFLTSPKDHERIMSGEAR
28812	59180	A	28987	2/5	/21	
		1				AILIASNSSVLVCAFRNFNKSFT
	i			1		DLLPSELAQSASERISFNNTLKD
				1		SGMPGSI*WLPSTMFLYILVRPF
				1		TSSDLTVSISCRVYAAPYASSA
		i		1		HTSISPKR*PPNTQRLLTGPVGT
		_				FWGRKPPLFPTP
28813	59181	В	28988	1	2082	
28814	59182	Α	28989	1	1567	
28815	59183	A	28990	1	453	
28816	59184	Α	28991	1	777	
28817	59185	Α	28992	1	1431	
28818	59186	A	28993	1	561	VDSRGYPYGSRGAGKCRESERL
			i			GSESRNPGSIGLENELTAEDVAS
						ADMVILTKDIGIKFEERFAGKTI
						VRVNISDAEFLMTNRISRLKTA
						LFANTREISLERALLYTASHRQT
			İ			EGEPVILRRAKATAYILEHVEISI
						RDEELIAGNRTV/ITARRDYVA
			}			GNGPLLAAERAGSIPDASAGPL
						CYQRRRL
28819	59187	В	28994	I	3414	
28820	59188	Α	28995	1082	1297	MIMWLAAVAIREINHDSGSATF
					1	RTPRDPRTVAGKYNLGASLYK
	1					SELLA*LHSAGAGCLSCQRAKL
						GLGRRR
28821	59189	Α	28996	1	2115	
28822	59190	Α	28997	168	317	
28823	59191	Α	28998	133I	147 I	RWSNGTLENGTL*LLTLPSASL1
1						STNKSPLDDVE*RSLISKAPGDT
28824	59192	Α	28999	147	1456	
28825	59193	A	29000	1	439	
28825	159193	ĮΑ	29000	μ	439	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ĺ		sequence		
28826	59194	Α	29001	722	2805	TPRAERTASSVALPTSRLLRAR
						AETTTAPSTPMKTHRVISMVFF
		l				TCSOTGTPSASPVKSSLKVSSLN
		ļ				IIIASTTNRPS/VQQF/WPVSPPG
		ŀ				DGTRRYP\SISLTVLTGNDNVNL
		l				LRAGIDLAIYFDDAPSAOLTHH
		l				FLMDEEILPVCSPEYAQRHALT
		l		i		DTVINLCHCTLLHDROAWSND
		1				SGTDEWHSWAQHYAVNLPTSS
		ł		İ		GIGFDRSDLAVIAAMNHIGVAM
					1	GRKRLVQKRLASGVYPPRCAY
						PRTHLLETSTTSGVNGVGTYSA
		l				PFWRMLLNSFVMAFSITLGKIT
		l				VSMLSAFAIVWFRFPLRNLFFW
		1		i		MIFITLMLPVEVRIFPTVEVIAN
						LQMLDSYAGLTLPLMASATAT
		l				FLFRQFFMTLPDELVEAARIDG
		l			1	ASPMRFFCDIVFPLSKTNLAALF
		l		i		VITFIYGWNOYLWPLLIITDVDL
		l				GTTVAGIKGMIATGEGTTEWNS
		1			i	VMVAMLLTLIPPVVIVLVMOR
		1				AFVRGLVDNPAANYIHYGVRE
1		1				
1		1				SGMTAIANGIAHHGGFVPYTAT
						FLMFVEYARNAARMAALMKA
						RQIMVYTHDSIGLGEDGPTHQA
	İ					VEQLASLRLTPNFSTWRPCDQV
İ	1					EAAVGWKLAVERHNGPTALIL
					1	SRQNLAQVERTPDQVKEIARGG
		l				YVLKDSGGKPDIILIATGSEMEI
						TLQAAEKLAGEGRNVRVVSLP
		l				STDIFDAQDEEYRESVLPSNVA
		ᆫ				ARVAVEAGIADYWYKYVG
28827	59195	A	29002	2253 279	2546 629	NGAGHL*RPPVDGATAAPAGG
28828	59196	A	29003	279	629	
		l				RYAHLRVCPESLPWLHLPAWRI
					1	YRSGS*SAPCHCRNHRSGSAWQ
						KHYGNRFRFRTVRPYRGRALH
		1				LRGRNTAITQAADWRLATAQL
		_				LEIAGVGDE
28829	59197	Α	29004	313	638	RWRQRWFWCLHCLVLFRITPR
		l				TFALSQCRPWDDSRSQDTSMSH
		l		1		SIQWNRMYCNCSMQDEQEADE
		l		1		ANGKGPAQVGDRQAWAGR/CR
		l				SHRREGTIPGNPHPRAS*RAGW
						QR
28830	59198	Α	29005	I	1182	
<u> </u>		_			•	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28831	59199	Α	29006		535	RPYVLPWAGSNALGA/LGYVES ALEINAQ/CEGAVNISSVVVASG SAGTHAGLA/GLEHLMPESELI GVTVSRSVADOLPKVVNLQQA IAKELELTASAEILLWDDYFAP GYGVPNDEGMEAVKLLARLEG ILLDPYTGKAMAGLIDGISQK RFKDEGPILFIHTGGAPALFAYH PIV
28832	59200	Α	29007	1	1953	
28833	59201	Α	29008		656	MKLMAIQEQARGECCFRDSEW LQFHIQVALATONSALAAIVE KMWTQRSHNPYWKKLHEHIDS RTVDNWCDDHDQULKALIRKDP HAAKLAMWQHENTIKIMDP HAAKLAMWQHENTIKIMDP ETSDDFEFNADRVLFAENPVAI AKELELTASAEILUDPYFAPG YGVPNDEGMEAVKLLFRLEGIL LDPVYTGKAMRGLIDGISQKRF KDEGPILFIHTIGGAPALFAYHP HV
28834	59202	Α	29009	1172	1371	
28835	59203	Α	29010	338	528	RHPRCDPYGFCPFTADADDA** LGACHHYWRGQRKIYAGSGDS RCQPDGRRSAPARRPLRRQR
28836	59204	Α	29011	413	2798	
28837	59205	А	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P SSFKEGIDHSATFFFAARFALVA AAIFCVFADGFFAFLASFFAAFG FVFFSPRKALSGSKFTFLPT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
				sequence		
28846	59214	A	29021	878	1267	LNSWLPSVPTV*SSVFNAL*TG
20040	37214	l^	29021	070	1207	ISPAFNPFADM*SASGLP*IKSPL
						STSTLFFTSLRASLIRLAVRTSP
		1				FSVAVSL**SKSIMLLCRSVVSM
					*	IRRSTVAAFTLAAISVARSVAL
		1				RFLIKSTGNACK
28847	59215	A	29022	294	2305	REERSTONACK
28848	59216	Ä	29023	5	337	GAPOHOMMSTYRINGRESPML
200.0	0,210	Γ.	27025			TYPSTPNFFWLAWQARDFMSK
		1				KYG\RRFPIARFLWRSTPAPGVF
						KTIFIFISLVFVLMCANSWITIW
						RTSAAAGCHCQVVCAGMNTW
		ļ.				RVG
28849	59217	A	29024	1	1753	MPSTRYQKINAHHYRHIWVVG
		Γ.	-,	-		DIHGEYOLLOSRLHOLSFFPKID
		1				LLISVGDNIDRGPESLDVLRLLN
		ı				OPWFTSVKGNHEAMALEAFET
İ	ì	1				GDGNMWLASGVYRIPLAVIWII
		1		1		GSLTSKAYKAEVQORREAFNR
	İ	1				AKMDYDHLVRQIQQVGGLEGF
		1		1		IAKRTMLEKMKDEILGLPEEEK
		1		1		RALAALHDTARERQKQKFLEG
				1		FFIDVASIPGVGPARKAALRSFG
						IETAADVTRRGVKOVKGFGDH
	1	1				LTQAVIDWKASCERRFVFRPNE
1	1					AITPADRQAVMAKMTAKRHRL
		1				ESALTVGATELQRFRLHAPART
1	1	1				MPLMEPLOPTVŠVVDKVVEKK
1			ĺ			GTKEVAEAYLKYLYSPEGOEIA
1	1	1				AKNYYRPRDAEVAKKYENAFP
		1				KLKLFTIDEEFGGWTKAOKEHF
		1				ANGVIAVVAAGIGYWKLTGEE
1		ŀ				SDTLRKIVLEECLTNOOONONP
		ŀ				SPCAEVKPNAGYVVLKDLSGPL
		ŀ				PYLLMPTYRINGTESPLLTDPST
		ŀ				PNFFWLA WQARDFMSKKYG\R
	1	ŀ				RFPIARFLWRSTPAPGVRKTIFIF
	'	1	l			ISLVFVLMCANSWITIWRTSAA
			l			AGCHCQPTGIAQALLSTRQHGC
	1	ŀ				AQCPLLPLSPLLSSSSF
28850	59218	Α	29025	865	974	IMPRISGSQSGEHQQPLVATAR
		1	1			WFARA*ILIIPL
28851	59219	Α	29026	1936	2490	
28852	59220	Α	29027	1105	1518	
28853	59221	Α	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	Α	29030	3338	3553	
28856	59224	Α	29031	95	1289	
28857	59225	Α	29032	1	732	
28858	59226	A	29033	I	672	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amine acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTTRL
		1				AEGLLEAAEEAGIPLVVNHVGG
		1				MFGIFFTDAESVTCYQDVMAC
		1				D/GGTL*AFLPYDAGRRCLQHG
		١.				RYQ
28860	59228	A	29035	852	933	PAPYALLLLPMHPHGLRRRDR
		ı				QGRIHNLNDRRRHWHRVRVCH
		l				LLRRERSRKDAPADGHPPL\RA
		l	ŀ			VGGRNQN*FGELRTTTCFTQTD
		l				FLTFNLTSVTSNEASFTQFRTQG
1		l				LVVFHQSAGDTVTDRTSLTRDT
		1				TTFNGDVQVQFLNHVDQFQRL
		1				TNYHAGSFTTEVLFQRTLVDYD
		1				FTVARFDENASCGTFAATSAVV
l		1				LIFSHCLRLLCRVVVLVTRVNF
		1				QFTEHSTTQRAFWQHAFNRDF
		1				NHTLRTASNHLFKGRLFDTTDV
		1				AGVVIVHFVSTLVAGYSNFVSV
						QNDDVITGIYVRSVFRFVLTAQ
						ATSQFSSQTAQSFTGRVNNIPV
		l				AFYGFWFSCAKYYRHGARWCS
		l				NGRKIDQRHTHCFFCPCIRTDFA
						VEIGKEEFIT
28861	59229	Α	29036	1	797	MIVFIENFKTSSPKYADILLPDL
						MTVEQEDIIPNDYAGNMGYLIF
						LOPVTSEKFERKPIYWILSEVAK
						RLGPDVYQKFTEGRTQEQWLQ
		1		1		HLYAKMLAKDPALPSYDELKK
		1				MGIYKRKDPNGHFVAYKAFRD
		1				DPEANPLKTPSGKIEIYSSRLAEI
		1				ARTWELEKDEVISPLPVYASTF
		1				EGWNSPERRTFPLOLFGFHYKS
		1				RTHSTYGNIDLLKAACRQEVWI
		1				NPIDAOKRGIANGDMVRVFNH
		1				RGEVR\LPAKVTPHPVGTWTAE
28862	59230	A	29037	1	1019	
28863	59231	В	29038	1	2727	
28864	59232	A	29039	1	2250	
28865	59233	A	29040	1	2850	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
l	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
			l	sequence		
28866	59234	A	29041		1339	MTGKCGKFGNFLESWRAQKTG
20000		ľ.				ICGKVWNFLENLLNGFGONAY
						SDTDNEVQAEVVSDKDKELVG
						NWSKGHSCYAKRLAAFCPCLR
1			İ			DLWNFELERDDLGYLVEEISKO
		1				QTIQEEADHKNLESLQTEDAIE
		1				KKTPFSGEKFKLAAEICISNKDP
		1				NINSQDDGENVPRVAVHPNGC
		1			İ	FAWKLPVLSRKFERKPIYWILS
		1	i			EVAKRLGPDVYOKFTEGRTOE
						OWLOHLYAKMLAKDPALPSY
		1				DELKKMGIYKRKDPNGHFVAY
		l				KAFRDDPEANPLKTPSGKIEIYS
		1				SRLAEIARTWELEKDEVISPLPV
		i				YASTFEGWNSPERRTFPLOLFG
		l				FHDKSRTHSTYGNIDLLKAACR
		l				QEVWINPIDAQKRGIANGDMP
		l				YVFSSQMAKFTPRT\GLSSLIWK
		l				AHKCGEALETLOKO*C*OSGAT
		l				LPAGPRARAWPPYPRLFPTGLA
		l				CVDLHGNARKAT
28867	59235	A	29042	378	530	AFLPYDAGRRCLPGTVSV*SGL
		1				YVRGAQHGRYQ*HHRCCTSDK
		1				IWRADKG
28868	59236	В	29043	1	1617	
28869	59237	Α	29044	417	607	
28870	59238	Α	29045	954	1163	
28871	59239	Α	29046	444	3793	
28872	59240	Α	29047	475	732	
28873	59241	Α	29048	1	219	
28874	59242	Α	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	Α	29051	1	411	
28877	59245	Α	29052	172	378	LSLLRELGPVVAALLFAGRAGS
						ALT/VRNRPDARYRATLQYGD
		1				DGGGSAASGYFSPFLGWGYFIT
						TVDG
28878	59246	В	29053	1	1641	
28879	59247	Α	29054	1	3036	
28880	59248	A	29055	1	1419	
28881	59249	Α	29056	1	1500	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l			sequence		
28882	59250	A	29057	2	1760	KSQLHDPCCAPIQQEAVRAVV
						GOPPOOHLGFPVERGVCOREC
l				]		DFEKELEARIASLSDSVSNAREE
		1		1		RMALRQEQEQLQSRIQSLMOR
1			İ			APVWLAAQNSLNQLSEQCGEE
						FTSSQRTHGHSEGNITKRGLLG
1						ELRFENGDPSNDQSYGRHKDG
1		1				MAEIGTFHGGDLRGLTNKLDY
		1				LOOLGVNALWISAPFEOIHGW
		1				VGGGTKGDFPHYAYHGYYTO
		1				DWTNLDANMGNEADLRTLVD
		ı	1			SAHORGIRILFDVVMNHTGYAT
		1				LADMQEYQFGALYLSGDEVKK
		l				SLGERWSDWKPAAGOTWHSFN
						DYINFSDKTGWDKWWGKNWI
						RTDIGDYDNPGFDDLTMSLAFL
ļ					1	PDIKTESTTASGLPVFYKNKMD
		l				THAKAIDGYTPRDYLTHWLNO
l		1				WVRDYGID/GFRVDTPKCLRCN
		1				PSITIGTNYSAS*PQWSSIPGAL*
						G*/PAWAG/GLPWAPSVLLLDH
1						LROGFTMLEENLGNTIQDIGMG
						KDFMSKTPKATVTKAKIEKWN
						LIKLKSFCTAKETTIRVNRQPTE
						WEKIFAIYSSDKGLISRIYKELK
						QIYKEKNKQPHQQVGEGHEQT
		1		i		LLKRRHGCSQQTHEKMLNHQ
28883	59251	A	29058	I	1119	LLKKHOCSQQTHEKWLINIQ
28884	59252	Α	29059	3	2599	
28885	59253	Α	29060	225	1245	RGSTGAHPRSAGKHYAKTSAG
l		l			1	NAAGDP*YGOMGPHHRGCGKP
		1				VPLPDHQSENLRWW*RRAWCG
	1					SGGYR\MAEGRHAAOGIIDWLG
	1					LDVDKLGALEERRKVLQVKTE
						NLQAERNSRSKSIGOAKARGED
!	l	1		l		IEPLRLEVNKLGEELDAAKAEL
	i	1		1		DALQAEIRDIALTIPNLPADEVP
İ		l	İ			VGKDENDNVEVSRWGTPREFD
		1				FEVRDHVTLGEMHSGLDFAAA
		1	1			VKLTGSRFVVMKGQIARMHRA
		1	l			LSQFMLDLHTEQHGYSENYVP
						YLVNQDTLYGVGLYPLGALAS
		1				GWLPKRRERKDATPGPTGYPG
						AHGNLELPERSEGPRAGGEPRR
						RTGHTQKGSPDRGQTPPKGP
28886	59254	C	29061	201	1244	
28887	59255	Α	29062	1	2530	
28888	59256	Α	29063	675	920	RTYRLAGRQKQRRGGGTDSRS
				1		QNPWRSHRRHLP*RSSGAGKR
		1		l		GGKRFAGGAERRNPRLCRKPEP
	I					PAGGDGRRRRLAAAGAD

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
110.	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28889	59257	Α	29064	498	707	
28890	59258	Α	29065	510	554	
28891	59259	Α	29066	600	734	PECLSAPDH*YKHCCSTGTQAR
						QPDADCPLLPPRLAAHNERQTR
28892	59260	Α	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD
		1				LWPGEVLGIVGESGSGKTTLLK
		1				SISARLTPQQGEIHYENRSLYA
		1				MSEADRRRLLRTEWGVVHQHF
		l				LDGLRRQVSAGGNIGERLMAT
		l				GARHYGDIRATAQKWLEEVEIF
		l				ANRIDDLPTTFSGGMQQRLQIA
		l			!	RNLVTHPKLVFMDEPTGGLDV
		l				SVQARLLDLLRGLVVELNLAV
l		1			i .	VIVTSSPDQDWGFTPEPRLAAR
		l				FPGSTHSSRSRRNRGRRHPRPRS
		l				LPTPSAPHSRAPGDGVKLVPPP
		l				ARVTRNEPAPSDSVTLGVPHEP
İ		l				GACIGTPILTFVRPSTSAINAAA
		l				EESTGTILFGAGGFKRTDLNDT
		1				ESDSTTLVASRYWDLSSGWQR
1		l				AINLRWSLDHFTQGEITNTTML
		l				FYPGVMISRTRSRGGLMPTWG
		l			0.00	DSQRYSIDYSNTAWGSDVDFSV
		l				FQAQNVWIRTLYDRHRFVTRG
		l			İ	TLGWIETGDFDKVPPDL*LKSR
		l				VGQRSELGSQYTPRARVEPPKI.
		l				LSRKVRAHFGSRAPGAGRA*RH
	1	l				LRAPDCGVRWVWAGSGAGDG
						GGRGCGGSGTSEWILGSGRRGE
28893	59261	Α	29068	84	128	
28894	59262	Α	29069	1547	1822	CSRCSIPAFRVKPAPLKPRVFSP
		l				AWNVPERLWHLAPSTFSGGEQ
	l	1				QRVNIAR/ELYRRLPHSAA*RN
						YRLP*RQNSAALSRLYAAFLPR
20005	59263		29070	1520	1000	PQYHH
28895 28896	59263	A	29070	563	1656 976	
28897	59265	A	29071	1	1011	
28898	59266	A	29072	1	1097	
28899	59267	A	29074	1	2490	
28900	59268	A	29075	1	879	
28901	59269	A	29076	1	1317	
28902	59270	Ā	29077	1428	1619	YAARRALCGSPCPFPGGCNGE
I	1 - 2 - 1	Γ.	l	1		NCRLPPOLHADLTARIFYETRG
1		1				WWWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG*
	1-7	Γ.		1		HQLWARWQNNGLAHTPRADS
						THQQSALDGRISSLT
	<u> </u>					111QQ0/1LDOIG00E1

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28904	59272	Α	29079	1886	2329	PLLVWINTRPSLTTGRESASPAT LVCHATVPSLVIASHVLSFL*W SFTVLVISRIGVAFAHAIFWSIT ASLAIRMAPAGKRAQALSLIAT GTALAMVLGLPLGRIVQQYFG WRMTFFAIGIGALITLLCLIKLL PLLRRTVKYTSGC
28905	59273	Α	29080	1	2319	
28906	59274	A	29081	3	194	STSSLAAQSLRFGYETSQTGLA TYCGEKIQ*FFADLQQPVCADS YPLLVQMKKLGPIVFFFDI
28907	59275	Α	29082	3109	3384	
28908	59276	A	29083	703	1000	DCFLRRLIKRPFGTSMKDQAVR FEEGFMAMGALGLAMVGMTA LAPVLAHVLGPVIIPVYEMLGA NPSMFAGTLLA\WIWAAVFLAK ELAGGVRLLVLIF
28909	59277	Α	29084	2040	4603	
28910	59278	Α	29085	3	94	
28911	59279	Α	29086	3	148	YAEHMLEVMSSIGDYT/NPRPA SRPVTKFDQRGHRLGHGVWNL MFERVK
28912	59280	Α	29087	27	227	
28913	59281	Α	29088	344	1067	
28914	59282	Α	29089	798	1049	
28915	59283	Α	29090	1	1473	
28916	59284	Α	29091	1	720	
28917	59285	Α	29092	45	208	
28918	59286	Α	29093	1	2499	

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SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
20010	100007		20004		725	MHPRFOTAFAQLADNLQSALE
28919	59287	A	29094	1	/25	
		l				PILADKYFPALLTGEQVSSLKSA
						TGLDEDALAFALLPLAAACART
		ĺ		1		PLSNFNVGAIARGASRRSAKNIP
						RAVRQVFWRILLFYVFAILIISLI
						IPYTDPSLLRNDVKDISVSPFTL
				1		VFQHAGLLSAAAVMNAVILTA
						VLSAGNSGMYASTRMLYTLAC
						DGKAPRIFAKLSRGGVPRNALY
						ATTVIAGLCFLTSMFGNQTVYL
		l				WLLNTSGMTGFIAWLGIAISHY
						RFRRGYVLQGHDINDLPYRSGF
						FPLGPIFAFILCLIITLGQNYEAF
						LKDTIDWGGVAGTYIASGGEPA
			ŀ			VNSHAFGVLRNVVSIAVFFHQF
						GDAIKRLFPTDLLPFIRTWRTVF
						RKLQTAFGVDEIHQASAFRTKC
						TAVDRVIRIAFDMDRLDFFSWR
						SGYISRIPLIGLYFACALERHQN
				ŀ		ERQPIILLSDQNAIATINQLAIER
						DVLNCRVIIARSLSELVAIREEIE
						PLLIINNSHYLLDDAVNNYITVK
						NIITAAGIEQIKHFLATAFIRQQP
						ERFFSAPGSFHYSNVRGESWQH
l		1	ļ			ITRQICAQLVAQHHITADEAQRI
						IAREGEGENLIVNRLAIPHCWSE
l			i	ŀ		QERRFR*TVAWWRAA*CAVCD
1						DGDCRSVLPDLHVWOPDGIPV
İ				İ		AAEHLRDDGFYRLAGDCH
28920	59288	A	29095	3	453	
28921	59289	В	29096	1	3684	•
28922	59290	Ā	29097	î -	231	LLVFINOEEADFHTORGGPVFO
		1		l		QATFTL*QLALFAIEPGLMTDP
1			l	l		DIOVRGTTLPYGRGAAHGVYT
1				l		SNWKLTFRRILY
28923	59291	A	29098	1	2862	
~6/25	07471	Ľ.,	12,070	·	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \≔possible nucleotide insertion)
				sequence	1	
28924	59292	A	29099	ii -	1567	MKLNKAGFNVPESYSLLKMPP
	İ					VGCLISALKKAEDROEVILRLF
				İ		NPAESATCDATVAFSREVISCSE
						TMMDEHITTEENOGSNLSGPFL
				1		RVRAGESIKFFNVLLADTPGLD
						DTMDKDVAHDSRSIQLAMLRD
				1		DEILTHPVFNRYHSETEMMRY
		l		1		MHSLERKDLALNQAMIPLGSC1
						MKLNAAAEMIPITWPEFAELHP
						FCPPEQAEGYQQMIAQLADWL
		1		1		VKLTGYDAVCMQPNSGAQGE
		1				YAGLLAIRHYHESRNEGHRDIC
	1	1				LIPASAHGTNPASAHMAGMQS
		Į				RKTAGICCVHLWAGFGKVAIIG
		ľ				AGPAGLQASVTLTTQGYDVTIY
						EKEAHPGGWLRNGIPQFRLPQS
		1				VLDAEIARIEKMGVP\IKCTTEV
						G\NTLTLEQVKAENRAVLVTVG
						LSSGSGLPLFEHSDVEIAVDFLQ
						RARQAQGDISIPQSALIIGGGDV
						AMDVASTLKVLGCQAVTCVAR
l		l				EELDEFPASEKEFTSARELGVSI
		ŀ				DGFTPVAVEGNKVTFKHGDLR
						TAPFLGVADKRNKSAGNHP
28925	59293	Α	29100	107	892	LAICTGTYSGRQVLPRFVDRGA
						SLIAEERNGAGRRRAGIRTTSA
						GGGLCAYAIVEF*CWRNCARFE
						LN/AGISVPI/SEFIGATMQQTVH
						AEQSAISHAWLSGEKALAAITV
						NYTPCGHCRQFMNELNSGLDL RIHLPGREAHALRDYLPDAFGP
1						KDLEIKTLLMDEQDHGYALTG
i						DALSQAAIAAANRSHMPYSKSF
1						SGVALECKDGRIFSSEYAENAA
						FNPTPDIQRAVLAEKADAPLIQ
						WDATSATLKALGCHSIDRVLL
28926	59294	A	29101	1	3100	WBATBATEICIEGGISIBICYEE
28927	59295	A	29102	1878	2699	GTARNLTVSLSLSYSSSGTPSNA
	F	ľ.		1		PNARMEELGPHPGEASSLFHPE
						SPLLDELFLPEYKAGRTPNPDI\
	1					GHYVRRADV\DGKSRLLRGLDS
1	l	1				NKDQSYFLYTLSHEQIAQSLFP
		l				VGELEKPOVRKIAEDLGLVTAK
	l					KKDSTGICFIGERKFREFLGRYL
	l	1				PAOPGKIITVDGDEIGEHQGLM
1	l		1			YHTLGQRKGLGIGGTKEGTEEP
	1	1				WYVVDKDVENNILVVAQGHE
	l					HPRLMSVGLIAQQLHWVDREP
	1			1		FTGTMRCTVKTRYRQTISLGPL
	1				[	RKPPHNRCLEI
28928	59296	Α	29103	358	1160	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclentide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28929	59297	Α	29104	234	930	KRAFLCSFCANRRNAANSALAL
						PGNCPVAHAOKRHSAPGTLSPD
1				l		ARNEKQPLYG\GAAPETPNPRL
				ŀ		PPLDSGILGGYIAPDNLTITLSV
1						GHSLFDERFGLAPQMPKKLQK
						MTRFPNDSLDAALCHGDVLLQI
1	1					CANTODTVIHALRDIIKHTPDLL
						SVRWKREGFISDHAARSKGKET
						PINLLGFKDGTANPDSQNDKLM
						QKVVWVTADQQEPAWTIGGSY
						OAVRLNOFRSVMN
28930	59298	В	29105	ī	837	
28931	59299	Α	29106	1	1701	
28932	59300	Α	29107	733	1323	
28933	59301	Α	29108	1	736	MKPSVILYKALPDDLLQRLQEH
į						FTVHQVANLSPQTVEQNAAIFA
					ł	EAEGLLGSNENVNAALLEKMP
				ŀ		KLRATSTISVGYDNFDVDALTA
			1			RKILLMHTPTVLTETVADTLMA
l						LVLSTARRVVEVAERVKAGEW
						TASIGPDWYGTDVHHKTLGIVG
				ŀ	ł	MGRIGMALAQRAHFGFNMPI/R
					1	L*RAPPP*RSRRTLQRPLLRFGY
						SVTRVRFRLPDPAVN**DASSV
					1	WRRTIRGPSLGLSPGWNTRVSL
						CAFFG
28934	59302	В	29109	1	1359	
28935	59303	A	29110	874	1926	
28936	59304	Α	29111	1	777	
28937	59305	Α	29112	137	376	
28938	59306	Α	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGN
						FC*RHGS*KITAGYIVPLPEESA
						TATGASWTHPWGRQDASW
28939	59307	Α	29114	1846	2126	LMELIEKHVSFGG WQNMYRHY
				ļ		SQSLKCEMNVGVYLPPKAANE
						KLPVLYWLSGLTCNEQNFITKS
						GMQRYAAEHNIIVVAPDTSPRG
				l		SHVADADRYDLGQGAGFYLNA
				l		TQAPWNEHYKMYDYIRNELPD
		1		l		LVMHHFPATAKKSISGHSMGG
				1		LGALVLALRNPDEYVSVSAFSP
						IVSPSQVPWGQQAFAAYLAEN
						KDAWLDYDPV\$LISQGQ/LRCG
	1		1	!	1	NHG*SGVE**FLRRQLRLQI*KD
						WPQ*EAAHVH
		_				

		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
59308	A	29115	184	985	LGKRLVTYHTDANGOPVNOIL VEAATDIAKELYLGAVVORSSR RVVFMASTEGGVEIEK VAEETP HLIHKVALDPLTGPMPYGGREL AFKLGLEGKLVQOFTKIFMGT ITFLERDLALIEINPLVITKQGDL ICLDGKLGADGNELFRSLILRE MRDQSQEDPREAQAAQWELN YVALDONIGCMVNGAGLAMG TMDIVKLIGGPANFLDVGGG ATKERVTEAFNPPGYIGPYQGV PPAGPGVTRMGKSVRRIVQVG CQVAAGSH
59309	Α	29116	1825	3186	
59310	A	29117	366	1903	
59311	Α	29118	1	2139	
59312	A	29119	345	431	AASGSADDNLHHQYN*GDIAF CLHALLP
59313					
59314					
59315					
59316					MWWGGLLYWLAALVTLLWA
					ASQIQALKKLTCAISQTLEEQPV LNSKSWLTSLQNDYSLPDSLTE RIWLTLISQRISRGELREF*TGRR KLVTEQCLV
59318					
59319	A	29126	1	884	MVDSLIARVGYMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTOQQTPAFGRRVSGVIEI GOGSRRRKAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLIELMRVEEG DVILVKKLDRLGRDTADMIQLI KEFDAQGVSIRFIDDGISTDGEM VLDKLARGYADLSKAESQWDE WMRTAGSLKLGTHASELIRSL LKSSRPSGLAQAIMEVGRVNKT LVLLNYIDDEDYRRILTQLING GEGRHAVARAICYGQNGEIRKR YREGGEDQLGALGLVTNAVVL WNTLYMEEALSWMRRNGEEII DEDIARLSPLMHGHINMLGHTT FFDLIKGELR*RILPPPSSSA SFALPIGHPVKHLLGDNRYPI
5! 5!	9314 9315 9316 9317	9314 A 9315 A 9316 A 9317 A	9314 A 29121 9315 A 29122 9316 A 29123 9317 A 29124	9314 A 29121 I 9315 A 29122 I 9316 A 29123 96 9317 A 29124 I 9318 A 29125 3	9314 A 29121 I 1521 9315 A 29122 I 783 9316 A 29123 96 215 9317 A 29124 I 292

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nuclentide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28952	59320	A	29127	143	523	NQTLMIKGAAHGIFNPLCIKAT AGIAGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPRLILPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	В	29128	I	4107	
28954	59322	A	29129	1892	2720	IPTAWSPRPISM'ISISW'ICCM ERSNLSQPMPATKGR'QARGAG EEVDVDWLIAERPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRGPGVVARFKGLL NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFRALISTA SALAGLILLCLFGPALLAGVITE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRNGRVFLLVFILPFS LERVGHAFH
28955	59323	Α	29130	1332	1635	
28956	59324	С	29131	I	1677	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of loca	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28957	59325	A	29132	<u> </u>	11114	MAEACNIGLEPLIKHNIPALTRI
20937	37323	^	27132	l'	11117	RLSWVKQNYLRAETLVSANAR
						LVDFQSTLELAGRWGGGEVAS
						ADGMRFVTPVKTINSGSNRKYF
1	l					
						GSGRGITWYNFVSDQYSGFHGI
						VVPGTLRDSNFVLEGLLEQQTG
					1	LNPVEIMTDTCGCLEKQEEPPS
1	l	1			l	LLRLNNRIKQLLPPVDLTELLLE
						IDAQTGFTHEFAHVSESGARAQ
		1			İ	DLHISLCAVLMAEACNIGLEPLI
		1				KHNIPALTRHRLSWVKQNYLR
		1				AETLVSANARLVDFQSTLELAG
	ŀ			l		RWGGGEVASADGMRFVTPVK
1		1		l		TINSGSNRKYFGSGRGITWYNF
		1		i		VSDQYSGFHGIVVPGTLRDSNF
1				l		VLEGLLEQQTGLNP/D*NHDRH
1			i			LRLSGETGRATIIASSK*SDQTA
1					ł	TPTGRFNGTVT\EIDAQTGFTHE
1					ŀ	FAHVSESGARAODLHISL\LRY*
						WLKPVIS/ALEPLIKHNIPALTRE
						RLSWVKQNYLRAETLVSANAR
		1				LVDFQSTLELAGRWGGGEVAS
1		1				ADGMRFVTPVKTINSGSNRKYF
ł		1				GSGRGITWYNFVSDQYSGFHGI
				l		VVPGTLRDSNFVLEGLLEQQTG
1		l			l	LNPVEIMTDTCGCLEKQEEPPS
		1				LLRLNNRIKQLLPPVDLTELLLE
	İ	1				IDAQTGFTHEFAHVSESGARAQ
	l	ı				DLHISLCAVLMAEACNIGLEPLI
		1				KHNIPALTRHRLSWVKQNYLR
						AETLVSANARLVDFQSTLELAG
28958	59326	A	29133	1	2908	RWGGGEVASADGMRFVTPVK
28958	59326	A	29133	735	932	
28960	59328	В	29135	1	1413	
28961	59329	A	29136	i -	1469	
28962	59330	Ā	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	Ā	29139	li	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNL\LL
20700	37334	l^	27141	1104	1033	RRFHEATAQNAPDVVVWGSGT
		1	1	1		PMREFLHVDDMAAASIHVMEL
1		l				
		1				AHEVWLENTQPMLSHINVGTG
	1	1	l	1		VDCTIRELAQTIAK VVGYKGRV
		1	l			VFDASKPDGTPRKLLDVTRLHQ
	1	1	l			LGWYHEISLEAGLASTYQWFLE
		$oldsymbol{ol}}}}}}}}}}}}}}}}}}$				NQDRFRG
28967	59335	Α	29142	538	1116	
28968	59336	С	29143	1	2967	
28969	59337	C	29144	1	2214	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28970	59338	Α	29145	1	469	
28971	59339	Α	29146	780	1052	
28972	59340	Α	29147	617	2408	
28973	59341	A	29148	2	488	
28974	59342	Α	29149	1	1083	
28975	59343	Α	29150	527	3213	SWRSVQLLPATSIPSWQTETNQ
						FMGRDRPTPTAESPYAVLLRQP
ł		1				LAKLNIIQ/RPVMNMVENMLDQ
		l				AFKKLNPHEHPVLHSDQGWQY
		l				RMRRYQNILKEHGCGVTPIMS
	i	ł	1			MRRWLAKNRPQADVRVIYNVR
	İ	l				TPODVIFADEWRNYPVTLVAE
		l				NNVTEGFIAGRLTRELLAGVPD
						LASRTVMTCGPAPYMDWVEOE
						VKALGVTRFFKEKFFTPVAEAA
						TSGLKFTKLQPAREFYAPVGTT
l						LLEALESNNVPVVAACRAGVC
						GCCKTKVVSGEYTVSSTMTLT
						DAEIAEGYAVVALIKPGAOIGR
ł						SPVNCDVASCHVISFNLRVELAI
						MRRLLCRIAVLMSYRIEORLMF
						LERLRHVGLIAHPAKKAİKKTR
			İ			KPGMKVTFEQLKAAFNRVLISR
						GVDSETADACAEMFARTTESG
						VYSIIGVNRFPRFIQQLENGDIIP
						DAQPKRITSLGAIEQWDAQRSI
						GNLTAKKMMDRAIELAADHGI
						GLLRLAGGGKRLYWHLLDQLH
		1				RRNDNISLDLGNNAEAVILRED
						MLPRENFRPGDRVRGVLYSVRF
		l				EARGAQLFVTRSKPEMLIELFRI
						EVPEIGEEVIEIKAAARDPGSRA
		l	l	1		KIAVKTNDKRIDPPTOHEDEED
		l	l	1		EGLYDDPFPLNECSVGPGHRHR
						FAPPEAOFRRPETLKGAPTSRIP
						ETSVGVSAGSDFEPHLMRELTC
			1	1		RLTALTWCYPGSAYAVHOPDE
28976	59344	A	29151	1	812	34,111,121,22
28977	59345	A	29152	1	1830	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
	sequence		09/540,217	sequence	or pepride sequence	deterion, (-possible nucleotide insertion)
		L				
28978	59346	Α	29153	I	1308	MMPLIDLEDPRLLVRREIGMLI
		1				HVDYLDLVHEKVTCRGRNGG
		1				DREKTTMEKVRSSGTICPQAPE
			İ			VVNHYFTTDDGYRIISARFGVP
		1				RTQVRTWVALYEKHGEKGLIP
		1				KPKGVSADPELRIKVVKAVIEQ
		1				HMSLNQAAAHFMLAGSGSVA:
		1				WLKVYEERGEAGLRALKIGTK
		1	1	l		RNIAISVDPEKAASALELSKDR
	}			į		IEDLERQVRFLETRLMYLKELK
						ALAHPTKKVTLSLHREGKQINI
						KAVQRLMGTLSLKAAIKVKRY
						RSYRGEVGQTAPNVLQRDFKA
		1				TRPNEKWVTDVTEFAVNGRKI
	1					YLSPVIDLFNNEVISYSLSERPV
	1					MNMVENMLDQAFKKLNPHEH
						PVLHSDQGWQYRMRRYQNILI
						EHGIKQSMSRKGNCLDNAVVE
						CFFGTLKSECFYLDEFSNISELK
						DAVTEYIEYYNSRRISLKLKG\L
28979 28980	59347 59348	A	29154 29155	1	836 1566	
28981	59349	A	29156	297	936	RTSSSLMRSSSSLLRICSGVSPR
20901	39349	^	29130	297	930	IPRWFTSVSLPSSFIR\RITTFRY
		1				PGHVAPASRRSCYKYRR*PMR
		1				YTMIQSLS/VGSRPSGLRAFSSD
						CSPLPRTCSLSRRRVLMITTSRS
		1				*SLTYGVDPSVRPVLAAASEYF
		1				SRR\YAGFQNPHNLLVSG*YQG
						NYRHFGILRGYPG/TLKNSNFQ
		1				TRSARISLSSRSSICTSTGGNTTI
		1	ŀ			PPSSPPDC
28982	59350	A	29157	5	861	SWRSVOLLPATSIPSWOTETNO
20702	37330	l^	27137	ľ	801	FMGRDRPTPTAESPYAVLLRQI
						LAKLNIIQ/RPVMNMVENMLDO
		1				AFKKLNPHEHPVLHSDQGWQY
		1			ŀ	RMRRYQNILKEHGCGVTPIMS
		1				MRRWLAKNRPOADVRVIYNV
		1				TPQDVIFADEWRNYPVTLVAE
		1				
		1				NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQI
		1				
						VKALGVTRFFKEKFFTPVAEA
		1	l			TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC
		ŀ				LLCALCONNVPVVAACKAGVC
		Ì			1	CCCVTV VVCCEVTVCCTVTI T
						GCCKTKVVSGEYTVSSTMTLT
20002	50251		20168	1010	1001	DAEIAEGY
28983	59351	A	29158	1818	1991	DAEIAEGY SPSHIRRTAPNGLRHYQR*IQQ*
28983	59351	A	29158	1818	1991	DAEIAEGY SPSHIRRTAPNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK
28983	59351 59352	A	29158	1818	1991	DAEIAEGY SPSHIRRTAPNGLRHYQR*IQQ*

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
28986	59354	Α	29161	2	501	
28987	59355	Α	29162	1	1347	
28988	59356	Α	29163	3	2461	
28989	59357	Α	29164	1419	1640	IFCASLSLGLYAGIEARILTKG
		1				TRK*IQQ*APSDQKRDFLVPH
		1				ADSAMAKHGGSHRAVLPQG
						DPHMESL1
28990	59358	A	29165	1135	2067	
28991	59359	Α	29166	1	1364	MAGNRRFMCTPKTHGLSISQ
		1			1	GTFPEHAGCKIRCAGRSGRVI
		1				AELLAPYTGDIAAEGISKAMI
						GAKFLHHGIKRQQRYVAEAI
						EWRMAPGPLEVAWFAGVIYI
		ı	l			YYYRARFFCAAQPLVSGFHE
			l			LSLDDAKWVLHPGPDAGFH
	1	l	İ			DVDGRFVLAWMLFQGSYLA
						ALGDQPVHIHLGQLLALWRF
		1				QITQLIEVMLVGRGGDQAVG
						ATLGIDTNGGLYAKGPLIAFI
						LMHLRIALLLFVLGRTGCAY
						GRPQLAEKLYSELRAQGIEV
			l			DDRKERPGVMFADMELIGIP
						IVLGDRNLDNDDIEYKYRRN
						KQLIKTGDIVEYLNAALLIAV
		1				VLTSMEASDLVDLGMTLSPA YAERLAALTOKCGLDGVVC
		1				QEAVRFKQVFGQEFKLVTPG
		1				POGSEAGDORRIMTPEOALS.
		1				VDYMVIGRPVTQSVDPAQTI
		1				AINASLORSA*CRDAGTLRLI
						WLC*FLORRYHRYKGPAVPO
						ELCQICQRNEFCTQRVPGMC
28992	59360	A	29167	627	854	NAGDRRNRNPSCTAAROYG
20772	139300	ľ	29107	027	054	RFYNCRR*RHGRKNLSAERN
	l					PEYRNCNPDHRPSVFLAAGR
						APTMCHDASE
28993	59361	A	29168	ī	1593	
28994	59362	В	29169	î	3789	
28995	59363	Α	29170	940	1326	
28996	59364	Α	29171	1	1377	
28997	59365	Α	29172	1	2547	
28998	59366	Α	29173	561	845	AKIVQLRPRILRPSRSARRCPS
		1			1	PRSRRQRRRSGPLPEPAPRVS
		l	1		I	IFPSQYWRYRQSTENQKQRL
			l	1		RGQIVNVPARRIIRQKRKCCK
	L					AGSA
28999	59367	Α	29174	1	1284	
29000	59368	Α	29175	624	866	
29001	59369	Α	29176	1	1384	

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29002	59370	A	29177	2268	2684	RCRRCKRRLLRRFRRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCHCG*RQC SSDGRKITSVHRGRNADGRELT HQAVRLLAYLSDRFARHHRHL RNAHRRGPDRIPKERHFPATKL RHTPAV
29003	59371	Α	29178	1	2142	
29004	59372	A	29179	]	2463	
29005	59373	Α	29180	3	126	
29006	59374	Α	29181	]	2013	
29007	59375	A	29182	891	1000	FDSFHWHSHPMLCCDRGQHKE NPQSRGPISCQ*IQQ
29008	59376	Α	29183	1	846	
29009	59377	Α	29184	90	411	
29010	59378	A	29185		1580	MSKPKYPEEKRLEVVNHYFTT DOGYRIISARGVPRTOVRTWV ALYEKHIGEKGLIPKPKGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGVARWLKYYEER GEAGLRALKIGTKERNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTIK AAEIPRSTFYYHLKALSKPDKY ADVKKRISEIYHENGRGYSYRGEVG GTAPNVLORDFKATRPIKEWV TDVTEFAVNGRKLYLSPVIDLF NNEVISYSLSEPVMNWYEN LDQAFKKLNPHEHPVLHSDQG WQYRMRRYQNILKEHGIKOSW RKGNCLDNAVVECLFGTLKS ECFYLDEFSNISELKDAVTEYIE YNSRRISLKLKDLYASCLTVL LFGVSTYMGLLIRLIGSIFQKAL NISKIESFVAVTTIFLGQNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI VKRFMAESHEVLPHLYGGNEIPAI
29011	59379	A	29186	1375	3174	
29012	59380	A	29187	604	1268	
29013	59381	A	29188	1	288	
29014	59382	A	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	Α	29192	1	3156	
29018	59386	Α	29193	1	1824	
29019	59387	A	29194	1	1922	
29020	59388	Α	29195	1369	1743	<u> </u>

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
29021	59389	Ā	29196	21	432	GPGCNGVHRLCTE\QRDVRGTV
	i					RIVLKTFNNCRDTVFVAFEVNN
	1			l		TVSLLVATTDMTSGDTAIVVTT
					1	TGFVSAANEVQILAFFQGDVSF
	1					FPVATTTDTLSVTFNFPFNYQG
		l				VNDFDFDFKQFLHSSFDFCFGR
		l				VFSNFE
29022	59390	С	29197	1	1743	
29023	59391	Α	29198	2005	2571	
29024	59392	Α	29199	170	486	LQTQKDGIPAVVERLEYDPNLP
		1				RTSRWFRNDFSVPVLQLLGSP*
29025	59393	A	29200	1	1713	
29026	59394	Α	29201	I	6729	
29027	59395	Α	29202	1	753	
29028	59396	Α	29203	I	1470	
29029	59397	Α	29204	665	1773	ASSQVKSGWLSAKIPVISSIYGP
1				ĺ		LLSVRLLSHAWPNSLCPQLHCF
				i		LPGAIWSASSLLKSGNRPLIRLA
						SIVLPVPGGPISKRLCPPAAV/HF
		1				QSSLSLFLTDNITEIML*RPDTW
		1				THVMYVLHHADKPNLYHGLPE
	1	1				NPEISETVKFWKGIWKPLAAVG
		ĺ		i	1	FAATFAASIFHYVGVGPNRADE
		1				EENNLHEEKDEERKCSQDIQLV
		1			i	KERVIFLTGQVEDHMANLIVAQ
	1	l				MLFLEAENPEKDIYLYINSPGG
	ı	1				VITAGMSIYDTMQFIKPDVSTIC
	l .	i .				MGQAASMGAFLLTAGAKGKR
		ı			1	FCLPNSRVMIHQPLGGYQGQAT
		ı		1	1	DIEIHAREILKVKGRMNELMAL
		ı			1	HTGQSLEQIERDTERDRFLSAPE
		1				AVEYGLVDSILTHRN
29030	59398	Α	29205	948	1620	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Aminn acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletinn, \=possible nucleotide insertion)
				sequence		
29031	59399	A	29206	11782	3667	I HRRRCRHGYPVPAYRCRIWKC
2,05.	3,3,,	Γ.	2,200	1	5001	GOFHPTGIAGCGRTGHRRLPW*
		ŀ				RRLSAEQTWRTFYGALCAERQ
				l		RPGGP*RG\SRSIMIEIREGRGCD
				1		GPWGPHAKLKLDHLGKEVLES
					1	RLPGILELSRTFAHVDPSRFRLS
		ŀ	100			HLSLHDGRYSDQSYRYNDTRD
ł						MVPINGSIHRIGREPHYHYQRG
		l				QQYIGLCRNCNVIDTHICIYLVE
1		l		l		QPIMDDIRRLLLYSEISSAIIWLL
		1				PVVQGEHYMLVDPDTNEREER
		l				GRSETRGFPRVPLGRTVSTVWY
						PLSNAATLAATRCSRSPHAFAE
		i i			1	PSSNNGFITATPLGRTHFLGMA
				l		FPPSACWRLLRAEPERVEAVLS
		1				ASGMNKAMRCGVSLICNFRLD
		ŀ	İ			YAPIEKQWDLHFADYFAEDLK
		1				LLAPLAKDGLVDVDEKGIQVT
i		l				AKGRIRRLRRIRHLSMMPDAAL
		l				VASYQAYDFLRIRHKQRASAK
		1				QPNHCGTQHGSNGSLRTLWNSI
		l		ł		DSGSVLTWCASLIFSSRKSLSPI
		1			1	QLVRSVDRGDVKKRYSMREFS
:					1	LGETHSEAEFRELLEQNPSFVFF
ŀ		1				KPQSFAPVKGASAVPLVGRASV
ŀ		l				ASDRSIIPPGTTLLAEVPLLDNN
		l			i	GKFNGQYELRLMVALDVGGAI
			l			KGQHFDIYQGIGPEAGHRAGW
						YNHYGRVWVLKTAPGA
29032	59400	Α	29207	1351	1806	VIVGITSNSVTVAAVSSWCRTW
		1				VPVSVLCLNCYPASMALVRGVI
		ŀ				RGV*TCLSLCPNCAAIFIFAFGA
}		l				VIFCITSVGFLFPPMVYKSGLRF
		1				FVFT*MRDTGVPQRLRAPRRSL
						SAKLGPACPFAYIVPHIWCRWI
						GWGTCVCLAICVCVCVAD
29033	59401	Α	29208	1308	1647	RSWEVSIVEFYVVRPTGHV*HA
						SGNLSHHRKRHPLADQAARKG
		1				ETVPPRGRRS\WRTQAHP*HLR
l		1	1	l		QHRGQHPASLPTRTGTPQPGRR
		1				AIYRIPVRTAGQFQRIEVGDFQR
						VGHQ
29034	59402	Α	29209	1	2184	
29035	59403	В	29210	81	1356	
29036	59404	Α	29211	1	2349	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequenec		
29037	59405	Α	29212	514	1136	ILRIMQRGMKQFAGLLRLSGIK
						MLPSA**LGELLHAAGSFFQRG
						CLLFSTGGKIGVARRNFTGTGI
						DGI*TFADMSDGVSQRALHM*
				ì		NALRQVAHFTAPVNGQGIRQV
						TTGDFANVSNNFCQRSKQHTA
						NAVPRHQQNQYHHQRDNRQLF
				ł		LGKSVIICVVSDDIAIQFFTAEG
						VLSKRFAHCLMPSLGGLSKIGP
						SMPLFRIISQFS
29038	59406	A	29213	1	2992 168	
29039	59407	A	29214	I	537	
29040 29041	59408	A	29215 29216		1881	
29041	59409 59410	A	29216	1532	2160	KHWSDSIPGTEADWSASTTSGC
29042	39410	A	29217	1332	2100	AGFAAFACSSS*VICLLSGAVA
		l				AYAPOLRHOAIRKVIIRRTSAFP
						LMD*TWSFLSSTNGLASCSASIS
						SAGSGAGSASGVTKVSVDTAS
		l				GWPIFVTDRLSSCSTRFTLPGAN
		l				RLITVEPSLKRPISWPFSSATEPS
				1		FSPAGQVQRLMIPSRGGVMVP
1						AOTVSMLPTIVAPTGPYSSHLL
						GSFTLSPP
29043	59411	Α	29218	1	1713	
29044	59412	Α	29219	2159	2715	TIPAKPVPSMVASGTVRFGFLTI
ŀ	l	ŀ				PVLTAADSTPTKAHRQSRILLMI
ł						A*PSVVSAVFQLAA*VAASNQC
						QPTIAVITTGIRTSTRPIVA/CITG
		1				FVTGAVEIVLVANSVIDISVGSP
		l		l		FSIPQMFSARLGIATMAICPIMV
						SFSVAAINSASHNRQGFALQFFF
	i					NDAACGSGEFRILMQEEHPDSV
20045	60412	<del> </del>	20220		102	VFC
29045	59413	Α	29220	2	102	DFADFGTTIKQDFRLLGQTSVD
	1	ŀ				RLLQLSQGQAVKGNQLLPVSL
	1	1				VKRKTTLAPNTQTASPRALADS
	1	1		I	l	LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM
						SVDLCHRDFADFGTTIKODFRL
		1				LGOTSVDRLLOLSOGOAVKGN
				1		QLLPVSLVKRKTTLAPNTQTAS
-	1	1		1		PRALADSLMQLARQVSRLESG\\
	1	1		i		IGGAGSLAFPLPALIWCAVRYT POVTCLLTFVTGILPISEPPSNRI
		1		i		FACWGKPAWTACCNSLRARR
29046	59414	A	29221	ī	1464	PACWUKFAW IACCNSLKARK
29040	39414	IA.	29221	11	1404	L

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /~possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
29047	59415	A	29222	3	29	MQTEQQR/AVTRLCIQCGLFLL
						OHGAESALVDELSSRLGRALG
			ĺ			MDSVESSISSNAIVLTTIKD/GOC
						LTSTRKNHDRGINMHVVTEVQ
						HIVI/LAEHHLPDPEP*EQQRR
29048	59416	Α	29223	5	307	
29049	59417	Α	29224	5	948	
29050	59418	В	29225	1	696	
29051	59419	Α	29226	1	1083	
29052	59420	Α	29227	817	978	LAGCYTMLPGNGPAGMHACIS
		1				KLDK*AAVKKRISEIIHENRGRY
29053	59421	Ā	29228	198	362	GYRRVPLSLH
29053	59421	A	29228	1198	2907	
29054	59423	A	29229	1	2541	
29056	59424	A	29231	<del> </del>	1566	
29057	59424	A	29231	3	601	
29057	59425	A	29232	1	1347	
29059	59427	A	29234	940	1326	
29059	59427	A	29234	1 l	2547	
29060	59428	A	29236	527	1383	SWRSVQLLPATSIPSWQTETNQ
29001	39429	I <sup>A</sup>	29230	327	11363	FMGRDRPTPTAESPYAVLLROP
		1				
		1				LAKLNIIQ/RPVMNMVENMLDQ
		1				AFKKLNPHEHPVLHSDQGWQY
		1			1	RMRRYQNILKEHGCGVTPIMS
		1				MRRWLAKNRPQADVRVIYNVR
		1		l		TPQDVIFADEWRNYPVTLVAE
		1				NNVTEGFIAGRLTRELLAGVPD
		1				LASRTVMTCGPAPYMDWVEQE
		1				VKALGVTRFFKEKFFTPVAEAA
		1				TSGLKFTKLQPAREFYAPVGTT
		ł				LLEALESNNVPVVAACRAGVC
		1			i	GCCKTKVVSGEYTVSSTMTLT
						DAEIAEGY
29062	59430	Α	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	Α	29239	1135	2067	
29065	59433	Α	29240	1	1566	

	01/0/300/	_				FC1/US01/08031
SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop eodon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequenec	or peptide sequence	deterion, (-possible nucleotide insertion)
29066	59434	Α	29241	Îı .	1605	MKVPRGDVMFQLNLRKDDGO
						FEDQLLLLVLLPKHRGHLLLQV
		l				ADDVWFKNRRAKCRQQRQQQ
						KOOOOPPGGOAKARPAKRKAG
				1	İ	TSPRPSTDFRSRDGIPEKATRTS
				ĺ		CPSDSSVFSLQRPPLSSTGRGSS
		Į.				LSWDSSQVLVILSTLTPSGTIVT
						AEPKYPFEKRLEVVNHYFTTDE
					1	GYRIISARFGVPRTQVRTWVAL
						YEKHGEKGLIPKPKGVSADPEL
						RIKVVKAVIEQHMSLNQAAAH
						FMLAGSGSVARWLKVYEERGE
		ļ				AGLRALKIGTKRNIAISVDPEKA
i						ASALELSKDRRIEDLERQVRFL
					i	ETRLMYLKKLKALAHPTKKVT
					1	LSLHREGKQINHKAVQRLMGT
						LSLKAAIKVKRYRSYRGEVGQ1
			ŀ	l		APNVLQRDFKATRPNEKWVTD
				l		VTEFAVNGRKLYLSPVIDLFNN
i				ŀ		EVISYSLSERPVMNMVENMLD
						QAFKKLNPHEHPVLHSDQGWQ
		ı				YRMRRYQNILKEHGIKQSMSR
						KGNCLDNAVVECFFGTLKSECF
						YLDEFSNISELKDA VTEYIEYYN
		L				SRRISLKLKG\LTPI
29067	59435	A	29242	3	1119	
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRREIE
						SIIEAGRVSDDGEIAKLGDNVE
				ļ		AWYRARLAGAFTLQECVMAA
	ŀ	1				STFFIPSVNVIGADSLTDAMNM
						MADYGFTRTLSVTDNMLTKLG
	1					MAGDVQKALEERNIFSVIYDGT
						QPNPTTENVAAGLKLLKENNC
						DSVISLGGGSPHDCAKGIALVA
						ANGGDIRDYEGVDRSAKPQLP
						MIAINTTAGTASEMTRFCIITDE
						ARHIKMAIVDKHVTPLLSVNDS
	50 100	<u> </u>	20244	104	1001	SLMIGMPKSLTAATGMD
29070 29071	59438	A	29245 29246	104	1381 375	
29071	59439 59440	A B	29246	1	5082	
	59440					PHONOD DIVICUL CTID OCCUPANT
29073	39441	Α	29248	119	343	RMPKRRRWGKLSTIRCSTTCKK
						RLT*IVLPVRTPGRLCSSLKSVP
1						ASHCLASCKAYSNKPWKRQPS
ı						KRHYVTMR

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first endon for peptide sequence		Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29074	59442	А	29249	468	935	VPLAVPYGRLWRTIFSPLPSSFR STRVRFEVSGRSSPSISSLASLVR PITYSLLIVMAHPVELLQVVPPTL DKHIAAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPTE AVDLFFHFNAVTKGFHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	A	29250	407	2145	
29076	59444	Α	29251	1	177	
29077	59445	Α	29252	1	1767	
29078	59446	A	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	A	29255	2	314	
29081	59449	A	29256	2977	3913	
29082	59450	Α	29257	1	2091	
29083	59451	A	29258	l	751	
29084	59452	Α	29259	1	927	
29085	59453	Α	29260	1	1113	
29086	59454	Α	29261	1	875	
29087	59455	Α	29262	1	450	
29088	59456	Α	29263	1	522	
29089	59457	Α	29264	1	912	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
29090	59458	A	29265	1	2416	MLAQSLQALEQDGFLNRIAYPV
l				l		VPPHVEYSLTPLGEQVSEKVAA
				l	1	LADWIELNLPEVLAVRDERTRY
		1				DIAVPRKRYGHAVSRNTFALRS
1				l	İ	QERYGHSVLETVGNSGSSKQFS
						MDILDPCARGPGQISLITVNHKL
						HVRCESIAYSVQTMVVKGGSA
			1			FAAFFIAVVLWMIGYVPNVEQS
					l .	TQALLGMQFIMIALPTLFFMVT
						LILYFRFYRLNGDTLRRIQIHLL
					1	DKYRKVPPEPVHADIPVGARLS
					ŀ	FAERVMEGLSDGGQSLQSPSAL
						FSKQTLKNMSIYKIPLPLNILEA
				1		ARERITWTLNTLPRVCVSFSGG
				1		KDSGLMLHLTAELARQMGKKI
				ŀ		CVLFIDWEAQFSCTINYVQSLR
				l		ELYTDVIEEFYWDALPLTTQNS
l						LSQYQPEWQCWEPDVEWVRQF
						PODAITOPDFFCFYOPGMTFEO
				ŀ		FVREFAEWFSQKRPAAMMIGIR
				ŀ		ADESYNRFVAIASLNKORFADD
						KPWTTAAPGGHSWYIYPIYDW
						KVADIWTWYANHOSLCNPLYN
		ł				LMYQAGVPLRHMRICEPFGPEQ
		1				ROGLWLYHVIEPDRWAAIGSP
		1				ADREEDAEEYLEAIMEARVTV
		l				AGMGLVMEVQDYFDGEA\DRL
		1				AKAWLP\EYTPOIKSLKDERKE
		1				AYRQIVEMSTEPQDVDLVRPA
		l				NKFEMTRVREGEKEADLPVWK
		l	l			HHLLCDESGNYPALLNHWETK
		l	1			VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	TI ELETRICOTAL WTRIT QTTO
29091	59460	A B	29266	/80 I	10161	
29092	59461	A	29268	1	882	
29093	59462	A	29269	1	2484	
29094	59462	_	29269	548	945	
29095	59464	A	29270	17	352	DI ODTCCEMI ADITCER A VIIVA
29096	39404	^	29271	117	334	DLQDTGCFMLMNTGEKAV/KS
						ENGLLTTIAC/GPTGE/VNYALE
						GAVFMAGASI/QWLRDEMKLIN
		1				DAYDSE/YFATKVQNTNGVYV
						VPALPGWSLLWTRTCHRIFPRH
		_				RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIIELN
		l				TDFLCLINHMVVGQHIAFTGVD
L						DDTGA*TFEGLCRLIR
29098	59466	A	29273	I	975	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29099	59467	Α	29274	65	562	DFRWHGDSRKYHRKNRLIKPL MILLTRLSNRTNWPLTAAVIPL GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSSTSS SIIIIINSSSSLQCQPCASKYLAH YFTVSSIAAYSTDVSTQEPWA TRHHPHHQQTDRRRPATRKSPR QYHNETNRQ
29100	59468	Α	29275	1409	1641	PENGRPVYAGGRDAAWRDVY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSALGLCL* RLAGGDWCRDYSL
29101	59469	Α	29276	1	3252	
29102	59470	С	29277	1	2760	
29103	59471	Α	29278	1	723	
29104	59472	Α	29279	14	338	
29105	59473	В	29280	1	1201	
29106	59474	В	29281	1	1866	
29107	59475	Α	29282	1067	2753	
29108	59476	В	29283	1	1144	
29109	59477	A	29284	3	724	LAQLYGDPPAWPITFRGYSEIR LALRFKSNDSLLRHFKDTSTLY LEIVDYPGEWLLDLPMLAQDY LSWSRQMTGLLNGQRGEWSA WRMMSEGLDPLAPADENRLA DIAAAWTDYLHHCKEQGLHFI QPGRFVLPGDMAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL QPLNSGHSIVDMRWPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	Α	29285	1	1863	
29111	59479	В	29286	1	813	
29112	59480	A_	29287	1	546	
29113	59481	В	29288	1	2691	
29114	59482	A	29289	1	1212	
29115	59483	A	29290	1	2328	
29116	59484	A	29291	1	531	
29117 29118	59485 59486	A	29292 29293	188 2545	358 2713	LLVVQFFFQHL*VPSGTSP*L*H LSGILWHFLLQALLYPRVFLVL LCRSLGAVCLY
29119	59487	Α	29294	I	2046	
29120	59488	Α	29295	3	654	
29121	59489	Α	29296	2	182	
29122	59490	Α	29297	1	1215	
29123	59491	Α	29298	141	266	

SEO ID	ISEO ID NO-	Mer	SEQ ID NO:	Nucleotide	Nucleotide location of tast	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	•			sequence		
		<u> </u>		L		
29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN
						ASGHAKRQSDGDLRSRAATGG
						DHSAGDWCGRRVQTSAG*LWR
						KARPWPNR
29125	59493	Α	29300	2353	2758	SQAYHQVLPVCEAAPIPDDNHT
						LAALR*HGVYEKHMDQDCWA
ļ					1	SFLPEERLFWRPIPAPRSDRVEC
1		1			ł	VDSLPLTAVGKVDKKQLRQWL
		1				ASRASARAQRRSPLAEARKPQY
						VHQGMDNARTALQKPEQARA
		1				HTEVHWT
29126	59494	Α	29301	5	793	FLQRFVADLPCGAQVVKFSTFR
		l				TQCRQTEATLKVLFLHGTFNVV
1		1	1			TSIGATTQVTNDARTDLRKQLV
l						IDILFGIRRQTLLHFLDRHNRHF
1		1				CRCRSRNTFLFQLLRMIRDFND
i						FELV/NPLSLDSVLGMQPLREEI
		1				QQADRDDDKHHQGAGLLELET
		1				ANRFPQGDADPACADHADDGR
						RADVGFEAIEGVGDQQWHHL
		l		i		WQHAVEDLFELVGTGGANAGP
						GSIASTASESSLESTPVVWINSA
		1		1		STPARQRTGRGRRRPRTAWRRP
29127	59495	A	29302	1	2457	
29128	59496	Α	29303	1	292	
29129	59497	Α	29304	ł	440	
29130	59498	A	29305	593	864	RTSAEPINPAPPVIRIFLISARLC*
ľ		1		1		WTLSPLITLN*L*STSITSTSAVA
i	İ	1				SASSSCARVQSPVSFFGNWWM
						LGSTTRVSPLCHWAISSADF
29131	59499	Α	29306	2	696	VPAGRYTGRDLHLHI/ILPFRES
						LPARHRVRRYRPLEAC*TPCTD
						GYHRIFYRLKGESAKDGSVMT
				l	1	LRSFLDKDGHPIDVEDINDQAR
						HLVRLMPVLRLRDARFMRRIR
		l				NGTVPNVPNVEVTARQLDFLA
	1	1	1	1	i	RELSSHPQNLSDGQIRQGLSAM
	1	1		I	i	VQLLEHYFSEQGAGQARYRLM
		1			1	RRRASNEQRSWRYLDIINRMID
		1				RPGGRSYRVILLGLFATLLQAK
						GTLRLDKDARPLLLIE
29132	59500	Α	29307	3	1405	
29133	59501	A	29308	1204	1411	LRPALYQPARLSDAAVRKTG*F
1		1				AVVSGSEHAESDAG*SGELLEQ
1		1		1		LSEVLR*PDEIFLWRCRAEREOL
1		1		l	1	GL
29134	59502	A	29309	236	645	
-7.54	1	L	1		L	L

NO:	SEQ ID NO: of peptide sequence	hod	in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29135	59503	A	29310	1	776	MELAALRSENPÖPDERPLGETL KOLFSRPVLDEMTDVHLENLN IEEFMGEOLHVTCDTDIYREHH AAEMSNIDGNTKLDALDIDSSQ GIVDASGTAHLSDNWPVDITLN STLIVEPLKGDKYKLKMGGAL REQLEIGVNLSGPVDMDLRAHT RLAEAGLSLNVEVNSKQLYCL AHCMSSMPKESGADEKNSDNR WCRVYWLGAGALYHQRNERR GOSGR*ADLRRKPDVAGTGRA
29136	59504	Α	29311	955	1095	HRRHPIPFLIHHRDQPFRHQLRK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	Ā	29312	1029	1490	RLPPAVDPTARLRRPASGRRYP CIPAFVGTPAVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWSGLJDRQANPAQVEIIEIRQ L/VRKSPQTAHSPARIWRRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSGKYQRSRRARRPASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQTL SLSDKCRQGTVSGRLSLRKSD TPISHASCSSSSLHGH*VSVAVR LRMTDFSRTVGKDVQRFDAGL GWTLERLLSAHAAFRVALKAG DMAILASRPPTVTPNSMRLLGR LYRSGVVGR

SEQ ID SEQ ID S of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, ^Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29139 59507	A	29314	2	2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWGYDYTGNADN ANYFGKAVPADFNGGSFGRGD SDEWFFGAQMEIWCSYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRCGAKSPFCAIT FRVRWTIRKSTKCANRAYKR NITVGRIRRIRGPLPDATLC VLSGLQTEHNIRRWPNSVCHFSS STFYNDLSGRMKNVRLMFNG HRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVLUGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLLSPESDLYHFERDD FWPPPGDINGREHHLHILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFVILEGESAEDSWMT LRSFLDKDGHPIECRGIPPIKAR HLVRILMPVLJRLRECPVLMRR IRINGTVPNVIVSVLTARQLDF LARGGQARYRLMRRASNEGR SWRYLDINRMIERPETRYTREI GFTSTINIDLYGLPKGTPESSAF TLKRVAELNPDRLSVRVNAHLP TIFAAQRKIKDADLPSPQGKLDI LQETIARLTGSGYGPIGMDHFQ GYTTQGDTDLLGMGVSAISMIGD CYAQNQKELKGYYQQVDEQG YTTQGDTDLLGMGVSAISMIGD CYAQNQKELKGYYQQVDEQG YALDLARDLARDLARDLARDLARDLARDLARDLARDLARDL

SEQ ID	SEQ ID NO:			Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, -possible nucleotide insertion)
				sequence		
29140	59508	A	29315	11	2237	MLTGYRAVSRHKSQRYTADDA
		1		-		EEMIGKLTGMPIPLNSLROWIL
						GLPGDATDYKLDDQYRLSEITY
						SONGKNWKVVYGGYDTKTOP
						AMPANMELTDGGQRIKLKMD
						NWIRADGYHTLQTLFQFLDYG
						DTISIELRDDGDIRLLTPVEGVE
						HEDNLIVRAARLLMKTAADSG
						LSSDGKR/RSSSCARVQSPVSFF
						GNWWMLGQTTRVSPLCHWAI
						SAISHRRAFAQVINIRFKRQTK/
						GDFQFTGAFIGSRQAISHRRFHI
		İ				IDNPERFVIVHFARGTDKPRLLO
						VLCHDKPRINSNAVTAHARAR
				i		LKNINARVTIROANOFPDVNPL
		1				GTNORHFISKSDIHIAEAVFEPS
İ		1		1		IAADRLNPLVNELIIMPDIEKRL
			i			DAFVRIAHEELLYLLGILMNPA
				1		NKDHVLPLILTGPKESADYFRV
						LDEFVVHTLGENARRHYRIIIDI
		l	İ			AAEVARQMKKSMPLVKENRR
						DTGDAYSFNWSMRIAPDLQMF
1	1	l .			1	FEPSHENMANLKLYPDQPVEV
						AADLRRAFSGIVAGNVKEVGIR
						AIEEFGPYKINGDKEIMRRMDD
						LLOGFVAOHPGSYNDLLLMEL
		1				LPHLLVEGMLISAVSAESLPWL
						HLSCVANISKROLICAVPLPKPI
		1		l		KAGLLGKNIMGTGFDFELFVH
		1				GAGRYICGEETALINSLEGRRA
		1				NPRSKPPFPATSGAWGKPTCVN
ļ		1				NVETLCNVPAILANGVEWYQN
20141	50500	<del>  -</del>	20216	1	2892	NVETECHVFAILANGVEWTQN
29141	59509 59510	A A	29316 29317	19	649	
29142	59511	A	29318	2471	3036	KVTWVTCSILPMTLSPSAAFSSI
27143	37311	^	27510	2471	5050	FRMKILSLK**KRILR/SSGKPA
	į.				ł	RQGDMTQYGGSIVQGSAGVRI
						GAPTGVACSVCPGGVTSGHPV
						NPLLGAKVLPGETDIALPGPLP
						ILSRTYSSYRTKTPAPVGSLGPC
1		1				WKMPADIRLQLRDNTLILSDNC
						GRSLYFEHLFPGEDGYSPORVT
					1	VACAPRRGKTG
29144	59512	A	29319	1	1476	THE RESIDENCE OF THE PARTY OF T
29145	59513	A	29320	688	1578	
29146	59514	A	29321	1	1653	
29147	59515	A	29322	1	218	MLIVFSLPSDTLVLSPL*PNFRT
l				1		RPFRPSSVPR**PKKDLKIATSA
		1		1		MMEAAYSSVIANVVLVPVMDA
1				1		KWLAR
29148	59516	Α	29323	3	260	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR
23100	0,50,10	1				WLGHDKRATLLLWKLEAAGSP
		1			1	LRPLSVQVTTPQEVAETDNHAD
		ſ				NSYNAGLFIVNSLYTAEGVMD
						KHSLWQRYVPLVRHEALRLQV
		1				RLPASVELDDLLQAGGIGLLNA
						VERYDALOGTAFTTYAVORIR
		1				GAMLDEL\AAVTGCRAACDAT
		1				RVKWHRQ*GNWSRNLAAKPR
						KLR*RNV
29151	59519	Α	29326	1	2349	
29152	59520	В	29327	1	747	
29153	59521	Α	29328	275	729	
29154	59522	В	29329	1	2469	
29155	59523	Α	29330	1	969	
29156	59524	Α	29331	148	1180	
29157	59525	Α	29332	56	170	VHA*GSLFFPELSMHQDLSQGH
		┸				EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	A	29334	482	765	
29160	59528	В	29335	1	1713	OR OR COLUMN OF THE COLUMN OF
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNTT**A
		1				SAPGN/ARWNSYVG*KHH\SCQ
22112		١.	20002	ļ	3189	WGDYRRQCFRGE
29162	59530	A	29337	1	1344	
29163 29164	59531 59532	В	29338	1	1233	
29164	59533	A	29339	1	1572	
29166	59534	A	29340	1	3591	
29167	59535	A	29341	1	843	MNYSHDNWSAILAHIGKPEELD
29107	39333	^	29342	['	043	TSARNAGALTRRREIRDAATLL
1				•		RLGLAYGPGGMSLREVTAWAO
				ł		LHDVATLSDVALLKRLRNAAD
						WFGILAAQTLAVRAAVTGCTS
ļ			1	1		GKRLRLVDGTAISAP/GGGSAE
1		ŀ				WRLHMGYDPHTF\TDFELTDSR
l		l		1		DAERLDRFAQTADEIRIADRGF
						GSRPECIRSLAFGEADYIVRVH
			ł			WRGLRWLTAEGMRFDMMGFL
						RGLDCEVPDPKRRTNSLWRITK
						MVIWSLQVAIRGTVSLTAYKTQ
		1				LKNARHRLNEAPRRRILQMVQ
		ı				PLS
29168	59536	A	29343	2	3203	
29169	59537	Α	29344	227	634	IKTLPLSPDKLTRISKSIYRKQR
		1		1	1	AALFTHSFTTWVLAILEHRRFF
		1	1	1	1	AK*TRSISKAHVISCVAGHTLA
		1	1	1	1	AAPQPHYFTRETYSPERVSTLM
			1	1	1	TSPICTNSGTLTTAPVDRVAGLP
	1	1	1	I	1	PVPAVSPFRPGSVSTISSSTKFG

SEO ID	IEEO ID NO.	Th.1	SEO ID NO:	INdaeld	IN	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon fur peptide sequence	codon for last amiño acid uf peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29170	59538	A	29345	1	1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29172	59540	Α	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTIGSPGHRGKPGT REDEHGVIELDRRLINFEWWK PEYGINLYQDYYKQDGFVEIPD QNNPSLGDMVIMQIGQNYPVW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGYFHR FAVDSYPEARLALSSQVDGFKE YMQSEIGSRSKFAIFVDGYNVG HHEEKEFKCAKEIRIVPIPTGSK TGGLFQVVLGAAIMVAAFYTG GASLALMGTMSSSLFMMGGA MVLGGWMQMISPQPGWRNFEV QSSKNKPSYAFGGAVNTTGGGI PSPGPWISERRWRNFLSRFLC RGYELKLTRLARVFFRLYNEST
29175	59543	Α	29350	1	8043	
29176	59544	Α	29351	1	876	
29177	59545	Α	29352	2020	2224	CVESRCCHATRCGSK*YSGP\PE DTDLKTEAAGAGVACDAAEAP DEAPPAKLHVLPPIIPEIVLKITI
29178	59546	A	29353	1	2346	
29179	59547	В	29354	50	340	
29180	59548	A	29355	284	520	
29181	59549	Α	29356	2	304	
29182	59550	A	29357	79	177	
29183	59551	A	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHDRHHWH'GNRE NKVNCQLICVDIIINTAQPITSES /DQRQH/TLLRRQTRRDRRHWS HEP
29185	59553	Α	29360	2	388	YTVSFLLVITQLGFCSVYFMFM ADNLQQMVEKA/TRDLQHLPA QGDSDADPHPGHSFLHADNPA LPDPVGVYPEPQGAVRLLDIGQ HHHPWEHGSDL*VYHGGDSIS QQPTLDGKLEDLLAVLWYSHL
29186	59554	Α	29361	467	3014	
29187	59555	Α	29362	1	1174	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \≔possible nucleotide insertion)
29188	59556	A	29363	li -	986	MKVTFEOLKAAFNRVLISRGV
						DSETADACAEMFARTTESGVY
						SHGVNRFPRFIOOLENGDIIPDA
						QPKRITSLGAIEQWDAQRSIGN
						LTAKKMMDRAIELAADHGIGL
				1		VALRNANHWMRGGSNGWOA
		i				AEKGYIGICWTNSIAVMPPWVP
				l	/	KECRIGTNPLIVAIRSTPITMVD
						MSMIKHTLPORAAGTDRKLAM
		l				SREAQLLERHGYAFNELDLGK
		l		1		REPVTEEEKLFVAVCRGEREPV
		l				TEAERVWSKYMTRIKRPKRFH
						TLSGGKPOPGKKIVIRPLPGLPV
1		l				IRDLVVDMGQFYAQYEKIKP/V
		ĺ				PVE*WTKSASSRAFTDARAARK
29189	59557	A	29364	99	375	THOPARRFPAYHYAHPAAAAA
						PGDPLGADLQLCARHYHRORH
						CVPRHAGYPRSDGLHPOPRGR
						WRIRCSDCLRVP\SDRGDAGDY
			ŧ	1		FHL*LADR
29190	59558	Α	29365	871	1206	
29191	59559	Λ	29366	1784	1966	RPLDVSFMSSFTSNSPLTDLVG
l						YLTFSAIFLSWRLSLLSDAA*TP
						YPPWGSVHCRRFCSL
29192	59560	Α	29367	I	1276	FHIKLVLTGATWTALPYCHSHV
						GLRASLKPTPPFWGRAPLGTRP
l						SQQKTECRLINFPETPIFGNSFK
			ŀ			YDIEVSNKSPDEEVKLRRHHLA
						RCMKNFKTDIYFVSTFEPSTKS
						VDLLTVETFAGTVCEYADMPK
		1				EWTTTRGLYDPTHLISASCHKV
		1		l		EGLFSFEDRTVATLIRLFIHPVK
		l		i		SMRGIGLTHALADVSGLAFDRI
	1	l				FMITEPDGADIAVKTFTGIRLKV
		l				PCPPDHPAFSITNHQTEVTALV
		l				VFECDIAVRGSDRLRLSPGPGG
		l				SNTDWVIFGLLIKENPGSLLAV
	1		l			GVNLLGKILLSVVAAVSESGQN
						FLSVLPVRSEGPCFVVIDVDVEL
	1	ĺ	1			PGLRDIADEVKTGVIAVTPAVIP
		ĺ	ŀ			ALWEAEVDVNIAAFRSQKAYIS
	1	ĺ				GQVNKSGQQAITN/DATDYSRG
		ĺ	1	l	I	HQKLPCLQSECFHGIYHRIDVA

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Aminn acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletinn, \=possible nucleotide insertion)
				sequence		
		<u> </u>		ļ		
29193	59561	Α	29368	1	1815	STLEDPHÝYHIAEVSPVVIIISIY
						GATGEKYGFITYRCSEHAALSL
		1				TKGAALRKRNEPSFQLSYGGLF
						HFCWPRYTDYGYFELQINRLAI
		1				FSTNVTAETPYMHLAPPVGTQL
		1			ĺ	PLPHLSHDNSSKNSGGCLPGAS
		1			l	VSCNYREPA VRLALASTLPLLR
		l			ĺ	AQSPFFMHKDKDPLFWFLTVPF
		l			i	KWFRKGEVILSSRPRKKTEGSW
		l			l	FPKTFFGFGKSHVLVKEFYNRK
		l				HHIAKQQHAVERT\RELFCPKG
		l				LG\YSKPQTQGDYAIAQHF/L*T
						NLPTGCWAKYAVISFMRTD/TV
						DDKH\WPEEHLAKN*LGLLADS
		1			0	G\IR\IKLPWGAPHEEERAKRLA
						EGFAYVEVLPKMSLEGVARVL
						AGAKFVVSVDTGLSHLTAALD
		ŀ				RPNITVYGPTDPGLIGGAPENG
						DSDSALYRLRKEMEEFHLVVG
						SDIFGKHOHGTETDSTTCPSTLE
	ŀ					EFETQWFITGGINRILLATDGDF
		1				NVGIDDPKSIESMVKKQRESGV
		1				TLSTFGVGNSNYNEAMMVRIA
						DVGNGNYSYIDTLSEAQKVLNS
						EMRQMLITVAKDVKAQIEFNP
		1				AWVTEYRQIGYEKRQLRVEHF
		1				NNDNVDAGDIGAGKHITLLFEL
29194	50550		29369	2	1000	TLNGQKASIDKLRYAPG
29194	59562 59563	A	29369	3	1993 1782	
29195	59564	A	29370	Ī	3858	
29196	59565	A	29371	ī	705	
29197	59566	A	29373	104	471	LWWAGA/SYLCWMGYOMLRG
25150	33300	^	29313	104	J*/1	ALKKEAVSAPAPQVELPKSGRS
		1				FLEAIIYFGSVFSLFVGDNVGTT
		1				
1		l				ARWGIFALIIVETLAWFTVVAS
						LFALPQMRRGYQRLAKWIDGF
20100	60667		20274	60	(20	AGALFAGFGIHLIISR
29199 29200	59567 59568	A	29374	194	620	I DOWN COLVI ON A COVEY COL
29200	39368	Α	29373	1194	767	LWW/AGGLYLCWMGYQMLRG
						ALKKEAVSAPAPQVELAKSGRS
			l			FLKGLLTNLANPKAIIYFGSVFS
						LFVGDNVGTTARWGIFALIIVE
1		1				TLAWFTVVASLFALPQMRRGY
						QRLAKWIDGFAGALFAGFGIHL
						IISRLALIVPGLLQKNGGWRRM
				1		AIISAVIALVCHAIALEARILPDG
						DSGQNLSLLNVGSLVS
29201	59569	Α	29376	1	1038	
29202	59570	Α	29377	1	513	
29203	59571	Α	29378	485	1166	

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29204	59572	В	29379	54	275	
29204	59573	A	29380	2	215	IFLLLLPPHHLLLLLLLLLLLLLL
2,203	37373	ľ.	27500	l <sup>2</sup>	15	LLLLLLQ/MIPLEFCRLYRKQG
						CICFWGSLGEILLMAEGEAGAS
						PSH
29206	59574	ΙΛ.	29381	100	393	FLULLLULLLULLULLULLULLULLULLULLULLULLULL
				1		LFSSSFLLLSSSFFFFL\SSFSFSSF
,		l				SFSSSPSSPSPSPSFFLLSSSFFGV
			1	1		ISLDVVTLAWQSARITGVSHRT
29207	59575	Α	29382	264	911	ILGFLRDGNFWRKSQSFFPVHH
		1				LLICLLRKSSETMQLTDEHLIHD
		ſ				HPKRPPITELVVPGLHEHLRSN
						VGDYRCEPPHLTKRNIFCILSEA
		1				TDITY*LTSISFPGFCFRLT*LLPI
1		1				TEITGEAVVQIPIKFCPMCFFQS
1		1				CAKIWTRGMQWHLEAWRCQK
		ļ.				PQSPKGGVTALAQEAPKSGLLE
		i i				GQFMPMPPQYLAVQKKVVWF
		<u> </u>				DVSVDESKLVNRVYG
29208	59576	Α	29383	1	261	
29209	59577	Α	29384	3	195	L DDL O L DOVOL L ODOL OOL OL OO
29210	59578	Α	29385	1	399	LERLSAPCISLLLSRSLSSLSLSS
		1				LLFFFFFFLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL
		1				LL/SPPPLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL
	1	1				PSRGYHPRDTIQGAPSRGHHPG
	1	1				DTIOGVPSRGYHPGGTIOGAP
29211	59579	A	29386	15	159	SPLHLSLV*VKQLLLLLLLLLLL
29211	39319	l^	29360	1,2	137	LLLLLLLLLLLLLLLLLLLLLLLL
		1				LLLLLSSSSFLPS
29212	59580	A	29387	17	429	SFFFFFFFFFFFFFFFFFFFFFFFFFF
				I		LLLLLLPLLLLLHRKHLICVTLG
		1				CLRWLGQLCVRLQGSCAWLQT
i		1				LGWVHTYACVCTFFLDQQVAG
	1	1				RILLVEDPRSSLLQCCLLLDA\P
		1				LCCRFQKNMHFIRT*R*VHC\$GI
		1				TSIQFNLEP
29213	59581	Α	29388	3	282	RELLRGGNVYIGP*SILSFFLLLL
		1				LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL
		1				LLLLVN*GVCCTLLSGPEISCRS
		<u> </u>				DFAQGPTPLQGAPQTALGNLAS
29214	59582	Α	29389	3	264	
29215	59583	Α	29390	296	421	
29216	59584	Α	29391	3	210	
29217	59585	A	29392	1	252	
29218	59586	A	29393	1.	1731	NI CTA ATI PEI PEPPPPPPPPPP
29219	59587	Α	29394	1102	1362	NLGTAATLFFLFFFFFFFFFFFFFF
	1	1	1	1		FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
1	1					L/VPLLLLLLLLLLLSSSSCSSP PPSSSSLEKLYLSI
29220	59588	A	29395	3	2368	FF0000LENLTLOI
29220	27200	lv.	47373	2	2300	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29221	59589	Λ	29396		318	MEKKSPA YFCCRDMQVIHSDA ALORILTERFINDFEGWSNLAKN QYLSTSMKQKIWQRALSHIKN NPKADSDAYETSADMILSELIS HGEVDDQMILNATALIRSDDW DFLESALISWDNLPAVVLKELQ QVTFRNDIWAKFFLRQENSSRA QVDEALRYYYALDPDALAQLD YLAKRPYKTAAFRGEKTHRVP RSVRQNIDQADRLHGAQRLV INTNRTRVVDQLIEFLHHQHVN AHLAEIVRHIQPNRAGTSDRHL NAMVNSRLDVRNNEQTEYRHT RGLTRGIMLLMMLNKLDSTSP CRMLVCCVPRAPPNPGGLNPR AHSLNRSP*PPLKLLSPTGPEG
						MRPLGTHFWGGIGHGQGPEWG PQFGLGMNLLVKSLGHWATW VLARAKILRFELGASMMVAST
29222	59590	А	29397	2	4002	WQE-VHYIWGVMHGDLGISMK SRIPVWEEFVPRFQATLELGVC AMIFATAVGIPVGVLAAVKRGS IFDHTAVGLALTGYSMPIFWW GMMLIMLVSVHWNLTPVSGRV SDMVFLDDSNPVTGFMLIDTAI WGF/DHGTFMGAAPIRILPAYG LCTIPVAGFGRMTRSSMLEVLG EDYIRTARAKGLTRMRVIIVHA LRNAMLPVVTVIGLGVGTLLA GALTETIESVPGLGRWLIDALQ RRDYPVVQGGVLLVAT
29223	59591	Α	29398	187	1710	
29224 29225	59592 59593	A	29399 29400	353	791 646	FYWNWVPFTNWQNPRLMGQK *HARWLHLRSLLPAM*ATLL*R ENNR*LLLLTLTSIFKTFRIRRLS VSKP*VKAKKKTRLIIWSTSKFL SCMMLKFT
29226	59594	Α	29401	406	1023	
29227	59595	Α	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLLIEKMRES GDIHSHHGWLHLPDHKAGFSE EQQAIWQKAEPLFGDEPWWVR DSPGYFALMVRAKFNNCVIVFR R*AQQRHRYTDVVVEIACRIKR VAALA
29229	59597	Α	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	A	29406	1973	2582	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or pepude sequence	deterion, (possible nacicolide insertion)
				L'		
29232	59600	Α	29407	1	1483	MFVLADFGHTRRTNRSLGHNIL
						PARIAPDAINKWLSGFFSREVQ
		l				LRWVGPQMTRRVKRHNTVPLS
						FADGYPYLLANEASLRDLQQR
						CPASVKMEQFRPNLVVSGASA
		1				WEEDRWKVIRIGDVVFDVVKP
						CSRCIFTTVSPEKGQKHPAGEPL
ŀ	ľ	1				KTLQSFRTAQDNGGGEGEARA
		l	l			ANTGATHRGRHRSPSAVRYRD
İ		ı				RLNMYVLRRMDLLYRVKTLW
		l				AALRGNHYTWPAIDITLPGNRH
						FHLIGSIHMGSHDMAPLPTRLL
ļ		l				KKLKNADALIVEADVSTSDTPF
l						ANLPACEALEERISEEQLQNLQ
1			1			HISQEMGISPSLFSTQPLWQIAM
						VLQATQAQKLGLRAEYGIDYQ
						LLQAAKQQHKPVIELEGAENQI
		1				AMLLQLPDKGLALLDDTLTHW
		1				HTNARLLQQM\RAGGWSVKEG
		1				REKEYFQSPRGWGRSLMPSLGI
l		1				IIRPP*RKPKNTENRRCISASVTS
		l				EKEAPETINQYKAAVRRPFLFL
						ATALAQSEVRVCIAWTN
29233	59601	A	29408	2	1406	
29234	59602	A	29409	1	1818	CHANDEN MESCA CHODOLLA
29235	59603	Α	29410	44I	583	GVYRFPWRFSSAGYGRSGLLV
						QVEPRLDA*HPGLHEARPGLSS VSSR
29236	59604	Α	29411	835	1143	RQLPVSLYVRAVAFENGCFGSC
						SVGG*GPPAARLGEEQVRGGSS
		1				SPCIIRAPRRLHSFLLLLLLLLL
		l				LLLLLLLLLLFHLSSSSSFSST
						SSSSCSRSFM
29237	59605	Α	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	Α	29414	1002	1145	GVYRFPWRFSSAGYGRSGLLV
		l				QVEPRLDA*HPGLHEARPGLSS
						VSSR
29240	59608	Α	29415	2	289	
29241	59609	A	29416	1	919	
29242	59610	A	29417	329	405	
29243	59611	Α	29418	48	268	
29244	59612	A	29419	2	4625	
29245	59613	A	29420	1	867	
29246	59614	A	29421	1	684	
29247	59615	Α	29422	409	543	
29248	59616	Α	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	Α	29425	3	202	
29251	59619	Α	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH
i	I	1	l			S

SEQ ID	SEO ID NO	Me	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		_				
29252	59620	Α	29427	1	1774	
29253	59621	Α	29428	3	184	MSENMRCLVFCPCDTLLRMMV
			1			SSFIHVPPKDMMSIFSICLSAASI
					1	SSL*ASVCSYPSLNF
29254	59622	Α	29429	667	834	
29255	59623	Α	29430	1	738	
29256	59624	Α	29431	39	230	QMAQHLPHLVFGSHSGSLWEL
						LSH*VYLLILSLPPPHTPQQAPV
						WDVPLPVSKCSHCSIPTYK
29257	59625	Α	29432	985	1205	IPGSRGKNWVVTGTGQGCHRG
		1				PAESDGPAG\GARHWEQPPA*Y
		1			l	LVLFLCSQRRWPGRQQRGQSG
	1	1				RSWPSVRAAP
29258	59626	Ā	29433	339	592	PLQAWGPSLCS*AIGTPSRKPSP
27230	39020	l^	27433		J	STAHVKHRRLCIPTRRGFSSDN
i			i			WDPVSSPTCNDAROLHAOVDL
						EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFOLHPCPFFOGS*LLCI
29259	39627	I <sup>A</sup>	29434	633	894	
l	1	1				GLAHAPLAQRSLLLSTF*CLLLS
						IHQTHSPSSFCPLLARSCDPLEE
		$\vdash$				KRHSGFRNFQPFCSGFSS
29260	59628	Α	29435	517	603	
29261	59629	С	29436	1	1188	
29262	59630	A	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIISEGSVLFHWSISLFWYQ
		1				YHAVLVTVVL*YSLKSGSVMPF
		1		1		ALFFWLRIDSAMRALFWFHMN
						FKVVFSNSVKKVIGSLMGMAL
29264	59632	A	29439	1	1308	
29265	59633	Α	29440	162	377	YSHCSIYTRKIQFLCCPSIKTHL
		1				GTNLTS*TFFT*VNIISIYLEASLF
		1				FSFLDLGRADKGSSLTGVRSIIT
29266	59634	Α	29441	1	480	
29267	59635	A	29442	731	850	
29268	59636	Α	29443	531	845	
29269	59637	Α	29444	11	649	
29270	59638	A	29445	1	2433	
29271	59639	A	29446	1247	2420	
29272	59640	A	29447	29	94	
29273	59641	A	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGGRRSSTSGKGTAGCPOSPCF
	370.2		25115	3703	1205	CRCSTLRRTAASPGISPPCPKICS
	1					CSPLESIWMSNGLCRSCPPSEDS
	i					
		1		1		TCGC*GCCCCCCCCCCCCR RRCPSLGSDAGTELETORPGAG
		1				TGPGPTVAPATFLQSRRLMVGA
		1				GTPTLGVRTPGFGLQLGFFYWL
						EDVERDTS
29275	59643	Α	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
29278	59646	A	29453	1	599	
29279	59647	Α	29454	1	504	MWNCLTNKLLFQESLQKTATR
						LSAFSWEEAKVQLSWVVLNLA
		1				TSAMLPKFYPNEIKVTYLRCTG
		1				DEVGATSVLAPKISPLGLSS/VK
		1				ALKEPPRARKKQKTIKHSG\NIT
						FDEIVNVAQHMWHRSLARELS
						GIIKEILGTPQSVGCNVDGCHPH
	10000	١			10/0	DIIDDINGGAVECPAN
29280	59648	A	29455	434	1269	PFSSPASSSGR*KTTSFPAKLFN
29281	59649	l <sup>A</sup>	29456	434	633	ACRISLLASAEVNPNISAYLAT
		1				WISOIPSCSCRVPSDFLIWSTNR
		1				YSIRF
29282	59650	A	29457	1	801	13110
29283	59651	A	29458	2	722	GRVGGGGGGANYLRVVPESGV
	5,001	1.	27.50	Ĩ		YSTPSRLPPLPPKVRPPTRFKSV
		ĺ		i		YLEVAPKGE\VGA\TSALGPORI
		1				GP\LGPVSKKKLG\DDISKA\TG\
	1	1				DWKGP*GITVKLT\IONRQAQD
						*GGCLSASALIIKALK\EPPRDR
		1		1		KKQKNIKHSGNITFDEIVNI\AR
				1		QM\RHRSL\ARETLWNHLKRSL
						GTAQSVGCNVDGRHPHDIIDDI
						NSGAVECPAVSDIFIVTVGVKG
						GPPSVFTEISWEVLEMVTGGVG
29284	59652	Α	29459	1	330	
29285	59653	Α	29460	140	214	
29286	59654	С	29461	181	381 957	
29287	59655 59656	A	29462	427	241	WLRAERAPEGSPETKGS\PPPPP
29288	39636	A	29463	3	241	RSVLHLSA\SSPGLRPPEGL*TC
1		1				RGSPSADSPRRGKHGGKTTHLV
1		i i				SWLSOOKIPMAR
29289	59657	A	29464	122	473	a To farm were
29290	59658	Ā	29465	1	771	
29291	59659	В	29466	1	1017	
29292	59660	В	29467	1	2568	
29293	59661	Α	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I
						SQ*PQQRYECRDNQQPLDQL/V/
		1		1	1	EQFIQTLEKAITQHRQQLNQWT
		_				QKVDIARRR
29294	59662	A	29469	1343	1714	
29295	59663	Α	29470	321	2645	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amine acid	*=Stup codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29296	59664	A	29471	611	I215	RWCVWSLFLQML/EMCPEFLPS
						GGFVVSLTSGVKLQTFTVNVTA
	l	1				HKGSVDPKRVKLKTLAVSVTA
	1	ì				LKAACLELFLLPGGFVVFAGFR
					1	SEAADLCAEGASSGLGQPREGL
		1				PRCSGGLKGSSSAARMGAEAK
					1	GAPRASQGCEGRHHAVTSHRS
		1		l	1	DMGEEEGESQRYLSCPQPSCPI
		1				NLLQEDASKVIVFAESGINPDSV
		l				LDLIMLH
29297	59665	Α	29472	335	453	KYIWNVNLQHSVSMLL*FITS*L
						SGMDSLFPAAHCV
29298	59666	Α	29473	1	1041	
29299	59667	A	29474	3	874	TEGQKNLIVEVTSNDAVRFYP
	ì					WTIDNKYYSADINLCVVPNKFL
						VTAEIAESVQAFVVYFDSTQKS
				1		GLDSVSSWLPLAKAWLPEVMI
						LVCDRVSEDGINRQKAQEWCI
		1				KHGFELVELSPEELPEEDDDFPE
					ł	STGVKRIVQALNANVWSNVVM
				1		KNDRNQGFSLLNSLTGTNHSIG
	ļ					SADPCHPEQPHLPAADSTESLS
						DHRGGASNTTDAQVDSIVDPM
						LDLDIQELASLTTGGGDVENFE
ŀ						RLF\SKLKEMRDKAATLPHEQR
		1				KVHAEKVAKAFWMAIGGDRD
		_				EIEGLSSDEEH
29300	59668	Α	29475	1	1773	
29301	59669	Α	29476	1	1023	
29302	59670	Α	29477	2	616	
29303	59671	Α	29478	1	972	
29304	59672	Α	29479	1	339	
29305	59673	A	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG
l					1	EGTYGTVFKAKNRETHEIVALK
						RVRLDDDDEGVPSSALREICLL
1					1	KELKHKNIVRCAGGGCSLPVW
						PLGGGGG*HWTSVRRTCLAEPF
					I	FCPRLHDVLHSDKKLTLVFEFC
						DQVKGGVWRTVALGR
29306	59674	A	29481	1	843	
29307	59675	Α	29482	1	873	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
29308	59676	Α	29483	13	945	NRGPAGVPAAAAMOKYEKLE
						KIGEGTYGTVFKAKNRETHEIV
					İ	ALKRVRLDDDDEGVP\SSALREI
						CLLKELKHKNIVRLHDVLHSDK
			l	1		KLTLVFEFCDQDLKKYFDSCNG
				ł		DLDPEI\VKSFLFQLLKGLG\FCH
				İ		SRNVLHRDLEAPATWLINREW
			ŀ		1	GSWKLG\DFGPGVRAFWGFPV\
		l				RCYSAEV/VSHLW\YRSPDV\LF
		l	İ			GAKLYSTSIDMWSAGCIFAELA
			İ			NAGRPLFPGNDVDDQLKRIFRL
						LGTPTEEQRPSMTKLPDYKPYP
						MYPATTSLVNVVPKLNATGRD
			l	ŀ		LLQNLLKCNPVQRISAEEALQH
						PYFSDFCPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV
						FGKVKEGMNIVEAMERFG\$RN
						GKTSKKITIADCGQLE
29310	59678	Α	29485	3	1225	
29311	59679	Α	29486	1	864	
29312	59680	Α	29487	I	1413	MVNPVFFDITVDGEPLGRISFEL
						FADKVPKTTENFRALSTGQKGF
						GCKSSCFHRIIPGFMY/QGGDFT
						RHNGTGGKSI\HGEKFDDENFIL
						KHTGPGTLSMAIAGPNTKGSQL
				1		FIYTAKSEWLDGKHVVFGKLSR
						GDSLKEPTSIAESSRHPSYRSEP
						SLEPESFRSPTFGKSFHFDPLSSG
		l				SRSSSLKSAQGTGFELGQLQSIR
		[				SEGTTSTSYKSLANQTRNGSLS
						YDSLLTPSDSPDFESVQAGPEPD
}		l				PPLGYTSPFLSARLAQQREAER
		1				HPRLVPTGPTHREPSPVRYDNL
						SRHIVASLQEREKLLRQSPPLPG
						REEEPGLGDSGIQSTPGSGHAPR
						TSSSSDDSKRSPLGKTPLGRPAV
						PRFGKPDGLRGRGVGSPEPGPT
	1					APYLGRSMSYSSQKAQPGVSET
						EEVALQPLLTPKDEVQLKTTYS
						KSNGQPKSLGSASPGPGQPPLSS
29313	59681	<u> </u>	29488	1	3126	PTRGGVKKVSGVGGTTYEISV
29313	59682	A B	29488	46	114	
29314	J708Z	В.	27489	40	114	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nocleotide	Nocleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	coden for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29315	59683	Α	29490	I	704	AALLALGPRNPWILWTPLTPN
1		ı				YPDRQPWTDKHPDLLTCGRCL
		1				QTFPLEAITAFMDHKKLGCQLF
l		ı				RGPSRGQGSEREELKALSCLRC
ł		ı				GKQFTVAWKLLRHAQWDHGL
		l				SIYQTE\QRPRRPRSWAWPRWL
		l				QPCRQWWGQQLRPRAPV/HSG
		l				SGLTRRSPTCPVCKKTLSSFSNL
		1				KVHMRSHTGERPYACDQCPYA
		ĺ				CAQSSKLNRHKKTHRQVPPQSP
		1				LMADTSQEQASAAPPEPAVHA
29316	59684	Α	29491	3	1605	
29317	59685	Α	29492	1	453	
29318	59686	Α	29493	2	128	
29319	59687	A	29494	1	543	
29320	59688	Α	29495	39	1092	
29321	59689	Α	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/
ļ						TLRPKAL*LTPSQIFSA*RLKTD
						TARSPRKPPSFQGPVSLASITVV
					ŀ	GIDGQASKPLKTPQLWCQLRQ
						YSFK
29322	59690	Α	29497	1	281	VSDHAGTPALVLHP*RQVPLF*
						GRGKYPSTPSPSPLAELATSAR
						NLTTRPRNACSPGFLPSRVPSVR
					ĺ	DPTGNRTVQLTWQPLPEPLEL
						WPKAL
29323	59691	A	29498	1	542	MRAPPKSGQLQHCRPSRGALRS
		l		l		GDLPWEINPLSSCSLLHEKDPP
			l			MTSGPQTNQPKEHLTNFKSGV
						RP/LQGRLPWSFTLSGKSRFSGE
						GASTPTPYIS/GAPIPYFRTPTSY
						LCAPIPYVRTPTSYLCALTPFPL
						FWRHIRTSKRLN/LQQPGIPPEPP
						PPG/CLLQVPEI*PPGQGMPAAQ
29324	59692	Α	29499	1	1044	
29325	59693	Α	29500	596	833	LLLDLPAED*CCLIASEAP*TITD
			1			AEL*VTLTVEGKSVPFLINTEAT
						HSTLPSFQGPVSLASITVVGIDG
	L					QASKPLKNE

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSPLFPRPDLLS
2,020		ļ'.		1.000	1	LWPNPLFLHPNLLYLCAPIPYFI
						APTSYLCTPTPYFHDPTPFPLFW
		1				KELATCAGNLATGTRNAGSPG
						FLLSRVPSVWDPTENRTVQLT
						WQPLPEPLELWPKA/HLTDSFP
		1				DLLGLAA\ED*HCTIASEAP*TI\
						TDAELWVTL\TVEGKPFPFLINT
						EATHSTLPFFQ\GPVSLASIT\VV
						GIDG\QA\SKPLKTPQ\LWCQH*
		1				TIRRFKHSFLVIP\TCQVPLLG\E
		1		1	1	DTLTKLSASLTIPGLQLYLIAAL
		1				LPNPKPPLRPPLVSPDLNPQV*D
		1				IGVEWGKGD
29327	59695	A	29502	6958	7935	IGVEWORGD
29328	59696	Ā	29503	1	486	
29329	59697	A	29504	1	492	
29330	59698	A	29505	2	502	RRAHACARRRRKKEMLGVNVI
		1	2,000	1		TSHSSOERMKLTFKKKAVNFA
						DAAAAOGPLLPAMVNPTMFFH
		1				IAVDGEPLGCVSFEVRGLESKK
		1			i	*LLI*SIKLC*QIG\LFADKVPKT
					1	AENFHALSTGEKGFGYKGSCFF
			l	ì		RIIPGFMCQGGDFTRHNGTGGK
						TSKKITIADCGOLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFFDIAVDGEF
						LGRVSFEVRGLDTKK*LLI*SIK
		1				LC*QIG\LFADKV\PKPAENFR/A
		ı				L*SIEEKGFGL*GVPCFHR\IIPGF
		1				YVSRGGDFTPP*MAPGGOVHL
		1				MGKKFER*RTSSLKHTG\PGHL
		1				VPWANAWTQTQMGSQFFICTA
	į	1			i	\KT\EWLDGK\HVVVLAKVKER
		1				HEILWEAM\ERFWVPGNGKT\S
		1				KKIISIADCGQLLISFDLCFYLNF
						QDHSLLCSPLRESTPLPHLLAGS
29332	59700	Α	29507	1	380	LCCSPCRRRLLGREEAGEEPTSP
						VTQYLQPRSPEECKMFACAKL
			İ			ACTPSLIRAGSRVAYRPISASVL
						SRPEASRTG/EGAATVGVAGSG
						AGIGTVFGSLIIGYARNPSLKQQ
						LFSYAILGFALSEAMG
29333	59701	Α	29508	76	385	EEPTSPVTQYLQPRSPEECKML
			İ		ĺ	ACAKLACTPSLIRAGSRVAYTP
		1				TSASVLSRPEASRTGEGSTAFN
		1				GAQNGALHL\IQRELHTSAIRRD
						IDTWCKFIGCSAATE
29334	59702	Α	29509	2	230	
29335	59703	Α	29510	242	427	SAPDLTCNSKTWKNGRIICFHP
ı		1		1		ASLVSLY*QPQLASWTMKKQD
	1	I	l		1	ENTQEGKSWDSFSRDVIHI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first eodon for peptide sequence	codon for last amino aeid of peptide sequenee	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<u> </u>				
29336	59704	Α	29511	1	1497	
29337	59705	Α	29512	199	766	EEPTSSCHPNISSRAVPEECKMF
1		1		İ		ACAKLAMRPPSLIRAGSRV\AY
		1		I		RPIS\ASVVISTQRLSRTG\EGST
		1		l		GI*MGPQNGVS\QLIPKGSFQTS
		l		1		CNQAGGHLITGCQIYLGAGCLQ Q*GVGWFLVAGIGNSLLGKPYP
		1		1		LGYGQKTLSPESQQLVPP*CYP
		1	1	ŀ		GDFALALKLKAMGL\FC\LMVA
						FLILFADVTEITA
29338	59706	A	29513	427	840	TELETABVIETA
29339	59707	A	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ*DGTLLC\RR
						CGS*GLPTFKKSTCGKCGYPAK
ļ		1				RKRKYNWSAKAKRR\NTFGTG
[			1			RMRHLKIVYRRFRHGFREGTTP
						KPKRAAVAASSSS
29341	59709	Α	29516	1	668	
29342	59710	Α	29517	649	992	
29343	59711	Α	29518	1	2994	
29344	59712	Α	29519	3	486	
29345	59713	Α	29520	2	898	NSRVDDFVCPRSRRSKRDLIEFS
						CRIILFPLPSLPPRISFHPSPTLAR
						VRIGGAVRRPHQSHSISSSSFGA
						EPSAPGGGG\SPGSLPRPWGPKS
						CSSSLCGARS*FFWRDVKN\TGL
		1				VFG\TTLIMLLSLGSFSVSSVVV
	ŀ	1				S\YLILGFSSSVHHQLSGI*QSSVI PSCNRKFRKKGHPFOKPNWNV
l		i .				DITLSSKSFSINNMNAAMVHIN
		1				RALKLIIRLFLVEDLVDSLKLAV
			1			FMWLMTYVGAVFNGITLLILAE
		1				LLIFSVPIVYEKYKTQIDHYVGI
l						ARDQTKSIVEKIQAKLPGIAKK
				1		KAE
29346	59714	A	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGFFFTQVANIIS
						VAWNLVFCIRFLENTVGIVTI*R
						RCPIPFSWAF
29348	59716	A	29523	I	4368	MLFSYLEKYFYVADELSHCVEP
		1				EPSQVPGGSSRDRQQGKPPPLP
ŀ		[				ALKAKTSSRSGPYATEIKKSTD
ľ		l				DSIFK VLD WFNRSSYSDDNK/LI
ŀ		1				PPTSPRNRVQRKNR\PKSQVAV
		l				DLVTDDTTLRENGSKTLSPSKIE
						LKPVRSDSPFQAEGDMLVSESC
	i	1				QDNNVNIKSKFMNLSQKGTPK
		1				EGPGILQPFESYGTPSQGSKNM
		l				DYSQDSKSPGKGNGASPSNSNY
1		l				SYSVLKESDAENQVPCNTNNIG
L		1		_	I	NLGEEEPKFHAH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
_	sequence		09/540,217	sequence	or peptide sequence	deterion, =possible nucleotide insertion)
29349	59717	۸	29524	33	3339	TDQAKVDNQPEKLVRSAEDVS TVPTOPDNPFSHPDKLKRMSKS
						VPAFLODESDDRETDTASESSY
						OLSRHKKSPSSLTNLSSSSGMTS
						LSSVSGSVMSVYSGDFGNLEVK
						GNIOFAIEYVESLKELHVFGAP
						VEGLNSSGWKKTGVIPY*KG\Y
						LLPNKGOMGKKKTLVVKKTLN
						PVYNEILRYKIEKQIL*TQKLNL
		1				SIWHRDTFKRNSFLGEVELDLE
						TWDWDNKQNKQLRWYPLKRK
						AKALQRFQLKAMGNS
29350	59718	Α	29525	946	1183	
29351	59719	Α	29526	2048	3359	
29352	59720	В	29527	I	300	
29353	59721	A	29528	1	1495	
29354	59722	Ā	29529	I	2769	
29355 29356	59723 59724	A	29530 29531	450	3061 1464	
29356	59725	A	29531	238	930	RLSLVSSHCGTILSSEVVCAPPT
29337	39723	A	29332	236	930	AYIDFARQKLDPKIAVAAQNCY
						KVTNVAFTGEISPGMIKDCG/AT
						WVVLGHSERRHVFGESDELIGO
ŀ						KVAHALAEGLRE*FACIG\EKL
						DER\EAGHI*GRLFFEOTKVIAD
						NVKD\WSKVVL\AYEPLLAIGT
						CKTSTPQQAQEVHEKL\RGWLK
		ł		i		SNVSDAVAOSTRIIYGG\SVTGA
		1				TCKELASQP\DVDGF\LVGGASL
		1				KPEFV\DI\INAKQ
29358	59726	Α	29533	1	929	
29359	59727	Α	29534	3	623	
29360	59728	Α	29535	3	202	
29361	59729	A	29536	1	1046	
29362	59730	A	29537	1	1320	
29363	59731 59732	A	29538	922	1052	NDOLCNEEK OF OH OVER ALLA
29304	39/32	l <sup>A</sup>	29539	922	1243	NRCLGNSFKCFLCILQVGRAHA FLLCSDFMPCEAVCSSIIYSFIPV
		l	l			TKTOGAAPHTR\AHSLTPDPKPS
1		1				CCCCCPRPGEDPGHMCVVWP
			İ			WOPSVIYAKYWTYEHAOW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS
29303	37733	<u> </u> ^	27340	ľ	150	GHYALQEAQETSQSGRESQA
29366	59734	A	29541	1364	1916	31112421421424
29367	59735	Ā	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ
						PWAMIIDVFS\RYSGS\EGSTSDP
			1	1		*PKGE\LKVLMDKELPRLSLQS
			1	I		GKDKDAVDKL\LKDPGRPMGD
	1		1	I		AQGGTFSEVHPCSVAAIT\SA\C
			1	1		HKYF\EKAGLKLMPWEMFTDF
I	1	1		j		LGQSIGSQGFPKMFCLGIYFP

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclentide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=pussible nucleotide insertion)
		<u> </u>				
29368	59736	A	29544	175	355	FSQQLLGQAD**SFLL\GCSRLL
						TAVSRPKRPGEAGITPRVRCLLS NMKDILVASKFWQL
29369	59737	A	29545	482	1196	MINDLEVASKI WQE
29370	59738	A	29546	196	818	
29371	59739	Α	29547	170	370	
29372	59740	В	29548	147	257	
29373	59741	Α	29549	1	1278	
29374	59742	Α	29550	2	152	
29375	59743	Α	29551	2	187	
29376	59744	A	29553	1	915	
29377	59745	Α	29554	62	430	RQQDELALIAETLKCVDH*LSL
						DVLPRGCA*HRELCIHDLLKGN
		ŀ				PLRRNILAG*TQERMQLQVESQ
		ŀ				SIPEEILGLQPQLGPMGGLWNV
		1		1		RFLLIPTVLWGFHCSQERAFPR
						KLQVKSFPVAQG
29378	59746	Α	29555	149	381	
29379	59747	Α	29556	1	656	
29380	59748	В	29557	146	1320	
29381	59749	Α	29558	629	1417	WCASHWGSGHAARHA*ASHPL
		1				HGLLCSPSLPEEHHPLLHGAQS
		1	1			HRPPKG*GM*AHGTGLAGSSTC
		1				SPAQGL*IHQSAPCV*LKVCECT
l		ı			ŀ	NRHSVSSCSDEDVCICSLCLGQ*
		ı				GP/ECI*CRIFLGPFNRLIEGAPH
		1		1		L/CRSAMLNPLQEGAREQASAR
		1				SGWLLRLLTQEQLLCRACIQTR
		1				RDREGKTRHRKGTPEIGKGRAF
		1				WKKSLKIILILFNCLRYWNAYM
	1	1				EIWVPALTGIPPNVTVNYATSSS
		<u>_</u>				KDSRTDGRVDLLMAVTDGM
29382	59750	A	29559	318	608	ISQARRAAPWGPVQPEPSR*APP
		1				PASGHPVPSTTQRLRSAGARRG
		1	i			TGGQLHLQPRCGDPLGETSWA
		1				PESRRSAASLLKPARPRAHWEE
		↓_				QTTPDALL
29383	59751	A	29560	88	564	SCLPVLRRALAFLSPWVVDGTG
		1			1	RRGAAGGGRWGGSGRTGAHG
	1	1				VGGRLRHGGLQVPSPALQEGS*
		1		1		GSVRNRAQ\PGGLALLGDPVHP
		1		ŀ		LQPLARVLSPSLPG/DQQGWPA
		1		1	1	APSVGPTKPTPTRNSSWPPSAA
		ı		1		HSPGSCSCLSLHTSLESCRCPSIN
		_	L			TSLHKHA
29384	59752	Α	29561	3	339	RYKDSPRPHQTQEPSWLHLVDP
		1				APRLQVELPASPALCARIPQPLG
		1				G\HGTGRRGQGAALVGEARAG
		1				LPSLPSFFFSFLLSFLSFFLPSFPL
			L			FFSLFFPFCPVNCGEQCPIGKM

SEQID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	s <b>c</b> quenc <b>c</b>	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
29385	59753	A	29562	327	890	VMRIOVLLYYLRFADOGTGFH
27363	37733	ı^	27302	327	10,00	LVLCLRHTAGVO*SWDS*SGLT
						PELV/HLDGSHV/LAASPRGSPG/
	İ		İ			SPK*MGADORSSESSPGPOPGG
		1	ŀ		İ	PRAEGPHHIQEAPRSA*AQGAG
		1				AEAARLGAGOASGCOSTRRPA
			l			GSRREPGVSLDGGHRAVVGIOF
						OAPSRRAAWGHPLHDAPGRRL
						MSROLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGOWLRKVYWVPOOCRPTG
27300	37734	ľ`	27303	007	1772	AVLDFSPGCSCLPAGOGSGPAA
1						RHA*ASHPLHGLLCGPSLPDEH
		1		ļ		HPLLHGAOSORPPKG*GMRAH
ŀ	i					SAGLAGSSTCSPGAGSTR*SQL
i						GS*VW*GRGESLCL
29387	59755	A	29564	1	2715	GS VW GRGESECE
29388	59756	A	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ
27300	37730	l^	29303	ľ	044	KLLHFLYSLQKGISPNAIPPHSP
	l					HPTTAPVYSSQCERRRQVISAF
	1	1				PT/GD*SLHSN*E*QGGVEGEAP
	1					AGTWAVRGA*GPAGVPGGRGL
			i			GGLRTRSSWPALLAPGROGSGP
	1					AARH/GLSLPOPPWAPVOPEPP*
		Į.				GAPPPAPRRPVPSATOGLRSAS
	Į.	ľ				ARRTGROLHLOPPCGIHLVKP
1	1					AGLLSLVGTWRVFMS
29389	59757	Α	29566	1	470	MGOPLLLVRDSGGLOLWOKV
2,307	37737	ľ.,	2,500	ľ	""	KGEPVQQHERRIIPPAREEKVK
ŀ						RSPAGPPPSGGLDSSRHKIPSHE
1		1				OA/SGVOPACRTNHOPRGIWCS
			ŀ			PSLPDEKCPLLHSAQSHRSPKG*
1		1				GVRAHGVGLAGSSTCSPSAGSN
1	1	1	i			G*SQLGS*V*NKGR*IYPRTGRC
29390	59758	A	29567	777	1063	OLPPPSVFPTTPKTELVLGTPGH
2,,,,,	137738	<u> </u> ^	12,507	l'''	1005	GOPHRGGHESSDSAGGHLP/LR
1						ALRSGWDPSPPSSVCATPTSSGL
1		1		1		SSTPQLPLHQRTSSSTASWSPG
		1		l		WGMGSC
		1				# GINGSC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /-possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29391	59759	Α	29568	1195	1899	GSASGVVRSSRWARGLAGFRS
		1				EAADLHSECYSS*KQCGPKD*A
		1		1		EARFIAKSEGTKLPQCGRGPH*
		1				QRFSTSPPDSGAQLASPSGSRTE
		1				AAGGAACQSWCRAP/STPQPLC
		Į.		1		GRWDWAPWSRGWRSSGTSGR
				1		TGAHGAGGR/PQAWRAAGPQP
l						CPAGROLRPETLKQNIILSLIQC
		1				GASLVPTGTAELEPSPSLQLRG
l		1				TDAAQAIKNEFARVQKRNLCR
	l l			1		RGPICFEGDALSWFFEKINKIDE
	I	I		1		RLARRIKKKREKNQIEAIKNDK
		l		1		GDITTDPTEIQTTIREYYKHLYA
		1				NKLENLEEMDKFLDPYTLPRIS
		1				QEEVESLNRPITGSEIEAIINSLP
		1				TKKSPAPDGFTAEFYQRYKEKI
				ł		IVLEVLARAIRQEKEIKGIQLGK
ļ						EELKLSLFADDMIVYLENPIVSA
					-	QNLLKLISNFSKVSGYKINVQK
		1				SQAFLYSNNRQTESQIMSELPFT
ŀ		ı	1			IASKRIKYLGIQLTRDVKDLFKE
		ı				NYKPLLNEVKEDTNKWKNIPC
	1	1				SWIGRINIVKMAILPKIEKQTWN
1		1		ŀ		NSQTLQCQPFCESDVCTSTLQK
!		1		l .		ERFEVAPLHKKALSSEEITIDKT
		1				DPSPAIEELTV
29392	59760	Α	29569	77	640	
29393	59761	Α	29570	384	746	APWSRG WCSSGRLGLHRSPWS
l		1				GWEAQAWRAAGPEPRPAGRQI
		1				GAMSCKVETGT*DSEQRHRFG
		1		1		ESWGHPWAGAQPTGPVLSGIL
		1	1			NVLSSFSVLALPRPTGWPRPCS
20201	50000	١.	20.571	100	545	AASPSRCPAQSHQH
29394	59762	A	29571	189	343	GLSCLPAGQGSGPAARHV*ASF PLHGLPCGPSLPNEHHPLLHGA
İ				1		
		1		1		QSHRPPKG*GMQAHDAGLAGS
		1		1		STCSPGAGSTR*SQLGS*VCCTC
				1		RLVGTQQLRPESG*VSQPSPRL
20205	60762	+	20572	87	374	WAAAEGSC AYSSQLGESRRYSLDQCLAK*I
29395	59763	Α	29572	l°′	274	
		1		1		CEGRTCIFEEPCNCSSLYVRSNC
1		1		1		GNHSHSTTTFKYNGSNWIPRW QGPSGSTQPSKARRPVAFSQGN
		1		1		CAMEKGN
29396	59764	-	29573	1	2453	CAMENUN
29396	59765	A B	29574	182	1356	
29397	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS
29398	39700	l^	2010	1-0	1	LGLSCLPVEQGSGPAARHA*AS
l		1		1	1	HPLHGLLCGRSLPDEHRPLLHG
		1		1		AOSHRPPKG*GMRAHGAGLAG
1		1		1	1	SSTCSPGAGSTRNREN
L	1	1			I	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29399	59767	Α	29576	142	442	PKGVGRALAAFPQDRAPGPAA
		1				RHA*ASHPLHELLCGQSLPDKR
						HPLLQGAQSHRPPKG*GVQAQ
		1				GTGTGRQLHLQPWCGIHWVKP
						AGLLSSLGPRCFYKL
29400	59768	В	29577	1	2464	
29401	59769	Α	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL
	1					SPWVVDGTGCRGAGGGAHRG
		l				GSGRTGAHGVGGR/PQAWQAA
ĺ						GPEPCPMGRQVRPGEKSSAVPV
		1				GQPGWGTQYTLRSHWLGC
29402	59770	В	29579	I	2598	
29403	59771	A	29580	1	2028	
29404	59772	A	29581	5917	6355	QEAQPEESANDAQGDGPPGGK
		1				POPOPEERSSCAOGVGPPGGOO
		1		l		ESODEERSSDAPEDGPPGGOOK
		1			1	POPEERSSDAPEHDPPGGOOOP
						OPEERSSDAPEHDPPGGOOOPO
	1					SEERSNDAPGDGPPGGOOOP*P
						EERSSGAPGHSSPDV
29405	59773	A	29586	875	2090	DEMOCRIT CONSCIENT
29406	59774	Ā	29587	228	505	MLGRKPNHTSASRNTRLRHCSR
2,400	1000	ľ.	2,50,	1220	1	ARAQVKRMRQQRREEREAK\R
			1			OPGTASGTSGIAERDSGKCSRK
						RGVQKVPG**NTRQSKLRPREQ
				1		CTTADP
29407	59775	Α	29588	188	592	AAPPRSPSYRMIRKTR*MLGR/E
2,40,	37773	1	27300	100	332	AEPHVCQQEHQVEALQHGQGP
		1				GETDATAAERR/RGRORROPGT
						ASGTSGIAERDSGKCSRKRGVQ
				1		KVPG**NTROSKLRPREOCTTA
		ŀ				DP*TLSTFPEGRGTELEPGFDSG
						ASVLMRGCRAALSASSSP\OGP
		l				GPQEM*ATRNSWGRRQ*GRHC
	1	1	1			KLPVLITGLQGDVVEGVHVGC
	1					ASQEPLIQNDQEDEVDAWQKA
		1			1	EPHVCQQEHQVEALQHGQGPG
		1	1			ETDATAAERRAGGKDASLVQH
		1		I		LVPAVLLSVTQGSVPEKEEFKK
		ı		i .		SLVNEILGKVNYDQGNNVPQQ
	1	I	1	1		TLEHCPPFPKGEARSWSLASTP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRRQPGTASG
		l				TSGIAERDSGKWSRKKREFKKS
		l		ĺ		LVNEILGKVNYDQGNNVPQQT
		l		i		PSHHPNLEHCPPFPKGEAGAGA
						WLRLRGLGSYEGLPGCALCFFF
						PSRVLGLRRCEOOEIAGOOOGR
	1					DTOHGOO/RSAEGRGRPG*GPG
						RTGPPAAOLPOSLRTTRRSRPW
						GRRQ*GRGR*PPOGLMRC*RRP
	l					HHTGWSPQNEKRQPGRSFQQH
						KSH*RE/RR/RARPVGOOVKAK
	ĺ					RSQQFDDECGEDVRQEHSSRRD
						RVAVKS
29409	59777	Α	29590	2	394	
29410	59778	Α	29591	353	693	GSLFLVKRREPER/QVQHEELTE
						GEADHSGYAGELGFRAFSGSG
					ŀ	NRLDGKKESPSPIKPGDIKRGIP
	1	1	l			NHEFKLGKTPFIRNACPLVKKF
						EEDEAGGRFVAFSGEGQSLSKK
29411	59779	Α	29592	1	561	
29412	59780	Α	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W
			İ			TALWEMLYAEEANPFSTIRILF
	<u> </u>					QLEQPALGTSQYKILCLSST
29413	59781	Α	29594	2	704	WRGGSGSGGWESGRRGFFVAL
	ļ.					PERSGVCQVVSIMFSFNMFDHP
						IPRVFQNRFSTQYRCFSVSMLA
				ŀ		GPND\RIMPPSALDQLSRLNITY
						PMLFKLTNKNSDRMTHCGVLE
	ł					FVADEGICYLPHWMMQNLLLE
	l					EGGLVQVESVNLQVATYSKFQ
						PQSPDFLDITNPKAVYLFQISGV
	1	1		l		LLDKGECAGECVCRLENALRN
	1		l	l		FACLTTGDVIAINYNEKIYELRV
		1				METKPDKAVSHECDMN
29414	59782	Α	29595	1	1680	
29415	59783	Α	29596	1	2220	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown,  *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	'			sequenec		
29416	59784	А	29597	2	1114	SGRRGFFVALPERSGVCQVVSI
		į .				MFSFNMFDHPIPRVFQNRFSTQ
						YRCFSVSMLAWPNDRSDVEKG
						GKIIMPPSALDQLSRLNITYPML
		İ				FKLTNKNSDRMTHCGVLEFVA
		l				DEGICYLPHWMMQNLLL\EEG
						GLVQVESVNLQVATYFQELSSC
1						YLPHW\LMQNLLL\EEGGL\VQ
1		ĺ			l	VESVQPFKWATY\SNFQPQSPD
l					1	FLDITNPKAVLENALRNFACLT
						TGDVIAINYNEKIYELR\VMETK
						PAKPVSIH\ECDMNVDFDA\PLG
		1				YKEPERQVQ\HEESTEGEADHS
ŀ						GYAGELGFRAFSGSGNRLDGK
						KKGVEPSPSPIKPGDIKRGIPNY
1						EFKLGKITFIRNSRPLVKKVEED
		_				EAGGRFVAFSGEGQSLRKKGR
29417	59785	Α	29598	15	569	
29418	59786	Α	29599	30	525	YCLHHFFFQVSLLVFAWCSEM
		1		l		HGNRQLWE\RTGEMGRRTPGL
l		1				SWTAKSPIGR/RSLRSARVPRTV
		1				AHSQRAKGSHSLWVLRPQKRR
		ĺ		l		CAGKSPPPSRLARSPRCPEPLVA
		l				LARQPLCVRRAGPEERARAQR
		l	i			RPPRVPPLLSQPGRALLLLLRS
20410	#0505	ļ.,	20/00			SFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	I DI O IDDDD II FOOTU A DIIDI A A D
29420	39/88	A	29601	/58	10/6	LPMNRPPRWTGTILAPIIELLLE
						LQQKENMALGSRTHHGSSPNS
	i	l				GSAFCQMACCSSLKPAL*SGRC
		1		Į.		SQP*WLWMSPLSRIFSISNSTSA SSSIGNAIRRRRSRPGP
29421	59789	A	20702	632	835	555IGNAIKKKKSRPGP
29421	59790	A	29602	428	1214	FIAITVLPHWRSPQWYYPYWRG
29422	39790	<u>۱</u> ۸	29003	428	1214	PVTA/LVRKVPAVAGERSSLWS
		1				VVGLIWKPGLGLALOGVGFAVI
		1		1		GTFVSLYFASKGWAMAGFTLT
						AFGGAFVVMRVMFGWMPDRF
		l				GGVKVAIVSLLVETVGLLLLW
		l				
			İ			QAPGAWVALAGAALTGAGCSL IFPALGVEVVKRVPSOVRGTAL
		1				GGYAAFODIALGVSGPLAGML
		1				
		ı				ATTFGYSSVFLAGAISAVLGIIV
		1				TILSFRRGQETAHQPDQQRAAY
		l				DLQRSNRRVLPASPASACRCSD AHSR
29423	59791	Α	29604	1	825	мпол
47443	29191	<u></u>	47004	Li	043	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequenee		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29424	59792	A	29605	242	1945	NGCIVRGKTSGSTFICVAMSVA
	37172	ľ	27003		7.0	ASTVRR*CWLPGRKAAAWRTC
		1				WAPMT*AVMC/WSRLMYGAR
		1				LSLLVGCLVVVLSLIMGVILGLI
		1				AGYFGGLVDNIIMRVVDIMLAL
						PSLLLALVLVAIFGPSIGNAALA
		l				LTFAGLPHYVRLTRAAVLNCL
						APLIVOASLGFSNAILDMAALG
						FLGMGAOPPTPEWGTMLSDVL
		1				OFAOSAWWVVTFPGLAILLTV
						LAFNLMGDGLRDALDPKLKQ
29425	59793	A	29606	1	2433	
29426	59794	A	29607	i	1383	
29427	59795	A	29608	1	218	
29428	59796	A	29609	1055	1873	
29429	59797	Α	29610	3	823	
29430	59798	Α	29611	183	1163	
29431	59799	Α	29612	4375	5125	
29432	59800	Α	29613	1800	2031	
29433	59801	Α	29614	2	848	
29434	59802	Α	29615	886	949	
29435	59803	Α	29616	123	315	
29436	59804	A	29617	34	343	HLCSYGRVYAADPYHHALAPA
		l				PTYGVGAMNAFAPLTDAKTRS
		l				HADDVGLVLSSLQASIYRGGY
		l				NRFAPY*MTKP*KPSNVGRKEA
						FRGLSIAIHAVVHHFSNS
29437	59805	Α	29618	1	305	AAAYRGAHLRGRGRTVYNTFR
		l				AAAPPPPIPAYGGVVYQDGFYG
		l		l		ADIYG\VMLHTATPSLPLPLPLP
		l				TVTVTDEFMTFSPLSPLTCSSPH
		1				LRRWCHECFCTFD
29438	59806	Α	29619	1	2115	
29439	59807	Α	29620	1	273	FFSRVVPP\DSYQAQA/MVDIVT
				1	1	ALGWNYVLTLASEGNYGESGV
		1	i			EAFTQISREIGYPSLFGIQGCLHE
Ì						CFAILCQVVYQFLLLMQLSDAQ
		1				TVY
29440	59808	Α	29621	1	405	
29441	59809	Α	29622	I	582	

NO: of			SEQ ID NO:			Amino acid sequence ( X=Unknown,
se		hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	quence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29442 59	9810	Α	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS
						ICYSHGRDLAPARPAQPPQPRD
						QPQVRPLCSPHAAAAAAAAAL
						TWSCGPPAGFLTAPSAGSRVRL
						AARQQKAAPRKASAEPRDKKP
						LAPKLPQNALLVGKGESPRFIPL
						SVFFSKTFQRTARILKRSASDRL
						PWVTSRTCPGGIRTCPAEMTRY
						LRFANLTGGISEVSGFRDESGIN
						FGSWIAIPPVEKMVCEGKRSAS
						CPCFFLLTAKFYWILTMMQRTH
						SQEYAHSIRVDGD
		Α	29624	1	2740	
		Α	29625	1	1614	
	9813	Α	29626	88	540	
	9814	A	29627	2	577	
		Α	29628	1	2169	
	9816	Α	29629	1	1619	
29449 59	9817	Α	29630	674	867	LDGDGIESINSLGQYGHFHDIDS
						SYP*AWNENVLPFVCILFYFVE
20.450	0010		20/21	746	1005	QWFVALLEDVLHVPCKLDS
		A	29631	746	1985 2211	
-,	9819	A A	29632	139	247	KTSAAHEKPKWRKE\RNARG*
29432 3	9820	А	29033	139	247	KRKRRKMLQRSQVNR
29453 59	9821	Α	29634	335	556	RKKKKKIVILQKSQVIVK
		A	29635	1	586	
	9823	A	29636	908	1260	
	9824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA
2,400		•	23037		1000	LSPDEFISPVCWLARLVRWRCF
						FAOKAR*SPAKYGILGELTTGS
						KLVKANGLMEASTIAAILLGSV
						AGGVLAYWHVLVAWPHAHWP
						TVSRQQQLMASTLPFTSPLAQ
						IFPWRAITQRTMRMPFVIDARD
						ALLOGVFAAVNPSAHLNDSRH
						RRINKNVIEPGISCORPOHLDRI
						AHPFGIHIHQLNAFTGRQFHRQ
						QLLYLRQTFVVDIDHHHPRRLY
						AAVNGVIDSANAHRTCTRQQC
1						NIAARFDAHAMLINILRGVIIGM
						ISTNNAAHRLCQRRRSKIRSRDT
						GNTQPKLMQI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH
29437	139823	^	29038	139	000	CWTTAVACHOCEDAPCANVCP
						VDAISREHGHIFVEQTRCIGCKS
						CMLACPFGAMEVVSSRKKARA
	l					IKCDLCWHRETGPACVEACPTK
	l					ALQCMDVEKVQRHRPRLNFLR
	1					LWYVVHAHTLMRMRPRFIQPW
	ł					EEVVPRHHQHAACFQALIELLG
						RNGQILKP
29458	59826	Α	29639	391	812	HSALCSCRMRRERLIRPTKTCK
		l				FNRLQRLCRPDKRSASGNFAVV
						IRLERVSLLAPFFYGVLLLKCL
l					ŀ	MPKRQCNEADHHQTHTCAGQ
ŀ						KKMATHPLPGENKFIIGEDREY
						RWALMFPNENAPVCWVGHVR
						*KSPLHQHIDRA
29459	59827	Α	29640	589	1075	
29460	59828	Α	29641	1	435	
29461	59829	Α	29642	9	661	
29462	59830	Α	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	A	29646	114	851	CDHRNIVIRSAENISANFSHTGS
l	i					V*GWMFTVP*SPSGRVVF*FCH
					ľ	L*ATCGN*LN*THSLSQGQRAF
	ļ					CILGFLPWHSRRIRSHVGLENEC
	l	ł				KVLLSGRSSQQMGEP*GR*FSP*
						VGPLGGRALLQLPQPNSV/YVL
						PVSGLLVPAGE/CPLNV*PLVCS
						SANVLLSTSSCFCLCLARVSGF
						YRHRMGA/SGGFL/M*V*RKGS
	i					SFNFLHMA\ASSWDSYSGHHFF
						*AGADYFFASSVSSLPLVLLHSL
		1			l	HSFF
29465	59833	Α	29647	1	1422	
29466	59834	Α	29648	1	768	
29467	59835	A	29649	1	885	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
29468	59836	Α	29650	li	1253	MVSVTALKAAFLELFIPPSGLV
						VSLASGVKLQTFAVSVTAHKG
į .						SVDPKSDOHGLVVSLASGVKL
}		1				QTFARRAEFPASQQQREVPRHD
			İ			GGNHADRFTIIDHROLMATGG
l						RHFAIHFVDRFGVPANGARRAG
						NIITQTVTNRFAGVESFOOCOLF
1						GIYAVCEROGAEIPGPYARLFL
-						ATFFIYTSSFKPPLPWLRSLPRN
					Ì	TTPAVVRTAKGOVTAKYVIVA
						GNAYLGDKVEPELAKRSMPCG
						TOVITTERLSEDLARSLIPKNYC
			İ			VEDCNYLLDYYRLTADNRLLY
						GGGVVYGARDPDDVERLVVPK
						LLKTFPOLKGVKIDYRWTGNL
						QLTLSRMPQFGRQDTNIYYMQ
				İ		GYSGHGVTGGSSRVGLMAGSQ
						ISRVSV/CINP*YHRFNLHWRYV
		l				ADAISADGAFRTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRTDISLYQHTAEQKHPYCW
29409	37637	<u>۱</u> ^	29031	ľ	334	YPYPADSADI\SVNKHRRNATQ
						LHVSCSFFLLSDORFHHEAVPR
						RVVLFTFNTCVDKYIADIRSRT
1						NGLGFLYAFKORNSHFVFNAQ
						RHRHSACLR
29470	59838	Α	29652	1164	1273	KINGISACEK
29471	59839	A	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT
				•		EEALDQSNADLITLLADWFKDL
				ŀ		GFNVEVQPVPGTRNKFNMLAT
				ŀ		RRHEGRYITCMQPLPIIAEQEQE
						PEMTVRYYISSADLTAEKFATA
						IRNHWHVENKLHWRLDVVMN
						EDDCKIRRGNAAELFSGIRHIAI
					ľ	NILTNDKVFKAGLRQGWEDIED
						FGETHLDFLKOYGDFENGIPVH
						DTIARVVSCISPAKFHECFINW
						MRDCHSSDDKDVIAIDGKTLRH
				1		SYDKST/RRRGAIH\VNNAFSTM
			l	1		HSLVIGQIKTDEKSNEITAIPELL
						NMLDIKGKIITTDAMGCQKDIA
			l			EKIQKQGGDYLFAVKGTQGRL
			l			NKAFEEKFPLKELNNPEHDSYA
				1		ISEKSHGREEIRLHIVCDVPDELI
			l			DFTFEWKGLM
29472	59840	Α	29654	2	1587	
29473	59841	Α	29655	236	666	
29474	59842	Α	29656	1	1953	
29475	59843	Α	29657	2202	2333	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
29476	59844	Α	29658	1	1126	MHEVTLEDPSSAQILITVITGHG
		i				EIITLKRSSRRQNDIRMYCRRRP
						EAFRDHHQLRFLPGTDQAIGIL
						MMSKVGTARPPDKTNIREMSV
	1					HTVVLICATRVFQCFNNAGNR
		l				DFIHRIAATRQAALHGREHRRT
	1	l				PRGVTTIGKMVRKTKTAAGWE
	i					HESGFYLDGVVKLNRFKSNVA
	1	l				GKMSSGGAANGSYHSNGLGGH
		l				IETGMRFTDGNWNLTPYASLTG
	ļ	l				FTADNPEYHLSNGMKSKSVDT
		l				RSIYRELGATLSYNMRLGNGM
	1	l				EVEPWLKAAVRKEFVDDNRVK
	1	1			1	VNSDGNFVNYLSGRRGIYQAG
		l				KDLDRFKNLVLVHAARYAADL
		l				SYLPLMQELEKRYEGKLRIQTV
		l				VSRETAAGSLTG\GYRH*LKVG
						NWKARLACR
29477	59845	Α	29659	1	1989	
29478	59846	Α	29660	3	159	YKELNLADSSLSEEALIQAMVD
	1	l				IPKLMKRPKVVANGKARIGRPP
	1	ᆫ				EQVL\EIVG
29479	59847	Α	29661	360	744	
29480	59848	Α	29662	1	996	
29481	59849	A	29663	441	446	ICRQYPSPDDRTASGAGGGDHQ
	1	l			1	QYGAGLRQTFCLCQRLSARTC*
		_				RLSASVCAT
29482	59850	В	29664	1	1608	
29483	59851	Α	29665	1	2568	
29484	59852	Α	29666	116	283	
29485	59853	Α	29667	207	1270	
29486	59854	A	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

SEQ ID	SEC IN NO.	Met	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		[
29488	59856	Α	29670	1	1167	MPWLSTGAAALITALAVVELN
1						DDDDHHHRNNSPLPPTPPDDES
		1				DDTPVPPTPGGDEIIPDDPDDTP
		1				TPPKPVSFNNDVILDKTEKTLTI
						RDSVFTYTENADGTISLQDSNG
		l				RKATINLWQIDEANNTVALEG
						GNTSACRQALKIPKGSSDYTVT
	1	l		i		WKGGHFTFYRRWRCKVHKVV
						FEGSPPVTICRYVLNRKNSWHV
						AHIFRRHAKPEEQ/CSHLFPYPF
		l				HANDLDEVLNDPDVKLVVVCT
	1					HADSHFEYAKRALEAGKNVLV
				l		EKPFTPTLAQAKELFALAKSKG
						LTVTPYONRRFDSCFLTAKKAI
						ESGKLGEIVEVESHFDYYRPVA
		1				ETKPGLPQDGAFYGLGALFTNO
		l				QGFFKSSLLSIFADSSSSVAGRS
1		1				PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	A	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	A	29674	282	660	GPSSSEPSWAVAPGKAGDPHHS
					ľ	AEWARNSTPSKDQA*RRPHT\IC
						VTAYOGKVLLVGOSPNAELSA
						RAKQIAMGVDGANEVYNEIRQ
					i	GOPIGLGEASNDTWITTKVRSO
						LLTSDLVKSSNVKVTTEN
29493	59861	A	29675	720	4525	
29494	59862	Α	29676	218	990	
29495	59863	Α	29677	54	723	
29496	59864	Α	29678	1	2229	
29497	59865	Α	29679	2	235	
29498	59866	Α	29680	279	1275	
29499	59867	Α	29681	692	1052	
29500	59868	Α	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD
		1			į	CWVDDARLVLANAOMVVRKG
		l				GEVLTRTRATSARRENG\GKKY
						SWOARGLESLSOPVERLSP
29502	59870	Α	29684	1	1941	
29503	59871	В	29685	1	4107	
29504	59872	A	29686	840	1006	CHESHROTDGGAVFRVYPGGG
		l	1			PRRECWFGSSLDEATPGWLLQ/
	1	l	1	I		LYERDRH*PASTG
			<u> </u>			

SEQ ID NO:	of peptide	Met hod	SEQ ID NO: in USSN	location of first	codon for last amino acid	Amino neid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRKRLLLLSRK
						TRMP/GFTNPRYGAGAATNPDP
ļ						EVFSWAATQVVTAMEATHKLG
						GENYVLWGGREGYETLLNTDL
		i i		i		RQEREQLGRFMQMVVEHKHKI
ŀ		1		ŀ		GFQGTLLIEPKPQEPTKHQYDY
	1	1		1		DAATVYGFLKQFGLEKEIKLNI
		t		i		EANHATLAGHSFHHEIATAIAL
		1				GLFGSVDANRGDAQLGWDTD
						QFPNSVEENALVMYEILKAGGF
		ŀ				TTGGLNFDAKVRRQSTDKYDL
		1				FYGHIGAMDTMALALNIAARM
						IEDWQLDKRIVQR
29506	59874	С	29688	1	2130	
29507	59875	Α	29689	238	1879	
29508	59876	Α	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR
		1			1	KSVRTQV\LSAADVRAKLFTLK
		l			1	VQDPKIDRANPTMVNMRWMM
		<u> </u>		1		SA
29509	59877	Α	29691	596	723	MCASAP*WCELPAGVVRPPAST
						TADYFPLFTLVHGGCAHGRF
29510	59878	В	29692	1	441	
29511	59879	Α	29693	1	1422	
29512	59880	A	29694	2	2856	24. 2 . 112. 112. 112. 112. 112. 112. 11
29513	59881	Α	29695	2	367	QKAGAVQVLLSLWSSLSAAAA
						GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS
						GSLDRPSALHSGTILSGKITSDIC
		l			1	CPHF*SPGRPCSKOHWAEMLV
		l				HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLGEITSPAHFSPTLHSPAAH
27314	39002	<u> </u> ^	27070	/33	1550	HOYRKALHGRFPARSRDPPALA
		l				PGWRSARRER*SSPARAARW
	1	1				CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE
		1				SYSFTDSV
29516	59884	Α	29698	279	732	PPGATLPTVARGTPQMGKEGSS
		l				PAKSLAPPLCEOMGOEDGHWG
						AGWGLAQVLLIALDGLLDAQQ
		1				HGGEPLGPAGRWSRIPSPTRCS
		1	1	1		CPHSAPRGPLAIFSSTCIPGNQR
			1			KLGTAPHTFGQPAWR*ACRCRS
		1				GRGPP*RSSLWRCTEEGAVH
29517	59885	Α	29699	353	2776	
29518	59886	Α	29700	158	605	PERSGLQEAGGGSRGWGKRSL
l		1				PPAETAGLSGYMCFRAWLSLSR
		1				WDSEDGHWGAGWGLAQVLLI
						ALGWSS*CASNGWLSHWFQPG
		1				R\*SRIPFTDSV*LVHILLPVGPL
İ				1		AIFFINLAFPGIRESWEQLLILLE
l			1	1		KPVGLEACPCKSGKGRP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
29519	59887	A	29701	1	753	MLALDQREAMRMIFPA\AGAP
		ĺ			\	APALSPYAS/ARILVDQQFCYRQ
		l				VVEQNAIAKSCAMIVAADEFIP
						GNGIPVDSVVIDRKINPLQIKQD
		ŀ				GGKALKLLVLWRSDEDAQQRL
		ı				DMVKEFNELCHSHGLVSIIEPV
		l				VRPPRRGDKFDREQAIIDAAKE
İ						LGDSGADLYKVEMPLYGKGPQ
				1		QELLCASQRLNDHINMPWVILS
						SGVDEKLFPRAVRVAMTAGAS
				1		GFLAGRAVWASVVGLPDNELM
		l				LRDVCAPKSGEPIL
29520	59888	Α	29702	294	479	KIHFGFFCHCAESGSLDGRHFA
						PGV*RSEQHESGSGAVSGTGY
		l				WCSRDYRSREIDGLYRNW
29521	59889	Α	29703	1446	2103	IHTDHRPGEIAATTLANRAALS
		1				GAALRRRRRQNQTIAVGWRLA
		ı				GTAHACNIISIRGYGSDEDA/Q/
						QRLDMVKEFNELCHSHGLVSII
						EPV VRPPRRGDKFDREQAIIDA
	ľ					AKELGDSGADLYKVEMPLYGK
		l				GPQQELLCASQRLNDHINMPW
		1		1		VILSSGVDEKLFPRAVRVAMTA
		1				GASGFLAGRAVWASVVGLPDN
		1		1		ELMLRDVCAPKLQQLGDIVDE
						MMAKRR
29522	59890		29704	370	1080	
29523	59891	Α	29705	547	928	RLTKVEMPFYGKGPQQ\ELLCA
		1				SQGLNDHINMPWVILSSGVDEK
						LFPRAVRVAMTAGASGFLAGR
1		1			l	AVWASVVGLPDNELMLRDVC
		l				APKLQQLGDIVDEMMAKRRFIP
l	1	1		1		LLRRWVDŁAŁTRWLITVSKP

	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29524	59892	A	29706	1	550	MESGVATRPIADFDVYIDKLTE
						FVYKTNLFMKPIFSQARKAPKR
						VVLPEGEEARVLHATQELVTLG
						LAKPILIGRPNVIEMRIQKLGLQI
						KAGVDFEIVNNESDPRFKEYWT
						EYFQIMKRRGVTQEQAQRALIS
1						NPTVIGAIMVQRGEADAMICGT
						VGDYHEHFSVVKNVFGYRDGV
1						HTAGAMNALLLPSGNTFIADTY
	100					VNDEPDAEELAEITLMAAETVR
		ļ.				RFGIEPRVALLSHSNFGSSDCPS
						SSKMRQALELVRERAPELMIDG
		ŀ				EMHGDAALVEAIRNDRMPDSS
						LKGSANILVMPNMEAARISYNL
	1					LRVSSSEGVTVGPVLMGVAKP
		l				VHVLTPIASVRRIVNMVALAVL
1			l			FVNADETTVVNFHACFACVEV
		l				FTVRHTTNRYQHGVVTLRFSG
						CFFAFHRHINAVFFRFNIQAVFV
						ALRPEVIAIMHKLREQGHRVVV
		l				LSNTNRLHTTFWPEEYPEIRDA
		l	i			ADHIYLSQDLGMRKPEARIYQH
						VLQAEGFSPSDTVFFDDNADNI
		1				EGANQLGITSILVKDKTTIPDYF
						AKDKARHRTRPLWAWLKLLW
						QRIDEDNMTTLAGNLAYVSLLS
						LVPLVAVVFALFAAFPMFSDVS
İ						IQLRHFIFANFLPATGDVIQRYIE
						QFVANSNKMTAVGAGQSGDQF
						LFALFNCQCFDADELKRIKNEL
						EPKMGMELNLVQLIAYTDWNE
						TQQKQPDGSWVNYNYDWMFK
29525	59893	A	29707	898	1163	
29526	59894	A	29708	81	454	NRLLAGRISSGTGDHFSGAAGI
			l			DSSLRPVW*T*TLRDQMSGGQS
		l				AKQPGRFAQWFYP*RLPETG*V
		ĺ	l			PE*CL**CELIRAN/DHFLVSILPL
		l	l			RSPCVPLHLSTTPLRLAMDLTG
L .		L				LSGFPIPLSQSA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	I	2218	
29529	59897	Α	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	С	29713	1	3126	
29532	59900	A	29714	642	825	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
1		1		sequence		
29533	59901	Α	29715	107	1315	KCADLPVRGLRHCWRRREDPS
29333	39901	^	29713	107	1313	GADRSFSALIHSGRAAFWPCR*
						QGALMSEDIFDAIIVGAGLAGS
l	1		ŀ			
l						VAALVLAREGAQVLVIERGNS
1		l				AGAKNVTGGRLYAHSLEHIIPG
		ŀ				FADSAPVERLITHEKLAFMTEK
						SAMTMDYCNGDETSPSQRSYS
1						VLRSKFDAWLMEQAEEAGAQL
l	1	1				ITGIRVDNLVQRDGKVVGVEA
						DGDVIEAKTVILADGVNSILAE
		ı				KLGMAKRVKPTDVAVGVKELI
1		l				ELPKSVIEDRFQLQGNQGAACL
		l				FAGSPTDGLMGGGFLYTNENT
		l				LSLGLVCGLHHLHDAKKSVPQ
ŀ		l				MLEDFKQHPAVAPLIAGGKLV
	1	1				EYSAHVVPEAGINMLPELVQIP
	l	1				CIERNAINAVKAVNAARMAMR
ŀ		1				RTSAPRVSLDKVIETMYETGKD
		1				MNDKYRETSRGGLAIKV
29534	59902	Α	29716	3	264	
29535	59903	В	29717	85	737	
29536	59904	Α	29718	171	820	LGVCAMTNSQCG/CDEYRSKN
	1	l				GYEGARKALTGLSPDEIVNQVK
1		l				DAGLKGRGGAGFSTGLKWSLM
1		1				PKDESMNIRYLLCNADEMEPGT
		l				YKDRLLMEQLPHLLVEGMLISA
		l				FALKAYRGYIFLRGEYIEAAVN
		l		1		LRRAIAEATEAGLLGKNIMGTG
	1	l		1		FDFELFVHTGAGRYICGEETALI
		l		ì		NSLEGRRANPRSKPPFPATSGA
		l				WGKPTCVNNVETLCNVPAIL
29537	59905	В	29719	1	486	
29538	59906	A	29720	1	605	
29539	59907	A	2972I	285	449	TPAARDAQLSGGRGWY*CSAG
						NGLMOHRSOSGDWRAGRPFTE
						GW*PTPDWOIEA
29540	59908	A	29722	411	557	
27540	27700	<u> </u>			122.	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29541	59909	A	29723	1244	3261	KTINRTSLWYWTLHDHWSVTG
						RCAFTDVTKVEDHHEPOTOTR
		l				GLVMTTS*ATT*KLTVSLTTAC
						VMNWV*MQVIPSPTAKIRL*LR
		1				TSNWLTSTTTLTT/NNDVNGDSI
				l	ŀ	DNGTEGSAVRVGLGTQFSFTK
1						NFSAYTDANYLGGGDVDQDW
						SANDLTGITAKDAQMLSVVKP
						LOEFELFVLAALESRGTLADILK
						AAGATTANITQAIEQMRGGESV
		ĺ			İ	NDOGAEDOROALKKYTIDLTE
				1		RAEQGKLDPVIGRDEEIRRTIQV
l				1		LORRTKNNPVLIGEPGVGKTAI
		1				VEGLAQRIINGEVPEGLKGRRV
						LALDMGALVAGAKYRGEFEER
1						LKGVLNDLAKQEGNVILFIDEL
1						HTMVGAGKADGAIDAGNMLK
						PALARGEWHCVGATTLDDIAS
ŀ						TVKRCWTSHQHQTKNRTRRTT
l						TRNIRFPNQMIEQINIALEQKGS
						GNFSAWVIEACRRRLTTGGPHV
1						MYVLHHADKPNLYHGLPENPE
						ISETVKFWKGIWKPLAAVGFAA
		l				TFAASIFHYERVIFLTGQVEDH
						MANLIVAQMLFLEAENPEKDIY
						LYINSPGGVITAGMSIYDTMQFI
						KPDVSTICMGQAASMGAFLLT
						AGAKGKRFCLPNSRVMIHQPL
						GGYQGQATDIEIHAREILKVKG
						RMNELMALHTGQSLEQIERDTE
		1				RDRFLSAPEAVEYGLVDSILTH
29542	59910	Α	29724	1487	1821	QYRPESVLEDPRRSDHHRRTDS
						FRETSFIVQSIVCRVSLSRAILQS
						KRL*EPGEFPPPDPSSPEQRWPV
						CYPPK*SDR*PEYPHSPPGRQES
		<u> </u>		L		QSRYLPAFRHRYSYQTTAY
29543	59911	Α	29725	4063	6544	
29544	59912	Α	29726	174	556	
29545	59913	Α	29727	1	1926	
29546	59914	Α	29728	I	1443	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
29547	59915	Α	29729	1	817	MAFNEPLMLEPAYARVFFCAL
						AGQLGITRLTDTVSGITLDAGQI
					ł	AEPLALFGEDDDMDPRPSRSYQ
ŀ	1	1				VANGIAVLPVSGTLVSKTRALQ
l				ł		PYSGMTGYNGHARLQQAISDP
		1			1	GVDGILLDMDTPGGMVSGAFD
l	1				1	CADIIARMRDIKPIWALANDMN
i						CSAGQLIASSASRRLVTQTART
		l				GSIGVMMAHSNYGAALKTNGV
		l				EVTLIYSGDRKV\DGNPYEKLP\
		l				KDVRADFQTRIDATR\SAYTGM
		l				SVQDV/LDTEAAVFSGQESWDN
				1		GLAE*LVHTDWL
29548	59916	A	29730	68	98	
29549	59917	Α	29731	215	871	
29550	59918	Α	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP
		ł				EQRDGAGRFCSLAKETVTPQW
						*GVLTSLIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLLGYSLVCSRVLLAC
						FWPGSDFWPRSRRKTSHLTVEA
		ŀ				FPV/VVIFVSWRNPQVAPTSAH
		ł				QNRPSRNPVSRPPNTQRVARRK
						HYALADGY
29553	59921	Α	29735	403	588	
29554	59922	Α	29736	1	743	
29555	59923	Α	29737	5	97	
29556	59924	Α	29738	756	935	
29557	59925	Α	29739	1	1056	
29558	59926	Α	29740	1193	1405	
29559	59927	Α	29741	1	2718	
29560	59928	A	29742	3	357	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
29561	59929	Α	29743	3	1307	KYGFVHYT.HTLGGTARALVA TDYPRIT.KLSLDAGFOTVDHLG ISQCPYIPPYNFPTDTSPGTPGLI QPPEGHAYDAYWRCVRAVRG QRYSALHGPPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YGSGVRSWVQPGGFARYKYDG TGNASTYKCDYYRMAAFGHH AYKMQALTCSMTACPCTTRGE TSSAWGSVSSWGDSRPPOGELIG QPLLGRRIKYNCTGIGPWDGKG DESGASRPRKQQASGWLWACP RIFLVIPHSSHPAARRTNGSVGG SNRNRRVIITGGFQLAPKGLW QWPIGQDPVEIATLIGTHDLIM FDCIGSVSAPTIQPLEKLLSIVR PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVTISAF APVAVTAPPRQSRRQPFRLSPL APHORMGDVSIOAVKEARTC

3814

SEQ ID NO:	of peptide		SEQ ID NO: in USSN 09/540,217	location of first	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	от рерине зециенее	deletion, \=possible nucleotide insertion)
29562	59930	Α	29744	1	2352	MLPDSSVRLNKYISESGICSRRE
		1		l		ADRYIEQGNVFLNGKRATIGDQ
		1		l		VKPGDVVKVNGQLIEPREAEDL
		1			1	VLIALNKPVGIVSTTEDGERDNI
		1				VDFVNHSKRVFPIGRLDKDSQG
		l				LIFLTNHGDLVNKILRAGNDHE
		l				KEYLVTVDKPITEEFIRGMSAG
		l				VPILGTVTKKCKVKKEAPFVFR
					1	ITLVQGLNRQIRRMCEHFGYEV
		l				KKLERTRIMNVSLSGIPLGEWR
		l				DLTDDELIDLFKLIENSSSEVKP
		l				KRRPNRKQRASNVQSLRWKKR
1		i				RKKAVARRPTQSSDDAIRGQQP
		l				DGVDCRDCRAGERQRQQTDSA MMELMVVHPHIFWLSLGGLLL
		i				AAEMLGGNGYLLWSGVAAVIT
		l				GLVVWLVPLGWEWQGVMFAI
1		l				LTLLAAWLWWKWLSRRVREQ
		l				KHSDSHLNQRGQQLIGRRFVLE
		l				SPLVNGRGHMRVGDSSWPVSA
		l				SEDLGAGIRQCQQLVAHGLQLL
		l				NVSFDLRHLFORGRLEFGCALR
		l				LLTDSQSRLSRKPRGWRGLYG
		l				YSPPCGDIVRYHHHDLSVATLH
		l				VHINHDDCLEIAVLKGDMGDV
1		l				QHFADDVIAQRGFFFAFSYEDT
		1				VIKIIEKDFTMSGKPAARQGDM
		l				TQYGGSIVQGSAGVRIGAPTGV
		l		1		ACSVCPGGVTSGHPVNPLLGA
		ı		l		KVLPGETDIALPGPLPFILSRTYS
		ı		l		SYRTKTPAPVGSLGPGWKMPA
		Ļ				DIRLQLRDNTLILSDNGGRSLYF
29563 29564	59931	A A	29745 29746	755	3075 1321	
29565	59933	A	29747	397	576	
29566	59934	A	29748	1014	1266	
29567	59935	A	29749	416	724	TPGLTKTPCPWEKVTLFSLQWS
		ľ		"	l'	AYROANTSGLRHSASSLLPLAC
1		İ				RY*R*WRWQKLAAVLTASARQ
1						SVKSLAYCWORFVTWRWGRFS
						LRRVQLPFPLKWGLRR
29568	59936	Α	29750	230	1829	
29569	59937	Α	29751	1	474	
29570	59938	Α	29752	137	586	KTKTNIKL*AAPITRMVMVRHA
						\PHSGSVKK*SDITMSFATISVIG
			l			LGYIGLPTAAAFASRQKQVIGV
			1			DINQHAVDTINRGEIHIVEPDLA
			I			SVVKTAVEGGFLRASTTPVEAD
			1			AWLIAVPTPFKGDHEPDMTYV
0000	50000	Ļ.	20752		000	ESAARSIAPVLKKGAL
29571	59939	A_	29753	2	557	

QGLSARQGCTKGHQVRRYG   HD	SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29574   59942	29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPVYT**PTA QGLSARQGCTKGHQVRRYGFR HD
29576   59943   A   29757   I   393   395   395   395   395   A   29758   I   3753   395   395   A   29759   I   1098   305	29573	59941	Α	29755	66	372	
29577   59945   A   29758   I   3753	29574	59942	Α	29756	I		
29577   39945   A   29759   I   1098	29575	59943	Α	29757	1	393	
29578   59946							
29579   39947			Α		1.		
WRIGLFYVGSVVLLWMLP    AYQAGQSPVTFFSKLGVPY    SIMNIVVLTAALSSLNSGLYC    GRILRSMAMGGSAPSFMAKI    RQHVPYAGILATLVVYVG    LNYLVPSRVFEIVLINFASLG    WAFIIVCQMRLRKAIKEGKA    AHFTPYHATPLRNVMLHITV    GVSRFSVIDTNQIAQRCNRF/    LCGA			Α		320		
29581   59949   A   29763   1184   2406							WRIGLFYYGSVYLLVMLLPIWS AYQAGQSFYTFFSKLGYPYIG SIMNIVVLTAALSSLNSGLYCT GRILRSMAMGGSAPSFMAKMS RQHVPYAGILATLVYVVGVF LNYLVPSRVFEIVLNFASLGIIAS WAFIIVCQMRLRKAIKEGKAAD AHFTPYHATPLRNVMLHIYVLN GVSRTSVIDTNQIAQRCNRFAL
29582   59950			В				
29583   59951							
GIVPAPPCTSGRIQL*IRLVLE							
FLGETGSLSCGLSLSFKSCCE   RCSGSRGSSP/G*PGVQEWN   FSRF/HGVGLASLRKQRAPG    FSRF/HGVGLASLRKQRAPG    FSRF/HGVGLASLRKQRAPG    FSRF/HGVGLASLRKQRAPG    FSRF/HGVGLASLRKQRAPG    FSRF/HGVGLASLRKQRAPG    FSFF/HGVGLASLRKQRAPG    FSFF/HGVGLASLRKGPARG    FSFF/	29583	59951	A	29765	444	699	CWPGKMSWGGFPLFLLIGIVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVYSGIQ LLPGLVLGGCMCRGIYA
29586   59954   A   29768   I   I401			A				GVDNWRIIPIISARLOR*AGSFFS FLGETGSLSCGLSLSFKSCCEAK NCSGSRGSSPG*IPOVOEWNQI FSRF/HGVGLASLRKQRAPGDQ SPTGLLGE*AHGEIPVGNGRSG KTRA/RGGPRGLEVSWSGSLTH SRG*ASLTSSINSCHIRRGHGPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29587   39955   A   29770   1366   1515   YDQAELDQLIHGSSSN/EQDF   RLFKGLTPQTLR/TLCQWIDA   QDYEFSTDG					362		
RLPKGLTPOTLR/TLCQWIDA   QDYEFSTDG   QDYE					·		
29589   59957   A   29772   419   1295							RLPKGLTPQTLR/TLCQWIDAH
29590   59958   A   29773   167   451			Α				
29591   59959   A   29774   94   304   SPAASLYVTGSDLCTARMGG VTRTGGLSRRAAYPLCHPPS RPSATSRASVDSG*TCGELGI GTRAN   29775   345   652   29593   59961   A   29776   596   2297							
VTRTGGLSRRAAYPLCHPPS:							
29593 59961 A 29776 596 2297			A				SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
	29592	59960	A	29775	345		
29594 59962 A 29777 184 283	29593	59961	A		596		
	29594	59962	Α	29777	184	283	

SEQ 1D	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29595	59963	В	29778	16	1058	
29596	59964	Α	29779	715	1234	FTWIGFYANRHFHCPVTTNDFP
		l				HFMKWRAAAHGGENIAFKLAN
		l				LPFFGDIRESHYQVVINRADRG
1		l	l			FNPDFFTGARQQQKFVLIAGGF
		ł				P*QLL*TNA VIGREFRNVQECIG
		1				LHTAGFANAVTKHF/W*M/PRL
1		1				HCTIWRSGSRTITGRSRWSTAII
1		1		ļ		NCRVCSFCAISTLASRTSAR
29597	59965	Α	29780	938	1250	PGRVSGKADGSV/LAGNGLLPG
						FFCPLRLRGKYQPEV/IASTIRRR
						YQLLFLAVASHQATAAGCGVN
						ALSDLRLCSVCRPDKTHSVASG
						NGCRMRALPSSPFSVIL
29598	59966	Α	29781	I	1389	
29599	59967	Α	29782	3059	3537	SEGKTANLFNKAITCSGAGECT
						RPWASDIKAQCAGGISRFATGN
						GFKRLCDTLRYLQAIENGLKN
						WRLIHIATVRRCPFPT/LSPATID
						AINVIGQWLAQDDFSGEVPYQ
						ADCVILAGNAVMPTIDAACKIA
ŀ			İ			RDQQILAEGDFGLRCEIRDWCA
						NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVLVHHFH
						AITHIRQQSQITRYIKLLRHRRH
ŀ						TQRRFTACRLRVDAPFPGNHQC
					ŀ	CALHCLRKIDRIQHNFNARFNIR
						IEKYRRRNTHTARSAA/DPPSGR
						H*FQFAVVKHGRNFAAPVQVL
1						RPSPALPLFAGQTPPPRRVPLPA
		<u></u>				GYQRHMLLQYDQATVN
29601	59969	A	29784	269	753	YRTPTLQLDQGRADARRGVW/
						HVPFSHESV/WENIVMTRQAQG
						ANFT*TLFCFGIGFAVIA*NCAI
						DPDISIRFFSKEETAT/GDRPDQI
						AAHLWRFPTPGGRFVHHRGAY
			l			AAIIFRP*YLNGRSMAEQSMILV
			}			TGELLVELNLEPSQVGNEFAEK
20.000		ļ.—	2000			YYGPASQVV
29602 29603	59970	A	29785	762 3703	1182	
29604	59971 59972	A	29786 29787	925	5889 1130	
29605	59972	A	29788	658	1212	
29606	59974	A	29789	904	1473	
29607	59975	A	29790	1205	2222	
29608	59976	A	29791	1203	194	
29609	59977	В	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	
27012	27700	<u>'^</u>	-1170			L

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
29613	59981	A	29796	1	738	MQPWALPTVGELWVCGRPGA
	.,,,,,			1		ALRAGTEPSSRALGVSETALPA
				l	l .	EIKLRVIRVGHSSPLAQLASFQK
1				l		PVLFVLRLNSRRFLFLSLARSED
		l				GILFAKSKHSSPLSLTPLRCIVL
						MRMYEQLMSGDLCQRVMMPS
						RNNPGYWNPQ**SEIFKGSPAQ
				l		TMATLTCSFKKPPPKIPYKAIAL
						ATVLFLIGAFLIIIRLPSCCOGYI
		l				KQRGGRPGPFQLLIIGHSWCSY
i	1	i			1	PGFYPPAHRFTMHPKGLPWVN
						PNE
29614	59982	Α	29797	1	186	DCRLRAGDPRRSHCAVSPTGGS
			1			RALSGYRY*SVDQPRNDGVDQ
						*ATLRASAHLQTAVVEFSA
29615	59983	Α	29798	724	1015	RSHPQCGYLQNHTSSASFSAPA
						RKG*NRHYAFARNDRLVPAPCS
1						HHHQ*PAFPAPVHLH*PVDLST
						AIDAPAVNGDGKARPSKRRYQ
				l		RLSVPEVVQY
29616	59984	В	29799	1	4182	
29617	59985	В	29800	1	1191	
29618	59986	A	29801	167	504	
29619	59987	Α	29802	1541	1852	FALFANRVSLAANVSGRGSPC
	İ	l				WWRRIAVVCCSTNR/RSALDIA
	1	i				HQVDVLSLVHRLSQERGLTVIA
	1	l				VLHDINMAARYCDYL\APCAA
20.000	*****	Ļ.	00000	10.0	2004	VK*LLRERLRKLCAAKPSK
29620 29621	59988 59989	A	29803 29804	407	3584 150	
29621	59989	A	29804	1	921	
29622	59990	A	29805	300	560	IRDKNRVFLRESWRRLFTTAND
29623	39991	l^	29806	300	360	OPHRPARRIISIAGIKWRYSDFLI
			l			NYCAGRAVF*RETGSVVERWH
			l	İ		HHAGWKTPFRKRAGRTAGH
29624	59992	A	29807	100	315	PIKITSALASASRYVRATLSCSR
29024	39992	^	29807	100	313	NSTLRWKK*RKMALTKPSTTN
						GSRSNS**MNFFL*OAPPG*PSA
						LPFVH
29625	59993	A	29808	3	116	ELIVII
29626	59994	Ā	29809	1	1469	
29627	59995	A	29810	i	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYORA
		Ι.	T		"	CSGR*VPNLRLPEVQSTDRLLS
						ORRRVSPDROWWLACH
29629	59997	A	29812	438	1942	
29630	59998	A	29813	1	1464	
29631	59999	A	29814	3	602	

-	01/0/306/					PC 1/US01/08631
SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or peptide sequence	deterion,possible nucleonide insertion)
29632	60000	Α	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA
		l				SVVSRDGFVIAGGGGMVVVE
						LEHALARGAHIYAEIVGYGAT:
		l				DG ADMV APSGEG AVRCMKMA
						MHGVDTPIDYLNSHGTSTPVGI
		İ				VKELAAIREVFGDKSPAISATK
		l				AMTGHSLGAAGVQEAIYSLLM
					1	LEHGFIAPSINIEELDEQAAGLN
					1	VTETTDRE\LTTVMSNSFGFGG
						TNATLVMRKLMIISASTTSILR
29633	60001	Α	29816	1	2472	
29634	60002	Α	29817	1	469	LFNREVCCLGQGQS*QMAL*LI
				1	1	GIESYIT*L*SGGDN\ASIGVIPDI
					l	AAIAR*RPWRSACG**PKCPLA
		1		I	I	DVFAGHSGRKRPPSMAFTATLI
					l	SPGTGRRAINSVLAQFKAGESN
		1		l		WLSALPTPLTPTIRITNGALPST
						SGSSTFARISPISSFSRP
29635	60003	A	29818	884	1084	-
29636	60004	A	29819	1	1040	
29637	60005	Α	29820	2711	3854	
29638	60006	A	29821	1	957	MKIGTQNQAFFPENILEKFRYIK
		ı				EMGFDGFEIDGKLLVNNIEEVK
		1				AAIKETGLPVTTACGGYDGWI
1		1				DFIEERRLNGLKQIERILEALAE
		1				VGGKGIVVPAAWGMFTFRLPP
						MTSPRSLDGDRKMVSDSLRVL
			l		1	EQVAARTGTVVYLEPLNRYQD
		1			İ	HMINTLADARRYIVENDLKHV
		1				QIIGDFYHMNIEEDNLAQALHD
		l				NRDLLGHVHIADNHRYQPGSG
			1			TLDFHALFEQLRADNYQGYVV
		1		1	1	YEGRIRAEDPAQAYRDSLAWL
		1		I	i	RAGQVADKVHASYYCTRNDLI
		1	1			LVAVCDSRLSQAQALAEKYGN
						ASVWDDPQAMLLAVKP*FVGL
						V\GAGQVADKVHASYYCTRND
		1				LELVAVCDSRLSQAQALAEKY
		_				GNASVWDDPQAMLLAVKPDV
29639	60007	В	29822	96	821	
29640	60008	Α	29823	3	775	
29641	60009	A	29824	961	2073	
29642	60010	Α	29825	1	849	
29643	60011	Α	29826	319	541	
29644	60012	Α	29827	1142	1756	
29645	60013	A	29828	44	283	
29646	60014	В	29829	1	1812	
29647	60015	Α	29830	685	1146	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
29648	60016	Α	29831	202	918	AVDTGLADHRDRTEHGGAFAA
						IVHRIVKHFITAWAICQQRNHA
						ALVVIRRLEANHRRHRTGRG\S
						VDRVSAARSLSSGTMPGNGVW
						RIGVFTQLSVA/WHQ*VDLLIVF
		l				QFVRDTTDDHDVGIFALAAND
		l	ŀ			RAAFDNILDPTGSVDVLLPLPG
						RHNIANALAAAALSMSVGATL
						DAIKAGLANLKAVPGRLFPIQL
1						AENQLLLDDSFLVNAAQQNILS
						VHILNQQTGKPAADVTVTLQE
29649	60017	Α	29832	1184	2409	TLKACCLVRSMCRAVP*RC/GR
						QLVSSDNISNDPMNVIDWINMY
						ALAVSEENAAGGRVVTAPTNG
						ACGIIPAVLAYYDKFRRPVNER
						SIARYFLAAGAIGALYKMNASI
						SGAEVGCQGEIGVACSMAAAG
						LTELLGGSPAQNMEGKIDRPEE
						YADIATKCVTNFREKNRDRCL
						VILSRNDEALNSQRTSEELHHY
						YEIVWDEEQTHKFKNISPHLQRI
			1			KAFKTLGGPHGNITVDMVISAQ
			1			ELLQEDMATFDGHIVEALMKM
1						PEVNAMYPELKLHAIGWVKHK
						CIPGAKWPEIQAEMRIWKKRRE
						GERKETGKYTSVVDLARARAN
						QQYTENSTGKISPVIAAIHREYK
						QTWKTLDDELAYGRCFADRQN
						LMVCLRSMPNVFTGSCARMRC
		_				CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	II. CONTINUO VODEN DE CONTINUO
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA
			1			MIPNFNWAFLGVTTWIFMAAG
						GAESVA\CTLTTSKAVRNRSFK*
						SSSPGILSGYVSRSSGSPISSLISP
						ASLCAGHMRFFCSSSKPTCSNP
1						RTFAAALSSAWSSPSPNEGFSSN
						PAFLGTSLMMFHLELRRCIAPIV
						TTDLLPLTSGDVGLVLLCVGLD
						GSLWSDCRMTESVSTTNTPPIIT SRNS
29652	60020	В	29835	46	893	O.C.10
27032	00020	۳_	2,000		973	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	of peptide sequence	detection, (~possible nucleotide insertion)
29653	60021	Α	29836	3	2037	CTSSPDPPSGLPPGFAKLTSLIVT
						LVEVGVSPEPDEGWLYLAVVID
ļ				l		LWSRAVIGWSMSPRMTAQLAC
				l		DALQMALWRRKKPRNVIVHTE
						RGGOFGDRWKGWLTRSIFRWI
l				1	i	SFQPALAPTRKAALCYLAREVN
	İ					PDMADYIKKLKLPGIHVREESR
ĺ						RYYPSGEVTAHLIGFTNVDSQG
						IEGVEKSFDKWLTGQPGERIVR
						KDRYGRVIEDISSTDSQAAHNL
						ALSIDERLQALVYRELNNAVAF
						NKAESGSAVLVDVNTGEVLAM
						ANSPSYNPNNLSGTPKEAMRN
				l		RTITDVFEPGSTVKPMVVMTAL
						QRGVVRENSVLNTIPYRINGHE
						KDVARITTEEDFNHASAARFVC
	,	l				AAAERRCKTTINLVPENEVLNV
		i		l		LEGEDAETNALRAKRRCPKCG
						TAMDSYLIDPKRKLHVCGNNP
1		l				TCDGYEIEEGEFRIKGYDGPIVE
		ŀ				CEKCGSEMHLKMGRFGKYMA
						CTNEECKNTRKILRNGEVAPPK
		ŀ				EDPVPLPELPCEKSDAYFVLRD
						GAAVAARFNDDRHRRGLAVLY
						ADQADLYGVADSVSAGDSLSA
l						LYKHERRLVVPLLVSSSLLFLY
						RHGIRLPCGPSGGIWAPWQIRR
						GRQAVNCLAPM/HHPGKNRAW
		l		l		KTYCSQ*AIVPQLPVCGI*PRSD
	1	l				SYHDYQRDPRCQPLRALWRRS
						DSPIGGYSSAIGI*TERHCRSGNF
29654	60022	Α	29837	993	1832	
29655	60023	Α	29838	124	276	QEGRCQVTITRKMPLSSDLGSL
		İ				HGLAGNHSPPICARTPHVATVL
	l	ŀ				RQLLELEDKHWNGSG*FARLG
		l				WKPQSPHLCQNPPCGHCPQTAF GA
29656	60024	С	29839	64	267	GA
29657	60024	A	29840	3	86	
29658	60026	A	29841	i -	1481	
29659	60027	A	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK*VGGSSRVNVPQVFI
		1				SLVSQMFSENDLPLVRKRKTEP
29661	60029	Α	29844	115	903	
29662	60030	Α	29845	1194	2311	
29663	60031	Α	29846	368	502	
29664	60032	Α	29847	1156	1359	SEPVYPLCYLRQLAVQANPRR
				I		MRCIARHFNINGNRHLTTTINFI
	L	L.				*SMVSLIANRLLIIDLIHTVDFY
29665	60033	Α	29848	I	228	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29666	60034	Α	29849	102	296	YRNSHNLLQGWQIHRGDLLYH SSPHSR*KHRNRHNARARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	Α	29850	1	4185	
29668	60036	A	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVVIDQCVFLIRV TNPAGSFFELRIHH
29670	60038	Α	29853	2	834	
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNNLVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	Α	29855	1591	3150	
29673	60041	Α	29856	2	222	
29674	60042	Α	29857	16	359	TTHKTR WQAPVPLRGSPVVAL RIPSDQSEAV/HSLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLSFFNRHYICFTRI RRFR WHRSSLFHGMNVKYRRS KINN
29675	60043	Α	29858	207	470	ATIL*GDFYP/GSRNWLGVSSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTS/GHVLAGSCCW NGKTLRKSDSRWQQLLRRSLIR R
29676	60044	Α	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCIMAIRSPIRMASSR SWEIKTMVR
29678	60046	Α	29861	593	1881	
29679	60047	Α	29862	3	198	
29680	60048	Α	29863	1	1590	
29681 29682	60049 60050	C A	29864 29865	63	5421 185	LCQSHAPRKFPARPFRFFR*RQD COTSVFLLRPVANRAPA
29683	60051	Α	29866	1	715	
29684	60052	Α	29867	ī	1212	
29685	60053	Α	29868	886	1185	
29686	60054	Α	29869	190	433	AFAKLFIMAAALTSGVAHLSSS GTPFRPFCLPSC*LSSSRAAAIST CSLYAAWFPLTLIRCRGIRKSPII CGISRCRCWRQ
29687	60055	Α	29870	1	439	
29688	60056	Α	29871	14	106	
29689	60057	Α	29872	2518	3024	
29690	60058	Α	29873	448	537	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence (X-Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,21/	sequence	or peptide sequence	detetion, v-possible nucleotide insertion)
		1				
29691	60059	Α	29874	463	889	FFGLVTSSPSADSPAMLDTRNV
	1	1				SHTGLGPIIPLTFEAGIHTRPTPN
		1				SPPRSCLAPAIKA*FFSPAARITT
		l				CCASLYRSPLKTLRSVRFWRSS
	1					ASVLMRRSSSAAPMPEATLRVL
		l				SGLRGSRSDKAFTPHPTI*CLEA
						FPGSRAFVASAP*CLTLRANQR
		l				KGCW
29692	60060	A	29875	524	1006	SLLAWLSGINIFASSRIAIASPLA
		l				ASVPLSMDNISLCTPSGVPEKV
}		l		1		TSTVLTSVPQSCKLMMKDFSGP
ŀ		ļ				*FP*EKRVSETSPNCTLICLLSCA
	1	ļ				STHVLRRNDPLMLTVPSWANS
		1				SQPHVNPNKNRIQIIPFNITPSLV
						NOIKIETRRAFTPLLPLCGLITK
29693	60061	A	29876	2005	2517	
29694	60062	Α	29877	1	470	MQRRDGDIALIYRSKIGPRTSIT
		1				FTARRANPVQRIAARILLRDHLI
						CRMSCTAARHANTFDLIQGSG
l		l				ADNFAAIYGGANDRITRADA/V
l		l		1		SRGCWKLAPVRDIKRQTVAAF
						YHQDIQPGSCHDQNAL*STGFW
	į					REQSGGQ*P*AG*TNSRTRCCIT
						GR
29695	60063	Α	29878	734	1306	_
29696	60064	Α	29879	743	901	
29697	60065	Α	29880	771	1013	RLGTVGTDSLWCYQYQLCYQ*
	1	ŀ				ALPFSTLPAKLAGNGCQRRRCA
		ŀ				GTHSLWHADLGSVWPDADSLF
	1	-				QRDGRAGGGATRLLRR
29698	60066	Α	29881	1094	1345	
29699	60067	Α	29882	2	751	
29700	60068	Α	29883	239	483	PTPQHLTYHALTGSTIMSQRGV
		1				DIPCHWHDITCGHAHSLPHRRG
	1	1		1		RKA*SMGNR*YSCTWCYCEGG
						TEKAIWPGDGCPGLSV
29701	60069	В	29884	228	803	
29702	60070	Α	29885	488	636	
29703	60071	Α	29886	1	2117	
29704	60072	Α	29887	665	795	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
29705	60073	A	29888	1743	2013	LOCTOYAVGENPAVNFAGRPK
29703	00073	^	29000	1743	2013	GSPCFGPGGGLIN*AAADIPVAS
						DNPAHYADAIRYNARTPLOAG
						VYFVRDGPGPLASVRNKERYF
						ANNYIYDMGRNKDGROSTWY
			l			MGLGTDIDTGLPMSLSMNVYA
						KYQWQNYGAANENEWDGYRF
				ļ.		
						KIKYFVPITDLWGGQLSYIGFTN
						FDWGSDLGDDSGNAINGIKTRT
						NNSIASSHILALNYDHWHYSVV
			1			ARYWHDGGQWNDDAELNFGN
						GNFNVRSTARGWLPGTICRPDK
		ŀ				MRQHRIRHCAPIAGCGTGCRPD
						KTRQASHQAQMSNAYDYSEIQ
						PPSEGEILLDAQPLESWSSKAFA
						RKVAYLPQQLPPAEGMTVREL
						VAIGRYPWHGALALLGAADRE
						KVEEAISLVGLKPLAHRLVDSL
					}	SGGEPGVDRMLVAQDSRCLLL
				l		DEPTSALDIAHQVDVLSLVHRL
						SQERGLTVIAVLHDINMAARYC
						DYLVALRGGEMIAQGTPAEIM
						RGETLEMIYGIPMGILPHPAGA
						APMNTAHAAAIDPNRIVALEW
						LPVELLLALGIVPYGVADTINY
						RLWVSEPPLPDSVIDVGLRTEP
						NLELLTEMKPSFMVWSAGYGP
		1				SPEMLARIAPGRGFNFSVRNTP
						LARTLQLILREGPRGHPALVQV
1		l				VDLLIEPPQLPLLVP\$VQTRIPRI
		1				QPQSHPAHGVNEAVRNPTVWV
		ľ				APFIDEIISSIHKYSI
29706	60074	Α	29889	1	1584	
29707	60075	Α	29890	1	1188	
29708	60076	Α	29891	728	970	
29709	60077	Α	29892	2447	2665	
29710	60078	Α	29893	255	1360	

	01/0/300/					PC1/US01/08031
SEQ ID NO:	SEQ ID NO:	Mct				Amino acid sequence ( X-Unknown,
NO:	of peptide sequence	noa	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	.,			sequence		,
29711	60079	A	29894	I	1890	MYSRFDIVVAEPICTLTTFGKE
						VVSDSQTRTTTTDDPLQVLQQ
		l				LDRADIRPTHNEDLPFQGGALG
		1				LFGYDLGRRFESLPDIAEQDIVL
		l				PDMAVGIYDWALIVDHQRHTV
		1				SLLSHNDVNARRAWLESQQFS
						QEDFTLTSDWQSNMTREQYGE
		1				KFRQVQEYLHSGDCYQVNLAQ
		1				RFHATYSGDECQAFLQLNHGN
		ŀ			l	RAPFSAFLRLEQGAILKLSPERF
						LCDNSEIQTRPIKGTLPRLPDPQ
		i			ł	EDSKQAVKLANSAKDRAENLM
		1				IVDLMRNDIGRVAVAGSVKVP
		1				ELFVVEPFPAVHHL\TITAQLPE
		ĺ				QLHASDLLRAAFPGGSITGAPK
		1				VRAMEHDELEPQRRNAWCG/SI
ĺ		Į				GYLSFCGNMDTSITIRTLTAING
						QIFCSAGGGIVADSQEEAEYQE
		1				TFDKVNRILKQLENYRRALRDL
		1				KEEVAIRLSPFELSAFCSPSIASM
						ATRYPNGRHIPPDLRLPKERGIII
			1	- 0		VFTGNGKGKTTAAFGTATRAV
		l				GHGKKVGVVQFIKGTWPNGER
		1	i		1	NLLEPHGVEFQVMATGFTWDT
		1			l	QNRESDTAACREVWQHAKRM
		l				LADSSLDMVLLDELTYMVAYD
		l				YLPLEEVVQALNERPHQQTVIIT
						GRGCHRDILELADTVSELRPVK
						HAFDAGVKAQIGIDY
29712	60080	A	29895	159	475	VKVNLPWAMLLHSGYADHPYS
	1					RFDIVVAEPICTLTTD/GRCSHIS
		1				LYAAGIINSDSKGAVIMPPIIGA
		1				AIRLITSEPAPVPHRIGSRPAIITA
29713	60081	В	29896	158	810	TVIAFGRTRRTAP
29714	60081	A	29897	1	2070	
29715	60083	A	29898	1081	1218	
29716	60084	Α	29899	289	1014	
29717	60085	Α	29900	145	297	
29718	60086	A	2990I	452	568	
29719	60087	A	29902	21	185	VHDQPSQEIQQRTEAPGAPRSS
						RRVAQCHPQPGES*SRAQIPPAS TPKPGGGDL
29720	60088	A	29903	I	711	
29721	60089	A	29904	2	825	
29722	60090	Α	29905	812	961	
29723	6009I	С	29906	1	1587	

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide tocation of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29724	60092	A	29907	3	403	LVFDDGDVQMGFWCGCPFCLL
						VFLLTVRSLSCRSVGVCWRSTR
			l			DLVCLGISSGGCRTVNIAEQQM
				ŀ		LLPDCSSGIFVSEGYLAV*GVSL
						PLLGGASQLGLGSMAIFMILILP
						IHEHGMFFNLFVSSFILLSSCL
29725	60093	В	29908	168	863	
29726	60094	Α	29909	340	612	
29727	60095	Α	29910	1	834	
29728	60096	Α	29911	92	548	
29729	60097	Α	29912	1251	1682	VPVALAAARRSELSRTAAADT
		1				G*SAAAELVNPPDYVPDERKRH
					1	QSGCPASNSARDPSSYNHAPDD
1						ARCRHRGSGFASIPGGRASRLP
						APDADQNRLSLAPVLLQSPPER
						TELHAGGQSSWAPFEWEGAPR
						GEEWTLVSVGALK
29730	60098	Α	29913	1	1278	
29731	60099	В	29914	I	2007	
29732	60100	Α	29915	406	615	
29733	60101	Α	29916	52	391	SNRLLKLMHSSRSSCVMFFSSIR
						SFKDFSLVFDDGDVQMGFWCG
						CPFCLLSFPF*QSGPSAARSVGV
					ŀ	CWRSTPDPVCLGVSSRGCQTV
						NIAEQQMLLPDRSSGSFVSEGY
						PAV
29734	60102	Α	29917	759	1190	VPVALAAARRSELSRTAAADT
						G*SAAAELVNPPDYVPDERKRH
					İ	QSGCPASNSARDPSSYNHAPDD
		1			İ	ARCRHRGSGFASIPGGRASRLP
						APDADQNRLSLAPVLLQSPPER
		l			1	TELHAGRRSALGQLSEWQSGQ
						SPAGAAIAAFDNR
29735	60103	Α	29918	84	3661	

29737 60103 29737 60103 29738 60106 29739 60107 29741 60108 29742 60113 29743 60114 29744 60113 29744 60113 29746 60114 29747 60115	peptide quence	ide h	led	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
29738 60106 29739 60107 29739 60107 29741 60108 29742 60110 29743 60111 29744 60112 29746 60114 29747 60115	0104		1	29919	I	1230	MDAGWSDVGSWSSLWEISAHT AEGNVCHGDVINHKTENSVVY AEGGLVTTVGVKDLVVVQTKD AVLIADRNAVQDVKKVVEQIK ADGRHEHRVHREVYRPWGKY SIDAGDR YQVKRITVKFGEGL SVQMHHRAEHWVVAGTAK VTIDGDIKLLGENESIYIPLGAT HCLENPGKIPLDLIEVRSGSYLE EDDVVRFADRYGRGNDMKKL TCFKAYDIRGKLGEELNEDIAW RIGRAYGEFLKPKTIVLGGDVR LTSETLKLALAKGLQDAGVDV
29738 60106 29739 60107 29739 60107 29741 60108 29742 60110 29743 60111 29744 60112 29746 60114 29747 60115							GIEVTASHNPMDYNGMKLVRE GARPISGDTGLRDVQRLAEAND FPPVDETKRGRYQQINLRDAYV DHLFGYINVKNLTPLKLVINSG NGAAGPV/VDAIEARFKALGAP
29739 60107  29740 60108 29741 60109 29742 60110 29745 60113 29746 60115 29747 60115				29920	1	1398	
29740 60108 29741 60109 29742 60110 29743 60111 29744 60112 29745 60113 29746 60115				29921	426	1861	
29741 60109 29742 60110 29743 60111 29744 60112 29745 60113 29746 60114 29747 60115	J107		4	29922	863	1388	EPERTSIKSSGIFPGFSRQCVAPS GI*MDVVFTKQFDITINGDFCRS RDNHPVFRAVMVHLYRQALAR FHGDAFHLVAVARVDRVIFAPR THIFAMHPMIMATIGFDLIDHF FHILYRVTVGNQRIFGLHHYQ IFHPDGGDQARFSIHIAVFSFVIN HIAVANVALGGVGADLP
29742 60110 29743 60111 29744 60112 29745 60113 29746 60114 29747 60115	8010	. /	7	29923	1	2055	
29743 60111 29744 60112 29745 60113 29746 60114 29747 60115	0109	7	^	29924	I	2047	
29744 60112 29745 60113 29746 60114 29747 60115 29748 60116	0110	1	١.	29925	1	1294	
29745 60113 29746 60114 29747 60115 29748 60116	0111	1	١.	29926	1	1020	
29746 60114 29747 60115 29748 60116	0112	. /	١.	29927	1	1422	
29747 60115 29748 60116	0113	1	١.	29928	1	1698	
29748 60116			4	29929	210	340	YGDVEHESWLSCVRHAH\PRIP FA*PTLISLQKRLGKWSGVTGA
	0115	7	*	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK GYGHHHYRNLP/VPNGPPLSLL P*YCKAKFKPSTSQVP
29749 60117	0116	1	4	29931	63	281	
	0117	'	١	29932	345	467	LPTRCTYTNLTRRRSPPAWYY* *YWHRDICRSTPARRQTE
29750 60118 29751 60119				29933	29 520	281	MFGKELGRRDVSQLGAAEITYI LKD*T*ES*EILCGGRFLLPLRG RTLGQGEWPSLYFHSDCSSHAE QCLLYGFADWAPLAFFR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mct hod	SEQ ID NO: in USSN 09/540,217	Nucleotide Incation of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29752	60120	A	29935	222	527	LPSKLASGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAELGHLI SFHLALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGSLSPDIEG DLIQGQRHRDHIGP
29753	60121	Α	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRVILIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSYLNDALNGGD AESAGLTPPELWPRHHGHGPA GVKLVEQLOQRIRVPNEIDA RLVAEFHDLIHTFPMLNPKTIV KLFDSIDAWKKPQRVEQLALTS EADVRGRTGFESADYPGGRWI. REAWEVAQSVPTKAVVEAGFK GVEIREELTRRIAAVASWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVYSLREQIRSHEIRRSAAVS NHQHFRRACGHIDRRTVQTLA HLTFRFGDKGVTRPEDFVHFW HRFRTKGDPLLTFWPSAPVTAT ILRIPI.ANGFFRHDHKSSCMTR VPQVPEDFVKSHAPQQFWIHH GKWFAWYDVAIGIPGPFAGRS. CVILLGDA VREVTRVSNAVPAK RYIGGSPRRGFINSCMMPGIISPG
29756	60124	Α	29939	1	114	
29757	60125	В	29940	1	4191	
29758	60126	Α	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSSLLSLRAFW ASAPVTATNPPDTLGNGFFRHD HKSSCMTRVPQVRSPTELNRSQ GASRPRGVIQQLGHRDPNGDDS HRVRIGLIKHMP
29761	60129	A	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	Α	29946	1	936	
29764 29765	60132	A	29947 29948	1	966 675	
29765	60133	A	29948	1	792	
29767	60134	A A	29949	2	929	
29767	60135	A	29950	1	929	
29769	60137	A	29951	1	420	
29770	60138	A	29952	1	549	
29770	60139	A	29954	1	450	
29771	60140	A	29954	i	606	
27112	100170		27733	L	000	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon fur peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29773	60141	A	29956	I	726	MARGNAITLPVCGRDVKFTLE
				[		VLRGDSVEKTSRVWSGNERDO
1						ELLTEDALDDLIPSFLLTGOOTP
						AFGRRVSGVIECDNLKTCHTSH
						GSVMAETAVINHKKRKNSPRIV
						OSNDLTEAAYSLSRDOKRMLY
						LFVDQIRKSDGTLQEHDGICEIH
						VAKYAEIFGLTSAEASKDIRQA
						LKSFAGKEVVFYRPEEDAGDE
						KGYESFP\WFIKRAHSPSRGLYS
						VHINPYLIPFFIGLONRFTOFRL
29774	60142	A	29957	1	771	THE TENTH OF CHILD TO THE
29775	60143	A	29958	<del></del>	1491	
29776	60144	A	29959	145	1929	VSGVIEIADGSRRRKAAALTES
27			.,,,,,			DYRVLVGELDDEQMAALSRLG
						NDYRPTSAYERGORYASRLON
						EFAGNISALADAECDNLKTCHT
						SHGSVMAETAVINHKKRKNSP
						RIVOSNDLTEAAYSLSRDOKRM
						LYLFVDOIRKSDGTLOEHDGIC
						EIHVAKYAEIFGLTSAEASKDIR
						OALKSFAGKEVVFYRPEEDAG
						DEKGYESFPWFIK/RPSRGLYSV
					1	HINPYLIPFFIG\LONRFTOFRLS
						ETKEITNPYAMRLYESLCOYRK
						PDGSGIVSLKIDWIJERYOLPOS
						YORMPDFRRRFLOGFCRFRNH
						HOTGFSPAGANORGPLAATLSG
		1				PGGEGOSAVARLTGEKKNHPG
		1				AOYANRLSPRVGRFINAAGTTG
						FPTWKAGSERNAINDDVTYAIK
		1				PTCWPGLDIIPSCLALHRIETEL
		[				MGKFDEGKLPTDPHLMLRLAIE
						TVAHDYDVIVIDSAPNLGIGTIN
						VVCAADVLIVPTPAELFDYTSA
						LOFFDMLRDLLKNVDLKGNSN
						GSOSPWMEEOIRDAWGSMVLK
						NVVRETDEVGKGQIRMRTVFE
	1					QAIDQRSSTGAWRNALSIWEPE
						CNEISIGVSLDQDGGSNSVLRK
29777	60145	A	29960	1	1731	CITEDIO VOLDQDGGGIAS VERK
29778	60146	В	29961	1	3345	
29779	60147	A	29962	1	1959	
27.19	001-7/		27702		.,,,,	

	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29780	60148	Α	29963		1302	MKLMETLNOCINAGHENTKAI ALAGPINDSEPARKITERWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTTEQI NHMRDVFGTRLRRAEDVFDV NVSKSDDTLKINGVEDHKTIFD GOGKTYQNVQGFIDEGNYSD DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTHFFREKSGKLQQSAK RDAELANGALGHELNDYTLK KYMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAVSLSRDQKRMLY LEYDQIRKSDGTLQEHDGIGEN VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL
29781	60149	A	29964	1	1557	SETTO DETTO DE LA CONTROL DE L
	60150	Ā	29965	ī	2259	
29783	60151	Α	29966	ī	1959	
29784	60152	Α	29967	1	2277	
29785	60153	Α	29968	I	2418	
29786	60154	Α	29969	1	2028	
29787	60155	Α	29970	1	1650	
29788	60156	Α	29971	I	1170	
29789	60157	Α	29972	I	1446	
29790	60158	Α	29973	1	1191	
29791	60159	Α	29974	22	1893	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
29792	60160	Α	29975	1	1375	MNMNIKKIVKQATVLTFTTALL
						AGGATQAFAKENNQKAYKETY
						GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
		l				DSWPLQNADGTVAEYNGYHV
		l				VFALAGSPKDADDTSIYMFYQ
						KIRRKNGPVSATFTSDGKIRLFY
						TDYSGKHYGKQSLTTAQCDNL
	İ					KTCHTSHGSVMAETAVINHKK
i						RKNSPRIVQSNDLTEAAYSLSR
						DQKRMLYLFVDQIRKSDGTLQ
						EHDGICEIHVAKYAEIFGLTSAE
						ASKDIRQ ALKSFAGKEVVFYRP
ł						EEDAGDEKGYESFPWFIKRAHS
						PSRGLYSVHINPYLIPFFIGLQNR
						FTQFRLSETKEITNPYAMRLYES
						LCQYRKPDGSGIVSL/KIDW/IIE/
						RYQLPKVPSPEARKITRRWRI\V
l						KQRI*LGFLLRLSEMPRKQGDY
						RTRIWKFEDGLSNVLVIQLNKLI
						ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGSVMAETAVI
			l			NHKKRKNSPRIVQSNDLTEAAY
			l			SLSRDQKRMLYLFVDQIRKSDG
						TLQEHDGICEIHVAKYAEIFGLT
			l			SAEASKDIRQALKSFAGKEVVF
ŀ			İ	1		YRPEEDAGDEKGYESFPWFIKR
						AHSPSRGLYSVHINPYLIPFFIGL
						QNRFTQFRLSETKEITNPYAM/R
						IPLH*LFR*TLRQTKPDNSAGKC
l		i		1		VKI**HTQNQRSGRSQNDF*RR
29794	60162	-	29977		1317	GI
29794	60163	B B	29978	78	215	
29796	60164	c	29979	225	422	
29797	60165	A	29980	1	368	MAETAVINHKKRKNSPRIVQSN
29/9/	00103	^	25500	l'	308	DLTEAAYSLSRDQKRMLYLFV
l						DOIRKSDGTLOEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
ŀ						FAGKEVVFYRPEEDAGD/EKGY
ŀ		1				ESFPWFIKRIYSR
29798	60166	A	29981	1	409	MAETAVINHKKRKNSPRIVOSN
27,70	00100	l^	2/701	Ι.	1	DLTEAAYSLSRDQKRMLYLFV
						DOIRKSDGTLOEHDGICEIHVA
		1	l	I		KYAEIFGLTSAEASKDIRQALKS
		1				FAGKEVVFYRPEKDAGDEKGY
		1				ESFP\WFIKHSTNITSLSLWFFSS
l		1	l			CTH

SEO ID	SEO ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /*possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
20,000	101.00	<del>  -</del>	100000	3	678	GSVMAETAVIN\HKKRKNSPRI
29800	60168	Α	29983	13	0/8	
						VQSNDLTEAAYSLSRDQKRML
1						YLFVDQIRKSDGTLQEHDGICEI
1						HVAKYAEIFGLTSAEASKDIRQ
l						ALKSFAGKEVVFYRPEEDAGD
		ŀ				EKGYESFPWFIKRAHSPSRGLY
1					l	SVHINPYLIPFFIGLQNRFTQFRL
	1	l				SETKEITNPYAMRLYESLCQYR
		1				YSFPPDYFHGLALNVCGFSRYT
		l				VQDVGGSIILGSGGQWLSSHSS
						SRQCP
29801	60169	Α	29984	2	660	
29802	60170	Α	29985	179	283	MGQGRNPQTRRTYGCQFRMV
		ŀ				K*HGIEMKCEELIL
29803	6017I	Α	29986	1	643	
29804	60172	Α	29987	2	1073	
29805	60173	Α	29988	1	1167	MNMNIKKIVKQATVLTFTTALL
	1					AGGATQAFAKENNQKAYKETY
	1					GVSHITRHDMLQIPKQQQNEKY
		1				QVPQFDQSTIKNIESAKGLDVW
		l			l	DSWPLQNADGTVAEYNGYNV
		l				VFALAGSPEDADDTSIYMFYOK
ŀ		1		1		CDNLKTCHTSHGSVMAETAVI
		1				NHKKRKNSPRIVOSNDLTEAAY
						SLSRDQKRMLYLFVDQIRKSDG
l				ł		TLOEHDGICEIHVAKYAEIFGLT
	İ					SAEASKDIROALKSFAGKEVVF
1	1					YRPEEDAGDEKGYESFPWFIKR
1	i	l				AHSPSRGFYSVHINPYLIPFFIGL
					,	ONRFTOFRLSETKEITNPYAMR
					ŀ	LYESLCOYRK\PDGSGIVSLK/ID
				l		WIIKRSQLPQSAFYQPFMGLRR
		1		1		ESFYFRWERRTLGPLKSFSVKR
						GTEAGKFRLAALLVRL
20806	60174	ļ.	20000	I	1692	GTEAGKFRLAALLVKL
29806 29807	60174	A	29989	1	1788	
		A.				
29808	60176	A	29991	I	960	
29809	60177	A	29992	I	1385	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
29810	60178	A	29993	Ti Ti	936	MWLVTTELESTDTEHFYHHSK
27010	00176	ľ	27773	Ι'	250	CYWPRAHLGECILSIEAACOAA
1			1		\	GGEAGNGGSAVTKATLGSROG
1						
						AQHWKALARTIRQEKEIKGIQI GKQEVKLLPFADDMIIYLENST
l .						
		l	l			DSSKKLSELCDNLKTCHTSHGS
						VMAETAVINHKKRKNSPRIVQS
						NDLTEAAYSLSRDQKRMLYLF
						VDQIRKSDGTLQEHDGICEIHV
1						AKYAEIFGLTSAEASKDIRQAL
				l		KSFAGKEVVFYRPEEDAGDEK
						GYESFPWFIKRAH\SPFQRALYS
						CTICNP*ILIPFSF\IGLQNRFTQF
		_				R\LSETKEITNP\YAL\RLYQSLC
29811	60179	Α	29994	1	1641	
	60180	Α	29995	1	1551	
	60181	В	29996	90	1515	
	60182	Α	29997	452	1523	
29815	60183	В	29998	9	2021	
29816	60184	Α	29999	.1	960	
29817	60185	A	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA
			ļ			SSSNCAPRGISPQELTVDLQTKC
						DNLKTCHTSHGSVMAETAVIN
						HKKRKNSPRIVQSNDLTEAAYS
1						LSRDQKRMLYLFVDQIRKSDGT
1						LQEHDGICEIHVAKYAEIFGLTS
1						AEASKDIRQALKSFAGKEVVFY
1						RPEEDAGDEKGYESF\PWFIKR
1						AHSP\SRGL\YSVHINPYLNSLFY
						GVQNRFTQFRLNFVQKSRLVD
1						LALKGLRVLLVEGNDPQGTAS
1						MYHGWVPDLHIHAEDTLLPFY
1		l				LGEKDDVTYAIKPTCWPGLDIIP
1						SCLALHRIETELMGKFDE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29819	60187	A	30002	li .	1756	MPASGNENDLNMPSGTIEIFVR
29019	00187	^	30002	l'	1750	CYVEVERIMDFADFGTTIKQDF
						RLLGQTSVDRLLQLSQGQAVK
						GNQLLPVSLVKRKTTLAPNTQT
						ASPRALADSLMQLARQVSRLES
				ļ		GHQAPCMKSNNALIVILGTVTL
				İ	ŀ	DAVGIGLVMPVLPGLLRDIVHS
						DSIASHYGVLLALYALMQFLCA
						PVLGALSDRFGRRPVLLASLLG
		1				ATIDYAIMATTPVLWIYPLCDN
						LKTCHTSHGSVMAETAVINHK
1		l				KRKNSPRIVQSNDLTEAAYSLS
		1				RDQKRMLYLFVDQIRKSDGTL
		1	ŀ			QEHDGICEIHVAKYAEIFGLTSA
						EASKDIRQALKSFAGKEVVFYR
	1	1				PEEDAGDEKGYESFPWFIKRAH
		1				SPSRGLYSVHINPYLIPFFIGLQN
1		1				RFTQFRLSETKEITNPYAM/RIPL
		l				H*LFR*TLRQTKPDNSAGKCVK
						I**HTQNQRSGRSQNDF*RRPVL
		l				LASLLGATIDYAIMATTPVLWI
		l				YPLCDNLKTCHTSHGSVMAET
		l				AVINHKKRKNSPRIVQSNDLTE
		l				AAYSLSRDQKRMLYLFVDQIR
						KSDGTLQEHDGICEIHVAKYAE
						IFGLTSAEASKDIRQALKSFAGK
1		l				EVVFYRPEEDAGDEKGYESFP
		l				WFIKRAHSPSRGLYSVHINPYLI
	ĺ	l				PFFIGLQNRFTQFRLSETKEITNP
		l	1			YAMQSPYTDYSGKHYGKQSLT
		l				TAQVNVSKSDDTLKINGVEDH
		1				KTIFDGDGKTYQNVQQFIDEGN
29820	60188	A	30003	1	1653	
2982 I	60189	Α	30004	1	1128	PWISAPVPVDVVEGAMDSVTV
		1	l			LSFGGLMLYFCAGWPPARRWC
						FPESISCGSMERDQWWGLQVA
						KRAGLAGGOSGRTVLRERVRIE
					1	IASTHIALAARHSDWRCCRNGR
	1					YPARGPAALQNFQRYTGIQHV
						HRIGMAERMWCDRNRERHTVS
						SSGGNRLPNPGPDRSCDNLKTC
						HTSHGSVMAETAVINHKKRKN
						SPRIVQSNDLTEAAYSLSRDQK
				l		RMLYLFVDQIRKSDGTLQEHD
						GICEIHVAKYAEIFGLTSAEASK
				I		DIRQALKSFAGKEVVFYRPEED
			1	I		AGDEKGYESFPWFIKRAHSPSR
			1	I		GLYSVHINPYLIPFFIGLONRFT
				I		,
			1	1		QFRLSETKEITDPYAMRLYK\SL
				l		CQYRAFVNGGGEEKARGKPIL
	l				L	CRYGVGM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29822	60190	A	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA QRKKKYPPWEKLQGSVRGETP VINHKERKINSPRIVQSNDFPEA AYSLSRDQKRMLYLFVAQIRKS DGTLQEHDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESPW EIKRAHSPSRGLYSVHINPYLIPF FIGLQNRFTQFRLSETKEITNPY AMRLYESLCQYRKPDGSGIVSL KIDWIERYQLPGSYQRMPDFR RRFLQVCVNEINSRTPMRLSYIE KKKGRQTTHIVFSRDITSMGFF LESPTQGLASPE
29823	60191	A	30006	233	1538	
29824	60192	Α	30007	I	2331	
29825	60193	A	30008		1857	MPLRFSSSSRIPYYVNLLHKAA TGFERIDYNFETHSSLEIATDAL TISDHHPCESAAINAETRFSTVL EELARAIRQEKEIKGIQIGKEEV KLSLFADDMIMYLENPKDSSKK LLEWIKESNKVSGYKTHVHKS VALLYTNSDQVENQIRTQPFYN SCENKIKYLAIYLTKESKDLYK RNYKYLLKEITDDTNKWKHIPC SWIYUKVAGVESWHHTPQVESWH TPPEETAGSTAHGSQDQPDQPR YTCETLEGETHTIKAS STTDPEEKPLDHLLFQKETSHTIKA STTDPEEKPLPPYKRYCDNLKT CHTSHGSVMAETAVINHKKRK SPRIVQSNDLTEAAYSLSADL KRMLYLFVDHIRKSDGTLQEH DGIGEIHVAKYAEIFGLTSAEAS KOIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWEIKRAHSPS KOLTSCHINDEN TQFRLSETKIPVIIQEAGLSQSEK QAADGIGQVAHPAFQVCDGCG QAADGIGQVAHPAFQVCDGCG QAADGIGQVAHPAFQVCDGCG QAADGIGQVAHPAFQVCDGCG ABSCHHFILALUFQCPPLINL RVLIMATLFTIACYVELRGYML HAFQLVSLAMSHLHLAHNQDT HARISDVLWCALSHEFHRA SDVRADLSNAYSEEVREFFLLH SUGLOCKSLEFFRLH SDVRADLSNAYSEEVREFFLH SUGLOCKSLEFFLH SOURGLESSFFLH SUGLOCKSLEFFRLH SDVRADLSNAYSEEVREFFLH
29826	60194	A	30009	1	944	
29827	60195	Α	30010	1912	1915	
29828	60196	Α	30011	1503	1961	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
29829	60197	A	30012	li .	6552	MAETAVINHKKRKNSPRIVOSN
29629	00177	l^	30012	i'	0332	DLTEAAYSLSRDQKRMLYLFV
						DOIRKSDGTLOEHDGICEIHVA
	1				1	KYAEIFGLTSAEASKDIRQALKS
						FAGKEVVFYRPEEDAGDEKGY
		1				ESFPWFIKRAHSPSRGLYSVHIN
						PYLIPFFIGLQNRFTQFRLSETKE
						ITNPYAMRLYESLCQYRKPDGS
					ŀ	GIVSLKIDWIIERYQLPQIRLGDP
						GSSRLSMEHGLRSIPAWTLDKFI
						EDYLLPDTTFGADVKSAVNVV
					,	CDFLKERCF
29830	60198	A	30013	1	2679	MAETAVINHKKRKNSPRIVQSN
						DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
	1					KYAEIFG\LTSAEASKDIRQALK
						SFAGKEVVFYRPEEDAGDEKG
					1	YESFPWFIKRAHSPSRGLYSVHI
						NPYLIPFFIGLQNRFTQFRLSET
			Ì			KEITNPYAMRLYESLCQYRKPD
			ŀ			GSGIVSLKIDWIIERYQLPKVPS
	ļ.					PEARKITRRWRI\VKQRI*LGFLL
	ł					RLSEMPRKQGDYRTRIWKFED
						GLSNVLVIQLNKLIICVMCLVR
						DCDVLKTYFHR
29831	60199	Α	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI
						NHKKRKNSPRIVQSNDLTEAAY
						SLSRDQKRMLYLFVDQIRKSDG
						TLOEHDGICEIHVAKYAEIFGLT
						SAEASKDIRQALKSFAGKEVVF
İ						YRPEEDAGDEKGYESFPWFIKR
1		ĺ				AHSPSRGL\YSGHINPY\LIPFFIG
						LONRFTHF\RFMEQKKSPSNRFT
		ĺ				OVRLSETKEITNPYAMRLYESL
1		l	1			COYRKPDGSSIVSLKIDWIERY
		l				OLPOSYORMPDFRRRFLOVCV
		l				NEINSRTPMRLSYIEKKKGRQT
			1			
	L				L	THIVFSFRDITSMTTG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK
2,002	00200	ļ.,	20015	1	0207	SESDIHLAEHHKOVLYDGKLAS
		l				SIAFTYNAKATDAOLCLESSPK
		l			ì	ENASIFVHSPHALMLOILTEOV
		1				CTOVVHKPHPEPDSTVKIONPS
		ı				EOMAVLYCIVLVGGEFDLEMN
		1				FIIODAESITCMTELLEHCDVTC
		ı				QAEIWSMFTAILRKSVRNLQTS
		1				TEVGLIEOCDNLKTCHTSHGSV
		l				MAETAVINHKKRKNSPRIVQSN
						DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
İ				l		FAGKEVVFYRPEEDAGDEKGY
ŀ				ĺ		ESFPWFIKRAHSPSRGLYSVHIN
						PYLIPFFIGLONRFTOFRLSETKE
				l		ITNPYAMRLYESLCQYRKPDGL
						SIVSL\KIDWIIERYQLPQSYQR
				l		MP\DFRRRFLQDVQNETHGNT
29833	60201	A	30016	1514	6335	MPDFRRRFLQDVQNETHGNT
29834	60202	A	30017	2033	4226	
29835	60203	В	30017	1	5670	
29836	60204	A	30019	1968	3130	
29837	60205	A	30020	34	431	
29838	60206	A	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	A	30023	3	1771	
29841	60209	В	30024	1	2299	
29842	60210	Ā	30025	2	488	
29843	60211	A	30026	1	127	-
29844	60212	Α	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	T	836	
29847	60215	A	30030	297	936	RTSSSLMRSSSSLLRICSGVSPRS
		ļ				IPRWFTSVSLPSSFIR\RITTFRYT
				ŀ		PGHVAPASRRSCYKYRR*PMRL
				1		YTMIQSLS/VGSRPSGLRAFSSD
						CSPLPRTCSLSRRRVLMITTSRS
		ł				*SLTYGVDPSVRPVLAAASEYF
		1				SRR\YAGFQNPHNLLVSG*YQG
	ŀ	l				NYRHFGILRGYPG/TLKNSNFQL
						TRSARISLSSRSSICTSTGGNTTL
						PPSSPPDC
29848	60216	Α	30031	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ*
		1				APSDQKRDFLVPHGADSAMAK
	1					HGGSHRAVLPQGW
29849	60217	Α	30032	2	501	
29850	60218	Α	30033	1419	1640	IFCASLSLGLYAGIEARILTKGY
						TRK*IQQ*APSDQKRDFLVPHG
						ADSAMAKHGGSHRAVLPQGC
						DPHMESLI

SEQ ID			SEQ ID NO:		Nuclcotide location of last	
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29851	60219	A	30034	1	1593	
29852	60220	Α	30035	107	195	
29853	60221	Α	30036	1480	1605	TILRITFQFCRSNRRRQRQ*NRF STSQRRCYFLLNGEDVTLP
29854	60222	A	30037	<u> </u>	373	MPSYFTSRIAAVHVSALREEQA
27054	00222	l^	30037	1'	573	HHESKHHESFIAQRMFRMFYQ
						ARNLLHAGQENLFSGLTALTAE
					l	FTVGEEATRGKTTGKRGPSPDG
						RILRTTKTRNPRGYMQGRYLES
						ORDVEATDKPFEFFMNRFRLLE
						AAPRVEFIAYTGLCEDVIRPOL
						DEAIAOGYLTECADYWOITEH
						GKLFLNSLLELFLADGYHMWR
						MIGAGAHLAVGIDPTOLFLCOF
						EAVRKLLGNDQRAHLLPLGIEQ
						LPALKAFDTVFSMGVLYHRRSP
		ŀ				LEHLWQLKDQLVNEGELVLET
						LVIDGDENTVLVPGDRYAQMR
						NVYFIPSALALKNWLKKCGFV
		1				DIRIADVSVTTTEEQRRTEWMV
1		1		ł		TESLADFLDPHDPGKTVEGYPA
l		1	ĺ			PKRAVSDCAQAVKMTNMISYQ
		1	l	l		GLVRTFLSTSPNNWLVFMQNG
		1		l		QEVVIDSGKSVS*RSVCFGCFIK
		1		1		HGICSMRDKKISFLV*RRLLLNS
l		ı	ŀ	l		LSAKKLHGAKQRAKGDLPRMG
		l		ł		AFCVPPKRVIRVVICKEGIWKA
						SVMSKPQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCPSA
		1				PRSRRQRRRSGPLPEPAPRVS*Q
		1				IFPSQYWRYRQSTENQKQRLDP
		l				RGQIVNVPARRIIRQKRKCCKV
		Ļ.				AGSA
29856	60224	A	30039 30040	1	1090	
29858	60226	A A	30040	1	1377	
29859	60227	A	30041	2268	2684	RCRRCKRRLLRRFRRSLLSLAG
29839	00227	^	30042	2200	2004	SPENHARFYCRNSLPDEWFFRH
1						HPRST*PPRSREIRRCHCG*RQC
	1	1				SSDGRKITSVHRGRNADGRELT
						HQAVRLLAYLSDRFARHHRHL
		1				RNAHRRGPDRIPKERHFPATKL
		1			1	RHTPAV
29860	60228	Α	30043	1130	1310	RLDKONRROGKRORNNGVFHO
27000	00228	l^	30043	1150	1510	QPQRR*RTDVIQMPHSHHRHA
1	1	l		1		QRRDHQQLGQHHAGRNFE
29861	60229	A	30044	395	689	VAASVSSSMSCAPVLMTVVTR
27001	00223	ľ^	20044	1	007	CTLLILSOFMRRKAIKK/LSGSL
		l				LPASEVKVLKRDGDYSE/VQQ*
						APSDOKRDFLVPHGADSAMAK
		1				HGGSHRAVLPQGW
	1					

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
200.00	100000	<del>-</del>	20045	1	2142	
29862	60230	Α	30045	1	2142	
29863	60231	Α	30046	1	2463 1066	
29864	60232	A	30047	1		
29865	60233	В	30048	790	820	
29866	60234	Α	30049	3	126	
29867	60235	Α	30050	1853	2257	
29868	60236	Α	30051	90	411	
29869	60237	Α	30052	1375	3174	
29870	60238	A	30053	5	206	
29871	60239	Α	30054	1	1986	DELIVER DESCRIPTION OF THE PARTY OF THE PART
29872	60240	A	30055	339	596	PPYKRRKRRRESVSDGMRNTG KTRRTR*IINLLGRS*NRNFVSV PSGQNYP*ISLDHGRENYGGYS TIQNRLLRLPLSRSGCILQ
29873	60241	Α	30056	634	924	
29874	60242	A	30057	42	665	KYGVNPGPYGGTTIRKLYEKK LILKLREQGTESRSSTPLPTISSSA ENTROMGSSDDRYSDNEEDSK EILKLEKREPLKGRAKTPYTLK QRRVEHNGSYSQAGITETEWTS GSSKGGPLQALTRESTRGSRRT PRKRVETSEHFRIDDPVISSSTPI AETIMASSNESLVVRRVTGNFK HASPILPITEFSDIPRRAPKKPLT RAEVG
29875	60243	Α	30058	1822	4791	
29876	60244	A	30059	310	1275	
29877	60245	Α	30060	52	390	
29878	60246	Α	30061	250	1530	
29879	60247	A	30062	1	1641	
29880	60248	A	30063	1009	1140	
29881	60249	A	30064	913	1218	
29882	60250	Α	30065	900	999	
29883	60251	Α	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	Α	30068	1	2229	
29886	60254	Α	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSRCFWWKTAWAQKMN LLPMARLTTIIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALSLLTVTT QATGRLRARQRKTATPRTIRPG ESTSSSPRSSGSLSAPACSVPWM

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino aeid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
29888	60256	A	30071	498	1155	KQPSAVSGTGAAGEANLHAVR TAEQTAVVYRHRQNVRIVLR YGILDWSPTYLKEVKHFALDKS SWAYFLYEYAGIPGTLLCGWM SDKVPRGNRGATGVFFMTLVTI ATIVYWMNPAGNPTVDMICMI VIGFLIYGPVMLIGLHALELAPK KAAGTAAGFTGLFGYLGGSVA
						ASAIVGYTVDFFGWDVGFMLS HELWESEFTKLKYEYNNSCPAS VSGWL
29889	60257	A	30072	670	1100	NCRKTSPKRRFSFODPKSDRAK DFLAKILH*SLWRAYPIARHLTI YRFAPRICYILALPLSQRSTQQG ATMALPILLDCDPGHDDAIAIV LALASPELDVKAITSSAGNQTP EKTLRNVLRMLTLLNRTDIPVA GGRGKTVNA
29890	60258	В	30073	861	935	
29891	60259	Α	30074	1	2510	
29892	60260	A	30075	3	119	NALRKSASSCSGRNRYPGS*PS RPDCQRSCSHKHAGYG
29893	60261	Α	30076	3	227	GGEGRASCSADTGWLPSDPPGC AAGALGGGGWAVAGAAAGGP CA*SAGGIGVHAPKAQHPATFS GPAEGVIPPQ
29894	60262	Α	30077	1	2277	
29895	60263	Ā	30078	1	2187	
29896	60264	A	30079	1	3666	
29897	60265	A	30080	1	699	
29898	60266	Α	30081	513	1019	TGGVCCWCARYVDALVVFAD QLFVAEVLASAHSPSRLYAHAH GDTPQRLRLNGRQALSP*FCCN HRAALQRHOPVRPLPARQSRQ MRRCNLLYQKASAQRSQRDSS *RSLFFRSVDADGG*R*SHGYA FRHGRPGCHRPHGLPGTGPPH ADSAFSRRLIYPACRWRL
29899	60267	Α	30082	389	462	
29900	60268	Α	30083	1	278	MGVNDAVLEMHGLGNDFMVV DAGFDQLLVVEPPYDLELDFHY RMFNADGS/DSGAVRQRCALLC PFCASERTDQ*A*YPRQHRQRA DGSDRHR
29901	60269	Α	30084	1240	4914	
29902	60270	A	30085	1	1308	
29903	60271	А	30086	30	164	VTWW*RAPTAGLMQC*YCRNR RARLRLTYGHAPAHRRNGPDV PS

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29904	60272	A	30087	3	264	TLRPANRF*HIPDAAGVIPVGY
29904	00272	l^	30007	ľ	204	AL*RGTSVSAVHRW/CSTVFGV
l	1					NWATLATKLMVAGIRRSGAAS
1						
29905	60273	A	30088	ī	3639	RISRASPPSFSVPACSVGRKKVI
29903	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLLV
27700	00274	^	3000	*	)31	FADCLAWTCRHDKLDDISDVA
						KITGLTSKAIRFYEEKGLVTPPM
	1					RSENGYRTYTQQHLNELTLLRC
						AROVGFNLEESGELVNLFNDPO
ļ						RHSADVKRRTLEKVAEIERHIE
l		l				
						ELQSMRDQLLALANACPGDDS
						ADCPIIENLSGCCHHRAGKYVG
	1	1				LIRRVKRRIRHRCWPIKTLSQRA
	i					VSEFQRLIQPNHQYQSYTRQCA
						PETDNHADNSYNAGLFIVNSLY
	1	1			i	TAEGVMDKHSLWQRYVPLMR
l						HEALRLQVRLPASVELDDLLQA
	1					GGIGLLNAVERYDALQGTAFTT
						YAVQRIR\GAMLD
29907	60275	Α	30090	1	699	
29908	60276	Α	30091	430	660	HQTHFIVEHRRIMQRTARQNIG
1		1				RHYQIQLSAVQRIRGAMLDELR
l						SRDWVPRS\RRNAREVAQAIGQ
						MSLPMLQVALS
29909	60277	В	30092	1	1575	
29910	60278	A	30093	1	289	MISANRPIINLDLDLLRTFVAVA
				i		DLNTFAAAAAAVCRTQSAVSQ
1					1	QMQRLEQ\PLGKNCSLVTVATN
				l		C*LNMAFNFLVTPGKSCVLMM
						RSCIQPNSD
29911	60279	Α	30094	1	1095	
29912	60280	A	30095	1037	1297	LILRCPWSYSRCIRILIAPSSS*Q
						TEAKPFASRASRTSDDCQWANI
		1				SSVMPVKPNSTTPSILRRFSTPK
						CSATNCGEN*LSIMIGS
29913	60281	Α	30096	905	2042	
29914	60282	A	30097	87	760 2793	
29915 29916	60283	A A	30098	308	485	KSLNAICYRNTRTSMACY*PA*
29916	00284	l <sup>A</sup>	30099	306	1402	VRWPKHSAGLMTISPVLHVISP
		1				
29917	60285	A	30100	1	2784	RHWRLECATRVGRLG
29917	60286	A	30100	453	1975	
29918	60287	A	30102	3	470	
29920	60288	A-	30102	1447	1773	QFAFTEHHQTQEHHHQRSYDC
17720	00200	l^	33103	1,	1	PORDPRHIDAQVSDQRPCPDSG
						LREPLHCAQPDSGG*ADNSADH
	1	1	l		1	IRRNGGDGAFORKRNRTLTDPH
1	1		l		1	KRQEHGGLTLRIKLSVEQAFAG
29921	60289	A	30104	1	449	KRYLINGE I LAIKESVE QAPAG
29921	100289	ĮA.	130104	I'	1447	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29922	60290	Α	30105	188	1508	
29923	60291	Α	30106	171	410	
29924	60292	Α	30107	3080	3232	
29925	60293	Α	30108	1	1272	
29926	60294	Α	30109	438	617	
29927	60295	A	30110	259	392	
29928	60297	A	30111	3	1545	RITTPSISVCWRPAAKRPILPRS LKQLKKIASKVTP'\SLQINAW NNLEKQRAYLSMMAQKRVDG LLVMCSEYPEPLLANLEEYRHI MVVMDWGEAKADFTDAVID NAFEGGYMAGRYLIERGHREIG GRSDDOVDCDIQFFFSTNTITGR GHFRTMVDGICPCKDGNLFFN RILEHREPFYPQIPATFAYA AIVKFKRNVHQDGGYCSVQIQ QCFALIFSDFCRMRHNGLIRR TISQQSVGRIRCVSIASGRVYYC FFALEGKKPSSISAAPTQMAVS ARLKVAKCQSFT*KSIISTTEFC
29930	60298	A	30113	1	1562	HRRSNRLPSAPPIISATRVHRQM RYSTSSGAAALLSITVTPS
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLLTS LLTSVV*IDAIDGIRFSFLSWAS GKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRR RREREKTSERTPAPV*VKITTRK LYPAEERTGRIFEA
29933	60301	A	30116		3095	MDKFLNTYTLPRLNREVESLN RPVTASGLEVINSLPIKKSPGPD GFTAAFYQRYKEDAGEREGEG GNQQWAVRGKRKTTERKKLLG EDVKYKESKNSGAYEVKQHRF FRSLDWNSLLRQKAEFIPQLESE DDTSYPDTRSEKYHHMETEEE DDTSYPDTRSEKYHHMETEEE DOTNDEDFNVEIRGYSSCSHRFS KAAEVSTRLLSTRVTEIEGWLI VQRNQKLLQSNLKQRSGEPLIL DDDSHYPPELRAGYRLLKNAG CLPPELEQRREAIQ
29934	60302	A	30117	1	2583	
29935	60303	Α	30118	1	3141	

SEQ ID NO:	of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequenee	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop eadon, /=possible nucleotide deletion, /=possible nucleotide insertion)
29936	60304	A		1	1037	MRVVILGSGVVGVASAWYLNO AGHEVTVIDEREPGAALETSAAN AGDISPGYAAPWAAPGVPLKAI KWMPGRHAPLAVRLDGTGFGL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRAPPDTLATMPIGK CTPDNRRAVWRHRAQTSPESR LLDMTAAWIEIANHHLQRFTTR LQQLGIKTNNLRHSGKTRAVIV YMIQSISLVDEMSCHLVLTTGG TGPARRDVTPDATLAVADREM PGFGEOMRQISLHFVPTALLSRQ VGVIRKQALILALPGGPKSIKET LEGVKDAFGVYCIQLLEGPY
29937	60205	ļ	20120	96	711	VETAPEVVAAFRPKSARRDVSE
29937	60305	A C	30120 30121	128	628	
29938	60307	A	30121	1024	1128	
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHVF ATTCNRALSIWYLMN
29941	60309	С	30124	202	321	
29942	60310	С	30125	150	491	
29943	60311	Α	30126	1163	1257	
29944	60312	Α	30127	929	1023	
29945	60313	A	30128	3	765	TARAWILLGPVWPCVSERWSK KPSPRGGRDPSDRDPAAFAARS TVPPRISAYERPVPWPGEWNDP RGPGRRASAVVSPREGNWGVL ROPELQAKEPMVRSRQMCNT NMSVPTGGAVTTSQIPASEQET LVRQESEDYSQP*LLVALFIAA KKM*KSLKGKKPKTKKRVWN LVCPLMPLNLV*FVKVDLKMV ALSMAKQDILWPALHDAKKL KKRNKPCYCRQ;HMSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	Α	30129	2	430	
29947 29948	60315	A	30130 30131	3 303	1088 529	GTGQCANTKMSVPTDGA\VTTS QIPS/SPEQETRVR\PKPLL\LKLL KSVG\AQKDTYYYGKRFLFNLG QYIYGLNDYY
29949	60317	Α	30132	3	619	
29950	60318	Α	30133	123	385	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
				sequence		
29951	60319	A	30134	66	413	HQSEQMYQSSESCLLGTTAKA
						RGHQLRTASACHFPSTPPFWSL
						TLESQREGRFKQPTLISCF/CLF
ŀ						MSVPVVSAPPFSSSSSSSSSSSSS
						SRPWFPDQEAR*LTSPVERPCR
						GLRPA
29952	60320	Α	30135	257	465	VPTSPASLESKQSCPHVLCPVW
						EVEGHSV*TGKPDRPPRRKLLT
						LLLPVPWVPGQLAIKQEGQEPK KRH
29953	60321	A	30136	1564	1857	KKII
29954	60322	Α	30137	33	265	
29955	60323	Α	30138	114	560	
29956	60324	В	30139	70	555	
29957	60325	A	30140	650	1045	
29958	60326	Α	30141	374	575	
29959	60327	Α	30142	1	1095	
29960	60328	Α	30143	1	981	
29961	60329	Α	30144	28	698	TACRIRHGHAGRECCSPCLLVIP
		İ				LKSSQHI\LRVLNPPNLDGRRKI
						A\FAHHCPFKGVG\RRYA\HVVL
	1	1				RKAD\IDLTKEGGENSLEDEVE
ļ		1			l	RVITH/ILQNPRQYK\IP\DWFLN
	1			ļ		KTRRM*KDGTYSPGP*PIGLGQ
		1				QAPVKDLGAD*KKIRAH*/RGL
		1				RHFLGAFRVRGQAHQEPLGRR
		ı				GRHPSGVSKEEIRSVGPCLVNKI
						VYIPKKKKKKKKKVDAAANLVV VVVVGGR
29962	60330	A	30145	107	340	VVVdok
29963	60331	Λ	30146	428	934	
29964	60332	Α	30147	I	1533	
29965	60333	В	30148	1	2652	
29966	60334	Α	30149	205	450	
29967	60335	Α	30150	1	879	
29968	60336	Α	30151	139	1029	
29969	60337	Α	30152	237	422	WFETPAQYTNRSPESGTHYRRA
						RSRARWHGCMECVCRRRKSPR
L						ANKPRRLPPVR*RCPPRA
29970	60338	Α	30153	1	1134	
29971	60339	Α	30154	136	411	
29972	60340	A	30155	1	3345	
29973	60341	Α	30156	194	475	TPATVRRGWRPAVRVFRWWK
						PLTVPPRRKGPLSRGTGCRPVPL
						TTPSTGTVMRAGICAVKMLIVQ
						KSPCMPPC*HRQWTMTGLWQA
2007	(0242	<del> </del>	20167	l. —	2988	PAAIRPV
29974	60342	A	30157	1	3939	
29975 29976	60343	C	30158 30159	308	749	
			30159		1338	
29977	60345	Α	30100	1	1336	L

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
		_				
29978	60346	Α	30161	1	4342	MTRDNPVIPRFIHRREVVFIGQE
						NGGIQNARFIAALFFQHGVNLC
						QRVGGLLKGIGVEVFRYTSVVE
						RVVVDYYIRPAGFSIDTNDRGS
						VTDDFAPDGQLAKAIPGFKPRE
	l	1				PQRQMAVAVTQAIEKGQPLVV
						EAGTGTGKTYAYLAPALRAKK
	1	1				KVIISTGSKALQDQLYSRDLPTV
	1	1				SKALKYTGNVALLKGRSNYLC
1	i					LERLEQQALAGGDLPVQILSDV
	1				ĺ	ILLRSWSNQTVDGDISTCVSVA
						EDSQAWPLVTSTND
29979	60347	Α	30162	1	1023	
29980	60348	A	30163	1	679	MFRVTWSSGRTGLGKRLFRTP
	1					YDNDDTGPYAFNKTHPKDNYT
	l					CTVLFIDDMSASGQSLDKAQD
i	1				ľ	NYRQAMKKLSSGRGNVLAQAE
ĺ	1				ŀ	AFRGLGVEIKREINPDLAEQAIR
	i				İ	LQDCVFDTQETMTTTFTGTVSS
	l l				i	ANSGNYYTIFNTDTGAAFNNVS
	1					LAIGNYVVLAFSAS/VGA/DMK
					l	MVNSTITASGSKRSTTVLRQGL
						SQRWLLSAGARNLLQHYSFRE
					l	TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	Α	30165	1	1353	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amine acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
29983	60351	A	30166	li .	1661	MRGEVLLAGVPRHVAEREIATL
						AGSFSLHEONIHNLPRDQGPGN
						TVSLEVESENITERFFVVGEKRV
ŀ						SAEVVAAQLVKEVKRYLASTA
						AVGEYLADQLVLPMALAGAGE
	1					FTVAHPSCHLLTNIAVVERFLP
						VRFSLIETDGVTROLLGVSYRIL
						AMGHAEFLIQIADMRNDGGWR
		l l				DFQFSGNLVMDEPNRSAQTYIK
						LVKSRLGTTKRYNHKDDCPRC
						RWIAAMIDNPPRIRKPTKSASV
		l				WHATATSASPERQMSTTVIMS
	ł	1				ARFISCWVMTPFCMPRSGPMRF
					ł	VHLPCRFRDAFNTGVGKLDQL
		l				GPSMSTRIRQRFTTLCPMTLSSS
					ŀ	STEFENVSDCRPSRARSCLRFRL
		-				CRSIRCVYRLADYVQRSLQAGF
						IQRPAIRHPYHHVKGAFTEYVR
						NNRLPETVIRVLQPALARFSPDI
						APLFSPFPLHDDDVTARLYAPS
						LMPKLRLIGLTLLALSATAVSH
					1	AEETRYVSDELNTWVRSGPGD
	1					HYRLVGTVNAGEEVTLLQTDA
1						NTNYAQVKDSSGRTAWI/HVET
						T*H*AKPALPCARSGKSGQNPD
						R*THQYR
29984	60352	Α	30167	254	496	RASRLKTCGDGCCSLSAVVSVC
						ASPFASRVKSSRRWV*S*VGPSS
						WPPGMSL*TAEIRRSRRIPVVSS
						GSLTASFANVVR
29985	60353	A	30168	1	984	
29986	60354	Α	30169	1	429	
29987	60355	Α	30170	1	523	
29988	60356	A	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	67 I	
29992	60360	С	30175	1	2649	
29993	60361	Α	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	Α	30178	3	108	

SEQ ID NO:	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29996	60364	A	30179	404	1347	DVTILARAVLQALLKILYH/KCE
		į.		1		FNDEMLTEGVIREKMGFNPQTL
		1				REVLQACQQQGCVANNLDLDV
						VMIIIDGAFSGIVQNWLMNMA
		1		l		GYDLYKQAPALVDNRTGMER
		1				ASNGGPWQVQSLPARSYRQLD
1	İ					SYYGEAMAIGERALVALLDFSG
	1					PSPSGDWRYQTHHTFPPTGWR
ŀ						RQATLVKMRACIEAVKAVGEE
ŀ	1					LCPALGLTIPVGKDSMSMKTR
ŀ						WQEGNEEREMTSPLSLVISAFA
ŀ						RVEDVRHTITPQLSTEDNALLLI
						DLGKGNNALGATALAQVYRQL
						GDKPADVRDVAQLKGFYDAIQ
2000	500.55	+	20100	10.1	1.402	ALVAQRKLLAYHDRLI
29997 29998	60365	A	30180	1092	1433	
29999	60367	A	30182	315	600	STPIEKTVSKAFSAGSCSILTVT
27779	00307	^	30182	313	000	NARASARSACIISITAAVSGSCA
						PTP*EVSSAFARSLICRSIRKPGL
						KLRSITIGALASKTVLPASPPRIA
			1		İ	REKSITIOAEASKI VEI ASI I KIA
30000	60368	A	30183	535	661	
30001	60369	Λ	30184	I	1491	
30002	60370	Α	30185	1400	1852 534	
30003	60371	A	30186 30187	2	539	
30004	60373	A	30187	1	690	
30005	60374	A	30189	127	939	
30007	60375	A	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLCL
		ľ		1-07		TDERTRR\NNLRHATNSELLCE
		1				AFLHAFTGQPLPDDADLRKERS
		1				DEIPEAAKEIMREMGINPETWE
		1				Y
30009	60377	Α	30192	242	709	NYMHYHADRCITRCHGNACTV
		1				NYAGLRSVPTSTVWTGLNLLT
		1				KRIKYLMAEWSGE/YISGPCVEP
		1				GKKSDQSKKITVSIPLKVLKILT
						DERTRRQVNNLRHATNSELLCE
		ĺ				AFLHAFTGQPLPDDADLRKERT
		1				AE\IPEAAKREHA*HGGLTPET
						WEY
30010	60378	Α	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263	514	PAHFSVAHSHLWQNINPLSSVQ
						CRQNHQAIPCRIFELLNVMRH/
	1	1		1		VTRDSSSGLGCSWRLTASVNAR
20012	(0201	١.	20106	ļ	1006	RFVDPVQILVMAMSGRRSR
30013	60381	A	30196	1	1995	
30014	60382	Α	30197	141	229	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
30015	60383	Α	30198	1	702	
30016	60384	Α	30199	36	144	DGLLLMDERNISPLLQKRMPT*
		1				QAV*VWWKDYGV
30017	60385	Α	30200	462	646	QWVPIARPNMPACHVQRRTSSI
		1				ERRQPVMLMVMLRILWYIYCS!
						HVLG*WICRLYYKTLLK
30018	60386	Α	30201	107	1200	
30019	60387	Α	30202	366	500	
30020	60388	A	30203		1193	LADCSRYNGLEMTILSCCAGAS TDAVGGIERGGLKSPRASEGEI APRLLLDGEPLALSGDKWRISP WLLVTDDTATITAFLOMIQEGK AITLREDGDYTISLSGI.KAALLFI DAQQKRYGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPLISLEERNDLLDYGNWRMNGLRC SLDPLRREVNYTALTDDKALM MISSQIFNGIMVHIIKDLVFTD APDKGISFGSDTGMDRPARGD HRLLVMHHDMTRFLR.PHHVE GVPLVTRSQLRQPHTIRLAGFQI IRDQIFVNRATVTGEEITAJAFQL TNFPANGNRFSYRHNAANNNS VNVAVHGVLIGDKYLFNORF
3002I	60389	Α	30204	3	1057	
30022	60390	Α	30205	I	955	
30023	60391	Α	30206	1281	1370	
30024	60392	В	30207	1	2199	
30025	60393	A	30208		589	MLKKREQTVFTHEKSYPGGL GRNEELGPKTFGVKGAQKON LQIFSEDKNFGPGGSGEIWGHR GPKWDIPRGKRETLGRPHFFW KPSQEFGRKGLGSFGPWERVSC NKNSGKRIYPWGPVDGINCRW REPRNVDVAEYRRDCGSRFRSL KHFYRSLSFLHRPASTRIQKAQ SSAVTVLQTNAQHGRRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRTCCAPL.SSVWRCR PPRSSPWPASWRSVPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCLWTSSLAPASRE CPS*ILQPPGQQRWGEPIGAIAV PL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuelcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequenee		
30027	60395	Α	30210	61	641	RHKHRRRIPGRWDQIRPAPNR
						WQTGFQWFALPVTGVRLISGY
						TELLPRL/PAQKNLPYTIHPAWR
						FVAHQGRESALECRYVPLPVRH
		l				*RNCRWREPRNVDVAEYRRDC
		l				GSRFRSLRHFYRSLFSLHRPAST
		l				RHPGAQTGAVTGFADECPARK
		l			l	AAALAKASVNKVVFHSTNATV
1		l				CHRPDRSRRASGSFRRYWRQE
30028	60396	Α	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLANSKNKRR
		1			İ	WRKNIKLR*SSLLK*TESPLPMA
		11				ILVLTSLTAI
30030	60398	A	30213	451	834	IWTGKKVDSARALIARGWGLH
						VILRRTDDWMDGRRSRHTDDT
ŀ		l			ŀ	DVLLRIHHVIGELPTYGYRRVW
		1				ASSQTGRT**FKVQNRYFPPVLS
1		l				DFEHLQEPYEYFGKLR*PWLPA
						TGEFHAEIYRSVDFCKHPV
30031	60399	Α	30214	1180	2547	
30032	60400	A	30215	341	505	
30033	60401	A	30216	293	4221	KPFSPCCRKGRWLFRNHSSARR
1						PTVLYYRRSTMR*NSW*PNLRR
i						QRGNPANRS/RQSMLELSGVKD
]		l				GELIPAKLFNHLVTWLQARQTL
1						SQQNTPRPGGGEIPPWCSSVLA
						ESERKKRGRKKQRGIDSPDVGA
						LLLVRATFYIWQQPPVNKIALGI
					ļ	EYAASKYYGWQRQNEVRSVQ
		1			ľ	EKLEKALSQVANEPITVFCAGR
						TDAGVHGTGQVVHFETTALRK
		1				DAAWTLGVNANLPGDIAVRW
		_			-	VKTVPDDFHARFSATAR
30034	60402	A	30217	1	1362	
30035	60403	Α	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWRR*SP
		_				QYARHTRKRTSAGCSA
30037	60405	A	30220	1160	2385	
30038	60406	A	30221	290	373	
30039	60407	Α	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	A	30224	1	469	
30042	60410	A	30225	241	615	
30043	60411	A	30226	1	1428	

	01/0/300/					PC 1/US01/08631
SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30044	60412	A	30227	862	1453	SFLLVSPSQACHHYYAP/KIFDI SGYTSTTEQMWGTVIVGLTNV LATFIAIGLVDRLGFLAMPAGN GVLGTMMIIIGIHSPSAQYFAI/ MLLMFIVGFAMSAGPLIWVLC EIQPLKGRDFGITCSTATNWIAI
						MIVGATFLTMLNTLGNANTFW VYAALNVLFILLTLWLVPETKI VSLEHI/ERNLMKGRKLREIGA D
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCCPPV: WHFFFHSRLCRDALNEAFHSC FQVVKCCDIARIHRNRYGDLI AIGVVHIANVNAHIHRNATTHOG QEIGGGFTNQOPI-SIGGAMN VDNFLQRPETYGDPFCQYHFH QVLLYRIFGNLIVGYOHQICPR KSPPLNADLTVNQAFINPA*NN IWHSVFLFVLLIGLHRLGGMR DVLNMVDNEFPWRWLQLAGA DVLNMVDNEFPWRWLQLAGA NFHVLQRQILADQRQRNW
30047	60415	Α	30230	2553	3845	
30048	60416	Α	30231	I	656	
30049	60417	Α	30232	3	228	
30050	60418	Α	30233	185	206	ATVDPPFITEPGDILAGGFA*PL SWFAGFALEHHNLPWATGDLI SLRA
30051	60419	Α	30234	12	155	
30052	60420	Α	30235	698	2684	
30053	60421	Α	30236	1	2004	
30054	60422	Α	30237	1	811	
30055	60423	В	30238	1	7521	
30056	60424	В	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPWNRKPVLSVIP* WKLKGPVALKTAYPAKRLPLF TSFSLPGVA
30058	60426	Α	30241	L	2067	
30059	60427	В	30242	1	2787	
30060	60428	Α	30243	101	947	
30061	60429	Α	30244	1	1917	
30062	60430	Α	30245	239	469	KRVSISSRRRFSAQKASASALA RWWRSAVNIYVFAI*TTAQRV QLRMTNCVRTTITACHSR*RIT SLSPVKPAS
30063	60431	Α	30246	1	4348	
30064	60432	Α	30247	1141	2244	
30065			30248	503	649	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide detetion, \=possible nucleotide insertion)
30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRLFIGAERFQHIAGSGHYR VV*NANAGSKIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNFFNFEIFQRLVDDDP HCTIGIMFANVDHGTTENRIRK LCFNLTNTGTQRKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	Α	30250	1	526	
30068	60436	A	30251	442	684	
30069	60437	Α	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPLPLPTENVP AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDRPRLAIRDATIGISG FCSLA
30071	60439	Α	30254	62	298	
30072	60440	A	30255	904	1530	
30073	60441	A	30256	701	1329	HRLSMCRGRCSRWWSARTNVI SMLYFALSFASWRIVSPRTMD ALTFAAESALPGSPTHISTDHOG QFVFVGSYNAGNVSVTRLEDG LTMLHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTPPEA CTTNKOPAQPORDKPQRGNQQ RLASVIFQCQQHDHEHKERHTY PAHQLAERHLVDRLLM
30074	60442	A	30257	8	382	
30075	60443	В	30258	1	2655	
30076 30077	60444	A	30259 30260	67 1109	231	TFLHSIPAAKTQGPPPRNTLVDT PQHL*HQQRRTRQPQLALSLRT *VFLNRILRGALFAPKACLKPD LVISPRGPPQGLGVTRVQVSAH TNPRTTHRNTPHYTRNTQTRPE STPRRDTTTPQQRHTPPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDRSDSPISQSKMKIIA SITTIRMEP*AIATPYSPSSTRLR M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSPISQSKMKIIASITTIRMEP *AIATPYSPSSTRLRM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	Α	30263	3026	3217	LPQCKWDPYGVTISPQVSIRSR ANPSCTSPFFV*SATKGLLYQQ TRIPALDIPPSSNRRNSHG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPHYGRWPQ HDPPPFKLLRPQSVTSRIPQFGSV VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSLRKTVVAHVFGE RSLFTGP*RERFATQIEVGKLFA AAVDMVLWLSGKAQPDTVVV KVVVL
30082	60450	Α	30265	3174	4135	
30083	60451	Α	30266	1	2771	
30084	60452	Α	30267	1	1281	
30085	60453	А	30268	10	233	LRIQASDPEINSRRESGIHLPYTT DKAPSPLTVDGAK*EVSRSSI/R QNSQVQHPPDAAKYPSGCHKS FRGFRRA
30086	60454	A	30269	300	564	SANSTLKRTQVNRRPLTVKLSA RKLPMLKVNTRNSLVVVVSMV MLLSTCTRWSRVQTRKATSSST TLKVV*SLANTSRPLIKVSRNS
30087	60455	A	30270	5259	8003	
30088	60456	Α	30271	1	819	
30089	60457	Α	30272	1173	1369	
30090	60458	Α	30273	1	4767	
30091	60459	Λ	30274	905	1162	FSSVVMCSSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSCRSS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	Α	30275	1164	1582	
30093	60461	Α	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGVS RLYAANQHRTCQ
30095	60463	В	30278	1	954	
30096	60464	A	30279	108	530	SIROTHVQIVRESCLAIRHQVPS TAIRVGIVKGNFAS*AGAQPSK TI.R*HRCTTRALTSGVLAVRLS AGCNFPELVHRRLTLWRAGRT YPPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLTP PFPAGQRC
30097	60465	A	30280	1	1389	
30098	60466	A	30281	1	380	
30099	60467	Α	30282	1	3255	
30100	60468	Α	30283	569	2547	
30101	60469	Α	30284	1	585	
30102	60470	Å	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGSLG PSSGPKTAGAPSSRPPSPSARRP RTTETRWTLLRSKDYWLITRKV GLGNLQDGGRAGSLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleutide location of first codun for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
30103	60471	Α	30286	737	1088	NMLMNVCNLPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRCLPIIVGR RKSGGSKIRANVCSLPIFPSGNG R*TTGESKRI.CRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAEST\SPLAMVGD GINDAPAMKAAAIGIAMGSGT DVALETADAALTHNHLRGLVQ MIELARATHANIRQNITIALGLK GIFLVTTILLGMTGLWLAVLAD TGATVL
30106	60474	A	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPP IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFIVOTSGLENHAENIDEAW KWHTAQILAKKSEQWGQVY AIVQNTDQAQAVMPYGPKCLY VLAQNDALQATENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTINASLAGIALNSMDLSP GGRVAVKESNQRWCSDGFEC CDNGERLRVTFALDCCDREAL HWANTTIGGFNSETVQDWILG AVETPLRQRSSVVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQSRHRPAPALRYPQLQ MPHWRRSICTSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIKSASLS*FK*LLKPAINAG*Q AS*WRASASKPCSASPDCAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	Α	30294	1246	1300	
30112	60480	С	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCGVD
30114	60482	В	30297	1	3081	
30115	60483	Α	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVATKLRR *RVFPAPCCG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30116	60484	Α	30299	3	421	QRRATGDLRLPTR*TARRGGRC
						DS*SSRRWHRAFTGACREISRQ
				l		QNRRHRQRPAGGVALVGSE*T
	l				1	SGILAGQRHYRVYRAGYRRSPP
	1	l		l		AGYAPD*SD*RPVDGRHECGRR
						PVWRRENVPATGGQIGARHET
					1	GGGLPRTVY
30117	60485	A	30300	1	3202	
30118	60486	Α	30301	317	554	
30119	60487	Α	30302	474	599	TTSVQRTFLPDTY*APTPVLLPA
						RKATAARKLHRFSGRQDR
30120	60488	A	30303	212	569	TSLKVVTPALRSMPSVPINNLS
		1				KVKCSKAFSASCP*NEADFLRN
		1				VPPGIRIVCSLSSSDSALTICRLL
		1		l		VITVMLLKRESRGTICKTVLPAS
		1				RMIESPSWIKLTAASAISSFLWV
						LMSVL
30121	60489	Α	30304	1	160	WSKMSRAVRPSDWESWTQTRE
		l				VVRQTVRCRPDPPSAAVCLTAS
		l				SPANCGIPIG**MLAEILA*RAV
		1				RPSDWESWTQTREVVRQTVRC
		1				RPDPPSAAVCLTASSPANCGIP1
						G
30122	60490	Α	30305	1	975	
30123	60491	Α	30306	1	762	
30124	60492	Α	30307	1	733	
30125	60493	Α	30308	493	948	LGAIFLAGALFAAAWLADFRL
	1					GLGARLYRYGADWFCADGGM
	1					SAEELKFISENGAVVDMDHKKP
	1					GSAAASGPKLHYIKQLLSNRM
		1				MLGVFFGQYFINTITWFFLTWF
			l			PIYIGNVVSDNR*YVAQITFITW
	1					IKTYGRCPSFQRDGDGFVNRCL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30126	60494	A	30309	153	2031	RRNYQRQQKKRGSEGAGRPDR RSRISAAYSPRSEFNNAAVTEH
		1				Y*NRF*T/LVPRSR/HANADTVT
		1				REAVNQVIALLDSGALRVAEKI
						DGLPTNQMQASRRAKEEEVHL
		1				TGQPSRVQSPPRRCEEKQYMVL
		1	1		i	MIVSGRSGSGKSVALRALEDM
		l				GFYCVDNLPVVLLPDLARTLA
		l	1			DREISAAVSIDVRNMPESPEIFE
		l				QAMSNLPDAFSPQLLFLDADRN
		l				TLIRRYSDTRRLHPLSSKNLSLE
		l				SAIDKESDLLEPLHGFPDYDTV
		l				GFSCKRRIDYVCRIKHSRRIRQV
		l				VLLNFAKSGAFSTTRGTDDKTR
		l		ŀ		RSLLVTLVRIFCVRVIFAYDIRD
		l			1	GIHVRIIQINSKSGKVGSKHNSG
						YSAAKFGGVGLTQSLALDLAE
		l		İ		YGITVHSLMLGNLLKSPMFQSL LPQYATKLGIKPDQVEQYYIDK
		l				VPFKRGCDYODVLNMLLFYAS
		l		l		PKAVVLAPDSRSMSPAVSGRFK
		l		ł		PRVVVAIALDDQQRIVDTLFMK
		l	1	İ		GLTVFARPOKIPAITGRHSGATL
						OKOGKCSVEELAQYFDTTGTT
						MRKDLVILEHAGTVIRTSGGVV
						PDSPPHTRRDPRRFSMAFPWFD
						NIRSAEFHHVTTLLAEIPRQQND
						IHRPAHAAAAPKVETRSGDETN
						RRWNRPAOHLFA
30127	60495	A	30310	720	872	EKVPVSIGPGGMQELPMQSPDR
		1				RSAGKPGPASRAGR*TGGGAFS
						TKRDYR
30128	60496	Α	30311	1967	2452	SRRCSASINORPRPGHEKMVSV
						RIAPASNVPTCRPITVTTGSIALR
						SAWTIITRMRVSPLARAVRM*S
						SPSTSSIEERVIRTMTASGIVPST
						MAGKIIWATASIKLPSSPQMAV
						SISIKPVNGLESSRNTISLTRPET
						GVRFQCTETSMISIMPHQKIGIE
30129	60497	Α	30312	1912	3960	
30130	60498	Α	30313	2	250	LIRKVST*SVLMKAFLRIA*KDC
						ERLGLKCFWSGSEKGCPLVNT
1				l		NAFGGHCEHHQWVSSVSRVRV
		L				SQSAGGCPLFNILLNTV
30131	60499	Α	30314	I	300	SVFSH*AKKIWKGVSQRALGQ
				l		NSRGSGSGCQASWTIRFPVGFH
1						TDGTRLRRNPGMQAFLGPVAR
				l		FLALEARSLDCAFSSSLLFKRKL
L						SGRWGRASRGTKL

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last aminn acid	*=Stop codon, /=possible nucleotide
i	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30132	60500	Α	30315	1	468	MTEKVKQQPAPVTASDEIDIGR
		l				LVGTVIEARWWVIGITTVFALC
i		1				AVVYTFFATPIYSADALVQIEQ
l		ı	ŀ			NSGNSLVQDIGSALANKPPASD
						AEIQLIRSRLVLGKTVDDLDLDI
i		l				AVSKNTFPIFGAGWDRLMGRQ
l						NETRRGFSARGTGQMLKKEGV
		l				TLMVEAIHASPGSEFTVTKYST
		1				LGMINQLHNSLTVTENGKDAG
		1				VLSLTYTGEDRYTNHAGVVNT
						MIIIAATHNLVFENNSCEYAHP
						MGNAPAGLTEYQNVFYKHDRI
						OGHYVWEWRDHGIOAODDHG
						NVWYKFGGDYGDYPNNYNFC
						LDGLIYSDQTPGPGLKEYKQVI
		l				APVKIHARDLTRGELKVENKL
						WFTTLDDYTLHAEVRAEGETL
	İ					ATOOIKLRDVAPNSEAPLOITLP
						QLDAREAFLNITVTKDSRTRYS
						EAGHPIATYQFPLKENTAQPVP
						FAPNNARPLTLEDDRLSCTVRG
						YNFAITFSKMSGKPTSWQVNGE
						SLLTREPKINFFKPMIDNHKQEY
						EGLWQPNHLQIMQEHLRDFAV
						EQSDGEVLISRTVKPRGPARCP
		1				DSSVGTTYCTENNPPFDNGLLN
	İ					AQLLQQAKPFVDERQSK*FGCH
						SPSYSCLWLSIIGLKKLIFGSRVS
						SDSPFTCQDVGLPLIFEKVIAKL
30133	60501	Α	30316	1	524	2201110421021011011111111
30134	60502	Α	30317	1669	4421	
30135	60503	A	30318	2	349	SMAKCPLRKNQGPVRSCGAWS
						GCLWLPSPSGTPWRSSLWILLL
						F/SQISQLLSLLHQGQFQPKPNH
						RGNKYLAKPGGSRSAIPDTDGP
						SARAGGQTDPEQEEGPLDPEED
						LSVKQLL
30136	60504	В	30319	217	368	
30137	60505	Α	30320	1	951	
30138	60506	С	30321	1	3729	
30139	60507	Α	30323	1	2437	

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30140	60508	Α	30324	1005	1815	PDLHCQKKHPTLCSGYWPTFRT
		1				PVHYAAFS**/HALGHLAFS/EA
		ĺ				SLHSHRGTQALTTQKKSPAKSP
	i	l				TAATTETRVMRKISHGTRDPPG
						FASL\MQ*MHYGKLCAFQSELL
						FQSLQRSHWTQSWWLCWPHW
						RLCWTONWWOCWPHWTLCW
					i	TQSWWLCWPHWRSCWTQRW
İ	i					WLCWPHWTLCWTOSWWLCW
	1					SHWRSCWTOSWWLCWPHWRL
1						CWTQSWWLCWPHWRSCWTQS
1				ļ		WWLCWPHWRLCWSOSWWLC
						WPHWRLYWTQSWWLCWPHW
		1				RVCWTQN
30141	60509	Α	30325	2436	3678	KMPPWPPGSPGPLGCSAWAEA
		1				PPAHCPDVLLHLHPACPHIQAP
1		1			ł	CGTGAPGTGLAAAADSEPLGSS
İ					İ	APPAGRPCPQAAAACGLAPPLP
						RGWCPPPTSSWMGRRLQSLSA
						HPTSPAPLLAAPTAVCSCSRCSA
l l		1				PRSRCVARPAARTGLPTPAPAS
					l	SPAPATSPAPAESPAATASHPV
					i	AEASPAPGAPPPRPAASPSPAAS
						PAPPAASPVLTASPPLPAASPAL
		1				AASPVHTASPPVHVASPPVHTA
						SPPVHTASPPVHVASPPVHVAS
						PPVSCSGDSTSDCFPPQPGAVFP
						HSL/VSFLRWLVSSCSCSTLDGP
						AGGCGARGSAVWFLSLNKLLP/
						MLLYQMYLMLLLLLRCANQ*I
ŀ						DVFSELTDYCGA*IQGYC*FLV
1						LAIPR*VVTTRSGCVRATAIDFL
						FPVSSCWNARALPLPICF
30142	60510	Α	30326	929	2910	
30143	60511	Α	30327	1	1488	
30144	60512	Α	30328	203	701	
30145	60513	A	30329	493	924	SDPGFRHGKARITDPRGQPGRR
						LQGGSSEGNGSDMKAARKVSG
						NKHSTSSHQHAVWCPGVPS*SG
						KAWAADQRFVPRILGKGRGHV
1						DAA*LSWKCRNHLSSVSLNGE
		1				NQRFVGDARYRTRLQRGSANL
	1	<u> </u>				FKRQRCGTLHQNLELL
30146	60514	A	30330	1	2193	
30147	60515	A	30331	1	2990	ELL DUDONUDUREUR VODU
30148	60516	Α	30332	2512	2560	FALRYRQPVRHRW*FHLVQRH
		1	1		1	GRFSRASGATWPASAAAFAWP
20115	50517	<del> </del> -	20222	ļ. — —	2020	LLVCAPLSAASAAPLARL
30149	60517	A	30333	1	2820	
30150	60518	C	30334	194	418	
30151	60519	A	30335	25	458	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30152	60520	A	30336	860	1209	IPGNCRDSSGVGIKERETNAGS QHMH/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPENPVYEKKPK KEVKKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	Α	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	Α	30339	1723	1845	
30156	60524	A	30340	6	983	IRRWACRSLSSGRRSLFRRMGF VKVVKNKAYFKRYQVKFRRRR EGKTDYYARKELVIQDKNKYN TPKYKMIVRVTNRDIICQIAYA RIEGDMIVCATYAHELPKY KVGLTNYAAAYCTGLLLARRF LINRRGMDKIYEQQVIELTGDE VTVESIDQQGAFTCYLDAGLA RTTTGNKVFGALKGAVDGGLS YPLTYPKRFPWFDDS*KPRNLI AEVHRKPHPWAQNVARLHAPT LMBEDIEDANYKKQFVRQYVKN SVTPDMMEBMYKKAHAAIRE ESSSMEKKAQGKKFKKKRWNR PKMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	В	30341	1	2043	
30158	60526	Α	30342	390	1180	
30159	60527	Α	30343	2	649	
30160	60528	A	30344	1	1929	
30161	60529	A	30345	1	773	
30162	60530	A	30346	.3	484	NSSCRDFGY/CPIVSLNSS*GSL LQDMPGPSKVISEILATRGAVNI TTVAYKSAVILSFTTASAVSLSS RNVIGPLFASQPSFTIHFSLFSHN GSAPLNAPDMANCFGLTALTSS LDERLFSRNSAGSCCGIRNCFIS TLPPNTSTLTSVNSKGSSSVHG
30163	60531	В	30347	1	2775	
30164	60532	Α	30348	1	1386	
30165	60533	Α	30349	439	555	
30166	60534	Α	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITECRTIV. EQRYALSQAKSIADELMTGCTN FAFSGKPGTGKNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMRSVGMLTNLNY EAMKTLLGERIMDRMTMNGG RW
30168	60536	Α	30352	1	786	
30169	60537	A	30353	1	288	
30170	60538	A	30354	711	953	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30171	60539	C	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	Α	30357	1	420	
30174	60542	Α	30358	1115	1561	
30175	60543	В	30359	501	555	
30176	60544	Α	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	A	30361	386	1647	
30178	60546	Α	30362	l .	1179	
30179	60547	Α	30363	1	1215	
30180	60548	Α	30364	1282	1657	
30181	60549	A	30365	388	804	
30182	60550	Α	30366	1328	1978	
30183	60551	Α	30367	455	1000	
30184	60552	A	30368	291	303	RVRRMMYTVTLYSFSTNKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSLQTVSLL LLSSFALDPSSTMLTTEESVE
30185	60553	A	30369	284	433	RVRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	Α	30370	290	425	RVRRMMYTVTLSSFSANKNTYI *E*E*GLGWRHHIFLG*IQHFNR
30187	60555	Α	30371	842	905	
30188	60556	Α	30372	784	3453	
30189	60557	Α	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSPSGSLGP RGGRGGCILRPSRGGRGRHGPT KAGPWSPESRGR*DWKARGPP APSRGSPSRARARRGGSGGGPA DEPGLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	A	30375	1	340	
30192	60560	Α	30376	2	3336	
30193	60561	Α	30377	22	419	
30194	60562	Α	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECWSLF*SH MHVLLPRNRKEKLIEIFRTQTY DVNAYKASAHRNSGPG
30196	60564	С	30380	169	415	
30197	60565	Α	30381	3	1324	
30198	60566	Α	30382	2	3455	
30199	60567	Α	30383	85	2695	
30200	60568	A	30384	69	303	
30201	60569	Α	30385	1	951	
30202	60570	A	30386	1	4749	
30203	60571	Α	30387	176	1553	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30204	60572	A	30388	1	425	MDQIISLFGRPDHVAYDIRSLER KANPDDTFEAQLFYGDLKAIVK TSHLVKUDYPKFIVHGKKGSFIK YGIDQQETSLKANIMPGEPGFA ADDSVGVLEYVNDEGVTVREE MKPEMGDYG/PRL*CVVSNHHF RCAKLROGI
30205	60573	A	30389	3	1890	PSQPLLWFAGRPEGRDTGCPRC KQNSTCIA AVKMEGPLSVFGGR STGETIRSQNDKESSPNEQKTCRI *RKRLV*LYEVAEHEIVMAAAS LAINVESSLEGVGLDKMLVVDI GDVTITNDGATILKLLEVEHPA AKVLCELADLQDKEVGDHTY VVIIAAELLKNADELVKQEHPT SVISGYNRLA/CKEAVRYIYNEMP MLTQDELGRDCLINAAKTSMS SQIIGINGDFFANMVVDAVLAI KYYTDIRGQPRYPVNSVNILKAH GRSQMESMIJSGYALNCVVGS QGMPKRIVNAKIACLDFSLQKT KMKLGYQVVITOPEKLDFSLQKT KMKLGYQVVITOPEKLDGPIGQREVIY VLKRDLKRIAKASGATILSTLA* NLEGEETFEAAMLGQAIEEVVG VLKRDLKRIAKASGATILSTLA* NLEGEETFEAAMLGQAIEEVVG VKIRVLESKISVVPRIGGAVEAA LSIYYLENYÄNTSMGSREQLAIAR VCKITLWLFPPTLSS*CLPRODST KNLKWIGLDSLAILKSTKARTSASIIS RVPIDSMCDEMERSLHDALCV VKIRVLESKISVVPRIGGAVEAA LSIYYLENYÄNTSMGSREQLAIAR VCKITLWLFPPTLSS*CLPRODST KNLKWIGLD.SNGTPRDNKQA GYFEPTIVKVRGLNFATEAAITI LRIDDLIKLHPESKDDKHIGGGS
30206	60574	В	30390	1	975	YEDA VHSGALND
30207	60575	В	30391	1	2577	
30208	60576	В	30392	1	3126	
30209	60577	В	30393	1	1134	
30210	60578	В	30394	1	2082	
30211	60579	В	30395	1	915	
30212	60580	В	30396	1	2658	
30213	60581	В	30397	1	2412	
30214	60582	В	30398	1	2454	
30215	60583	В	30399	89	2533	
30216	60584	В	30400	1	4083	
30217	60585	В	30401	1	1725	
30218	60586	С	30402	127	345	
30219	60587	A	30403	1	597	

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30220	60588	A	30404	3	3386	MPATASAGVPATVSEKQEFYQ
1						LLKNLINPSCMVRRQAEEIYENI
	ļ					PGLCKTTFLLDAVRNRRAGYE
						VRQMAAALLRRLLSSGFEEVYP
	ŀ					NLPADVQRDVKIELILAVKLET
	ŀ					HASMRKKLCDIFAVLA\RNLID
						EDGTNHWPEGLKFLIDSIYSTN
						VALWEVALHVFWHFPGIFGTQ
						ERHDLDIIKRLLDQCIQDQDHP
						AIKTLSARAAAAFVLANENNIA
	İ					LFKDFADLLPGILQAVNDSCYQ
						DDDSVLESLVEIADT
30221	60589	A	30405	1	1695	
30222	60590	A	30406	1126	1355	
30223	60591	A	30407	1	1610	MGSRCLNPPPPAHSDTTGKDSF
1						GNIRGAETGQGASACSVTSARV TCGAGSEPHSHRNPGISAOVGL
1		1				APSYGAARGRRRPLALQQSPQE RRHVGWNSTRGLLPASLPGTAS
	l					SOSASATASAALPLKVTGPLAR
1						NPTPPWTAAAALATRGORPEK
1		i				GLFPGPAPFSLGKRKRGRGRTW
						ERRRVSIETSTCFRPGCERLGA
						AAGANLSQLASSQRPLRERWV
	1					LYTIMAAAGAPDGMEEPGMD
						TEAETVATEAPARPVNCLEAEA
						AAGAAAEDSGAARGSLOPAPA
						QPPGDPAAQASVSNGEDAGGG
						AGRELVDLKIIWNKTKHDVKFP
						LDSTGSELKQKIHSITGLPPAMQ
1						KVMYKGLVPEDKTLREIKVTS
						GAKIMVVGSTINDVLAVNTPK
1						DAAQQDAKAEENKKEPLCRQK
						QHRKVLDKGKPEDVMPSVKGA
						QERLPTVPLSGMYNKSGGKVR
						LTFKLEQDQLWIGTKERTEKLP
						MGSIK\NVV\SDPI\EGHEDYHN
1						DGRFQLAPTEA\SYYWVYWVP
		_				TQYVDAIK\DTVLGKWQYF
30224	60592	A	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP
						SAAGRRAMKKKLVVLCLLAVV
		1				LVLVIVGLCLW/LPSASKEPDN
						HVYTRATVAADAKQCSEIGRK\
						AEVINAREVAPSVAFASMFNSS
20225	60593	_	30409	562	2376	EQSQKAL
30225	00393	Α	30409	302	2310	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
30226	60594	A	30410	604	2475	ROREVTRSPPERSGLRVLQLFPP
50220	0055		30.110	100,		NPPVFRGOHPROGLGPPSAAGR
						RAMKKKLVVLGLLAVVLVLVI
				1		VGLCLWLPSASKEPDNHVYTR
				i		AAVAADAKQCSKIGRDALRDG
				l		GSAVDAAIAALLCVGLMNAHS
				l		MGIGGGLFLTIYNSTTRKAEVIN
	1					AREVAPRLAFATMFNSSEOSOK
				1		GGLSVAVPGEIEGYELAHORHG
	ĺ			l		
				l		RLPWARLFQPSIQLARQGFPVG
				1		KGLAAALENKRTVIEQQPVLCE
				l		VFCRDRKVLREGERLTLPQLAD
				1		TYETLAIEGAQAFYNGSLTAQI
				1		VKDIQAAGGIVTAEDLNNYRA
				1		ELIEHPLNISLGDAVLYMPSAPL
				l		SGPVLALILNILKGYNFSRESVE
				!	İ	SPEQKGLTYHRIVEAFRFAYAK
				ŀ		RTLLGDPKFVDVTEASSGVSA\
				1		VVRNMTSEFFAAQLRAQISDDT
				l		THPISYYKPEFYTPDDGGTAHL
				1		SVVAEDGSAVSATSTINLYFGS
					1	KVRSPVSGILFNNEMDDFSSPSI
				l	ŀ	TNEFGVPPSPANFIQPGKQPLSS
				l	1	MCPTIMVGQDGQVRMVVGAA
				ŀ		GGTQITTATALAIIYNLWFGYD
						VKRAVEEPRLHNQLLPNVTTVE
						RNIDQAVTAALETRHHHTQIAS
						TFIAVVQAIVRTAGGWAAASDS
				ŀ		RKGGEPAGY
30227	60595	Α	30411	63	342	GRTLVPHGGLPHHYLVQCEWL
						PGTS*AEFPVVHLPAFVARARG
						ADROHHGPFLPLCHLHPARPRR
						EDLHRKSPGEPNPIEHHRSSGPG
						CRRI
30228	60596	Α	30412	1	910	MLFRPALGSRQVVRNMTSEFF
						AAQLRAQISDDTTHPISYYKPEF
						YTPVDGGTAHLSVVAEDGSAV
						STTSTINLYFGSKVRSPVSEILFN
						DEMDDFSSPNITNEFGVPPSPAN
1						FIOPGMGWR\KOPLSSMCPTIM
						VGQDGQVRMVVGAAGGTQITT
				l		ATALICVTAFLPGRAHPAQPPS
						HADHTPMPQAIIYNLWFGYDV
		l				KRAVEEPRLHNQLLPNVTTVER
		ı		1		NIDOAVTAALETRHHHTQIAST
		ı		l		FIAVVQAIVHTAGGWAAASDS
		l				RKGGAYRILSALQEDKADKQS
				l	1	RDKILTRTRKGTLGDWLPM
			L	L		KDWILIKIKKGILODALLM

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
30229	60597	Α	30413	110	868	DLCPLPTLPPHLLRPALGSRQV
		1				VRNMTSEFFSAQLRAQISDDTT
		1				HPISYYKPEFYMPDDGGTAHLS
		l				VVAEDGSAVSATSTINLYFGSK
		1				VRSPVSGILLNNEMDDFSSTSIT
		l				NE\LGVPPSPANFIQPGKQPLSS
		ĺ				MCPTIMVGQDGQVRMVVGAA
						GGTQITMATALAIIYQPSWFGY
						DVKRAVEEPRLHNQL\LPNVTT
1						VERNIDQAVTAAL\ETRHHHTQ
1						IASTFIAVVQAIVRTAGGWAAA
						SDSRKGGEPAGY
30230	60598	Α	30414	1	1626	
30231	60599	Α	30415	171	2097	PSGEREGCLIRESLKKILWLQAS
						AECEGDPGYFLSYFHQILLSFV
						ANTPRQGLGPPSAAGRRAMKK
-						KLVVLGLLAVVLELVIVGLCL
						WLPSASKEPDNHVYTRAAVAA
						DAN\LCSKIGRDALRDGGSAVD
1		l				AAIAALLCVGLMNAHSMGIGG
						GLFLTIYNSTTRK\AEVINAREV
				Į		APRLAFATMFNSSEQSQKGGLS
						VAVPGEIRG\YELAHQRHGRLP
			ŀ			WARLFQPSIQLARQGFPVGKGL
			ŀ			AAALENKRTVIEQQPVLCEVFC
						RDRKVLREGERLTLPQLADTYE
						TLAIEGAQAFYNGSLTAQIVKDI
			ŀ			QAAGGIVTAEDLNNYRAELIEH
						PLNISLGDAVLYMPSAPLSGPV
						LALILNILKGYNFSRESVESPEQ
						KGLTYHRI\VEVFRFAYAKRTL
l						LGDPKFVDVTEASSGVSA\VVR
l						NMTSEFFAAQLRAQISDDTTHPI
						SYYKPEFYTPDDGGTAHLSVV
						AEDGSAVSATS\TINLYFGSKVR
1	1					SPVSG\ILFNNEMGDLSSPSI\TN
1	l					EFGAPPSPANFIQPGKQPLLSMC
1	1					LTIMVGQDGQVRMVVGAAGG
l	l	ı	1			TQITTDTALAIIYN\LCFGYDVK
l	l	l	İ			RAVEEPRLHNKLLPNVTTVERN
			1			IDQAVTAALETRHHHTQIASTFI
						AVVQAIVRTAGGWAAASDSRK

SEQ ID		Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	detetion, \=possible nucleotide insertion)
30232	60600	Α	30416	645	2571	GRPRLFPQLFPPNPPVFRGQHPF
		ı				QGLGPPSAAGRRAMKKKLVVL
		l				GLLAVVLVLVIVGLCLWLPSAS
		l				KEPDNHVYT\RAAVAADAKQC
						SEIGRVLVGGPAYLLLLGKAEV
		l				INAREVAPRLAFASMFNSSEQS
		l				QKGGLSVAVPGEIRGYELAHQ
		1			ŀ	RHGRLPWARLFQPSIQLARQGF
		l				PVGKGLAAVLENKRTVIEQQPV
		1				LWYVCGKVLREGERLTLPRLA
		l				DTYEMLAIEGAQAFYNGSLMA
		l				QIVKDIQAAGGIVTAEDLNNYR
						AELIEHPLNISLGDAVLYMPSA
		l				RLSGPVLALILNILKGYNFSRES
		1				VETPEQKGLTYHRIVEAFRFAY
		l				AKRTLLGDPKFVDVTENSIAGL
		l				LCARMDSPALGSRQVVRNMTS
						EFFAAQLRSQISDHTTHPISYYK
İ		1				PEFYTPDDGGTAHLSVVAEDGS
		l				AVSATSTINLYFGSKVCSPVSGI
		l				LFNNEMDDFSS\PAFTNEFGAPP
					1	SPANFIQPGKQPLLSMCLTIMV
						GQDGQVRMVVGAAGGTQITTE
		1				TALPPSHADHTPMPQAIIYNLW
		1				FGYDVKRAVEEPRLHNKLLPN
		1		1		VTTVERNIDQAVTAALETRHH
		1		l		HTQIASTFIAVVQAIVRTAGGW
		l		l	1	AAALDSRKVPTPGAGFWEGLV
		<u>L</u>				EVGWWEAVITAQHLDITRGTG
30233	60601	Α	30417	5	439	
30234	60602	Α	30418	I	423	1

	SEQ ID NO:			Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		1		sequence		
20005	10000	<del>  -</del>	20410	97	lacia	WAR PERSON OF BUILDINGS TO THE
30235	60603	Α	30419	97	2012	WADEETWLCLPHLPVFSPTAHL
						PLLSSTPFSSLLPFISTPHPRGFA
1	l		l			LPLPPSARLYLELRKLPATLPWS
1			l			SVTDTGSYLSGRRERGGEGEGP
						GRRVRVADHGFALPRTGPQGS
			ľ			EEELANMQGL\VERLERAVSRL
						ESL\SAESHRPPGN\CGEVNGVI
						A\GVAPSRGKPLHKLMDSMVA
1						EF\LKNSRILSGDVETLAEIVHS
						AFQAQRAFLLMASQYQQPHEN
						DV\AALLKP\ISEKI\KEIQTFQRE
1				ŀ		/RTRGSNMFNHLSAVSE*IPCPL
						DGIAVSPKPG\PY\VKEMND\AA
1		1				TFYT\NRVLKD*KQSDLRHVDW
						VKSYLNIWSELOAYIKEHHTTG
						LTWE/SKTGPV\ASTVS\AFSVLS
		1		l		SGAWGFPPPPPPLPPPG\PPSTFS
i						EEWKGKKEESSPSR\SALFAQL
	l	l				N/QGEKAITKGLRHVT\DDQKT
		l		ļ		YKNPSLRAOGGOTOSPTKSHTP
1	i	l				SPTSPKSYPSOKHAPVLELEGK
		l	İ			KWRVEYQEDRIDLVISETELKQ
1	ŀ					VAYIFKCEKSTIQIKGKVNSIIID
	l					NCKKLGLVFDNVVGIVEVINSO
		l				DIQIQVMG\RVPTISI\NKTEGCH
						IYLSEDALDCEI\VSAKSIWKWN
						ILYPPOGWVD\YREFPHFP\EOF
						KTS/AWDGS\KLITEP\AEIMALT
						SLRDRTPSPESPSIKTNKKAAVK
30236	60604	В	30420	1	499	
30237	60605	В	3042 I	390	851	
30238	60606	В	30422	136	603	
30239	60607	В	30423	1	2190	
30240	60608	Ā	30424	82	242	
30241	60609	A	30425	1	330	
30241	10000	٠.	55725	·	220	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30242	60610	A	30426	215	1984	LLLVVTMSNNGLDIQDKPPAPP
ļ		l				MRNTSTMIGAGSKDAGTLNHG
						SKPLPPNPEEKKKKDRFYRSILP GDKTNKKKEKERPEISLPSDFE
						HTIHVGFDAVTGEFTGMPEOW
						ARLLQTSNITKSEQKKNPQAVL
		1				DVLEFYNSKKTSNSQKYMSFTS
1		i				GDKSAHGYIAAHPSSTKTASEP
						PLAPPVSEEEDEEEEEEDENEP
i i		i				PPVIAPRPEHTKSIYTRSVVESIA
		ŀ				SPAVPNKEVTPPSAENANSSTL
						YRNTDRQRKKSKMTDEEILEKL
						RSIVSVGDPKKKYTRFEKIGQG
		l				PASGTVYTAMDVATGQEVAIKQ
						MNLQQQPKKELIINEILVMREN
		1				KNPNIVNYLDSYLVGDELWVV MEYLAGGSLTDVVTETCMDEG
		1				QIAAVCRECLQALEFLHSNQVI
		1			ì	HRDIKSD\NILLGMDGSVKLTDF
		l				GFCAQITPEQSKLSTHG*GTPY
		1				W/M/APEVVDTERAYGPK/VLDI
		1				WSLGIMAIEMIEGEPPYLNENP
						LRALYLIATNGTPELQNPEKL\S
						AIFR\DFL\NRCLEMDVEKRGFS/
		l				SKELLQHQFLKIGQAPSPSLTPH
		ŀ				*LLQPKEATKEQSPKTHTHPQP
		_				HCAQAFCEINAHFRNSNS
30243	60611	Α	30427	2	337	
30244	60612	Α	30428	1	1644	
30245	60613	A	30429	1	330	
30246 30247	60614	A	30430	169	1689	
30247	60616	A	30431	17	283	GHAWOLASIWLLCLLWPAVPL
30240	00010	ľ	30432	l''	203	NCLSSYGWTLWWRIALVGA*R
						SLAPSRGSWSTQARPLKORRTK
						WCGKSWCLSGTSEPLSHWPRL
						RSW
30249	60617	Α	30433	16	346	RTDTYHLEDSKEQSGNRAGSG
						GWL*SCAE/GRRVALKSWPGRT
					1	GMSGTRRVTASSRGTSWYCGG
1			1		1	SAGRSSTPPTGRACSPGSFSSPE
L		L				PQPPGPSAAGSSVSGQLGPCGG
30250	60618	Α	30434	1	1772	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30251	60619	Α	30436	1	2607	MLTMSVTLSPLRSQDLDPMAT
						DASPMAINMTPTVEQGEGEEA
		1				MKDMDSDQQYEKPPPLHTGAD
	l	1		1		WKIVLHLPEIETWLRMTSERVR
	1	1				DLTYSVQQDSDSKHVDVHLVQ
		1				LKDICEDISDHVEQIHALLETEF
		1				SLKLLSYSVNVIVDIHAVQLLW
		1				HQLRVSVLVLRERILQGLQDAN
						GNYTRQTDILQAFSEETKEGRL
		1				DSLTEVDDSGQLTIKCSQNYLS
			l			LDCGITAFELSDYSPSEDLLSGL
						GDMTSSQVKTKPFDSWSYSEM
						EKEFPELIRSVGLLTVAADSIST
						NGSEAVTEEVSQVSLSVDDKG
						GCEEDNASAVEEQPGLTLGVSS
		1				SSGEALTNAAQPSSETVQQESS
		1				SSSHHDAKNQQPVPCENATPKR
						TIRDCFNYNEDSPTQPTLPKRGL
		1				FLKEETFKNDLKGNGGKRQMV
		1				DLKPEMSRSTPSLVDPPDRSKL
		1				CLVLQSSYPNSPSAASQSYECL
	1	1				HKVGNGNLENTVKFHIKEISSS
		1				LGRLNDCYKEKSRLKKPHKTSE
		1				EVPPCRTPKRGTGSGKQAKNT
		1				KSSAVPNGELSYTSKAIEGPQT
		1				NSASTSSLEPCNQRSWNAKLQL
		1				QSETSSSPAFTQSSESSVGSDNI
		1				MSPVPLLSKHKSKKGQASSPSH
		1				VTRNGEVVEAWYGSDEYLALP
		1				SHLKQTEVLALKLENLTKLLPQ
						KPRGETIQNIDDWELSEMNSDS EIYPTYHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	LITT I THYRRRITHEORYSI SS
30253	60621	В	30438	1	702	
30254	60622	В	30439	1	936	
30255	60623	В	30440	l .	1494	
30256	60624	В	30441	jl .	921	
30257	60625	В	30442	I	3342	
30258	60626	В	30443	I	1072	
30259	60627	В	30444	1	3711	
30260	60628	В	30445	15	674	
30261	60629	В	30446	ı	2127	
30262	60630	В	30447	1	3132	
30263	60631	В	30448	103	438	
30264	60632	В	30449	1	3042	
30265	60633	В	30450	1	1425	
30266	60634	В	30451	84	1954	
30267	60635	В	30452	1	1419	
30268	60636	В	30453	130	1615	
30269	60637	В	30454	1	1794	
30270	60638	В	30455	1	3255	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30271	60639	В	30456	1	945	
30272	60640	В	30457	1	7437	
30273	60641	В	30458	1	1122	
30274	60642	В	30459	317	1630	
30275	60643	В	30460	1	1716	
30276	60644	В	30461	46	915	
30277	60645	В	30462	I	624	
30278	60646	В	30463	244	2988	
30279	60647	В	30464	1	804	
30280	60648	В	30465	1	1455	
30281	60649	В	30466	1	732	
30282	60650	В	30467	340	777	
30283	60651	В	30468	1	714	
30284	60652	В	30469	166	1337	
30285	60653	В	30470	72	617	
30286	60654	В	30471	1	1002	
30287	60655	В	30472	1	4173	
30288	60656	В	30473	1	4488	
30289	60657	В	30474	1	3822	
30290	60658	В	30475	i	1866	
30291	60659	В	30476	1	1002	
30292	60660	В	30477	1	1407	
30293	60661	В	30478	99	1046	
30294	60662	В	30479	122	1113	
30295	60663	В	30480	302	4145	
30296	60664	В	30481	1	669	
30297	60665	В	30482	i	933	
30298	60666	В	30483	I	2136	
30299	60667	В	30484	1	4017	
30300	60668	В	30485	ī	1335	
30301	60669	В	30486	1	1095	
30302	60670	В	30487	1	2895	
30303	60671	В	30488	1	1215	
30304	60672	В	30489	ı	2001	
30305	60673	В	30490	1	1281	
30306	60674	В	30491	1	780	
30307	60675	В	30492	1	858	
30308	60676	В	30493	i	699	
30309	60677	В	30494	1	1624	
30310	60678	В	30495	1	2958	
30311	60679	В	30496	30	658	
30312	60680	В	30497	1	1755	
30313	60681	B	30498	i	631	
30314	60682	В	30499	1	1528	
30315	60683	В	30500	1	1056	
30316	60684	В	30501	i	2305	
30317	60685	В	30502	1	723	
20011		В	30503	1	2691	
30318						
30318	60686				2322	
30318 30319 30320	60686 60687 60688	B B	30504 30505	1 401	2322 2677	

30322   606 30323   606 30324   600 30325   600 30326   600 30326   600 30327   600 30328   600 30329   600 30321   600 30331   600 30331   600 30331   600 30331   600 30331   600 30334   600 30338   600 30336   600 30340   600 30341   600 30351   600 30351   600 30351   600 30355   600 30356   600	10690 1691 1692 1693 1694 1695 1696 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1707 1708 1707 1708 1707 1708 1709 1710 1711 1711 1711 1711 1711 1711	B B B B B B B B B B B B B B B B B B B	in USSN 09/546,217 30526 30527 30528 30528 30528 30528 30528 30528 30528 30528 30528 30527 30528 30529	location of first codon for peptide sequence  1	codon for last amino acid of peptide sequence  906  906  2865  820  783  410  840  945  2108  2457  1156  4677  964  4521  2460  1884  1367  419  1786  1443	*-Stop codon, /=possible nucleotide deletion, \=possible nucleotide inscriton)
30322 606 30323 606 30323 606 30325 600 30325 600 30327 600 30329 600 30330 600 30331 600 30331 600 30331 600 30331 600 30331 600 30334 600 30336 600 30340 600 30341 600 30351 600 30351 600 30351 600 30355 600 30355 600 30355 600	0690 0691 0692 0692 0693 0694 0695 0696 0697 0698 0699 0700 0701 0702 0703 0704 0707 0708 0709	B B B B B B B B B B B B B B B B B B B	30507 30508 30509 30510 30511 30511 30513 30515 30515 30516 30517 30518 30519 30520 30521 30522 30523 30522 30523 30524 30525 30526	1	906 2865 820 783 410 840 945 2108 2457 1156 4677 964 4521 2460 11854 118	ucteaus,possible nucronice insertion)
30323 606 30324 606 30325 600 30326 600 30326 600 30327 600 30327 600 30328 600 30329 600 30331 600 30331 600 30331 600 30331 600 30331 600 30331 600 30334 600 30338 600 30338 600 30338 600 30340 600 30350 600 30350 600 30350 600 30355 600 30355 600 30355 600 30355 600	0691 0692 0693 0694 0695 0696 0697 0698 0699 0700 0702 0703 0704 0704 0705 0706 0707 0708 0709 0710 0711	B B B B B B B B B B B B B B B B B B B	30508 30509 30510 30511 30511 30512 30513 30514 30515 30516 30517 30518 30519 30520 30520 30521 30522 30523 30524 30525 30525 30526 30527 30527 30527 30527 30528	1 45 1 1 18 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2865 820 783 410 840 945 2108 22457 1156 4677 964 44521 22460 1854 11367 419 11786 1443 486	
30324 606 30325 606 30327 606 30327 606 30327 606 30327 606 30328 606 30329 606 30331 606 30331 606 30333 607 30334 607 30334 607 30334 607 30334 607 30346 607 30347 607 30348 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30359 607 30359 607 30359 607 30359 607 30359 607 30359 607 30359 607 30359 607 30359 607	0692 0693 0694 0695 0696 0697 0698 0700 0701 0702 0703 0705 0707 0708 0709 0711 07112 07113	B B B B B B B B B B B B B B B B B B B	30509 30510 30511 30512 30513 30514 30514 30515 30516 30517 30518 30519 30520 30520 30522 30523 30522 30523 30525 30525 30527 30527 30527 30527 30527	1 45 1 1 18 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	820 783 410 840 945 2108 2457 1156 4677 964 4521 2460 1854 1367 419 1786 1443 4466 1260	
30325 606 30326 606 30326 606 30327 600 30327 600 30328 600 30330 606 30331 600 30331 600 30331 600 30331 600 30331 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30340 600 30341 600 30341 600 30342 600 30343 600 30344 600 30345 600 30345 600 30356 600 30356 600 30356 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600	0693 0694 0695 0695 0696 0697 0698 0699 0701 0702 0703 0704 0705 0706 0707 0707 0708 0709 0711 0711 0711	B B B B B B B B B B B B B B B B B B B	30510 30511 30511 30512 30513 30514 30515 30516 30517 30518 30519 30520 30521 30522 30522 30523 30524 30525 30525 30525 30526	1 18 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	783 410 8840 945 2108 2457 1156 4677 964 4521 2460 1854 1367 419 1786 1443 486 1443	
30325 606 30326 606 30326 606 30327 600 30327 600 30328 600 30330 606 30331 600 30331 600 30331 600 30331 600 30331 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30334 600 30340 600 30341 600 30341 600 30342 600 30343 600 30344 600 30345 600 30345 600 30356 600 30356 600 30356 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600 30355 600	0693 0694 0695 0695 0696 0697 0698 0699 0701 0702 0703 0704 0705 0706 0707 0707 0708 0709 0711 0711 0711	C B B B B B B B B B B B B B B B B B B B	30510 30511 30511 30512 30513 30514 30515 30516 30517 30518 30519 30520 30521 30522 30522 30523 30524 30525 30525 30525 30526	1 18 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	783 410 8840 945 2108 2457 1156 4677 964 4521 2460 1854 1367 419 1786 1443 486 1443	
30326 606 30328 606 30329 606 30329 606 30329 606 30329 606 30331 606 30331 606 30331 606 30333 607 30334 607 30334 607 30334 607 30334 607 30334 607 30334 607 30334 607 30334 607 30334 607 30344 607 30344 607 30344 607 30345 607 30346 607 30346 607 30347 607 30348 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30349 607 30359 607 30359 607 30359 607 30355 607	0695 0696 0697 0698 0700 0701 0702 0703 0704 0705 0707 0708 0707 0708 0710 0711 0711	B B B B B B B B B B B B B B B B B B B	30512 30513 30513 30514 30515 30516 30517 30518 30519 30520 30521 30522 30522 30522 30524 30525 30526 30527 30525	1 1 1 1 1 1 43 80 1 1 1 1 1 273 1 1 1169 1 1 13270	840 945 2108 2457 1156 4677 964 4521 2460 1854 1367 419 1786 1443 443	
30328 00333	9696 9697 9698 9699 9700 9701 9702 9703 9704 9705 9706 9707 9708 9709 9710 9711 9711	B B B B B B B B B B B B B B B B B B B	30513 30514 30515 30516 30516 30517 30518 30519 30520 30521 30522 30523 30524 30525 30526 30527 30526 30527 30528	1 1 1 1 43 80 1 1 1 1 1 273 1 1 1 1 1 169 1 1 3 270	945 2108 2457 1156 4677 964 4521 2460 1854 1367 419 1786 1443 486 1443	
30329 000 30330 600 30331 600 30332 600 30332 600 30333 600 30334 600 30335 600 30337 600 30336 600 30337 600 30341 600 30351 600 30351 600 30351 600 30355 600 30355 600 30355 600 30355 600	0697 0698 0699 0700 0701 0702 0702 0703 0704 0705 0706 0707 0708 0709 0710 0711	B B B B B B B B B B B B B B B B B B B	30514 30515 30516 30516 30517 30518 30519 30520 30521 30522 30523 30524 30524 30525 30526 30527 30528	1 1 1 43 80 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2108 2457 11156 4677 964 4521 2460 1884 11367 419 11786 1443 4466 11260	
30330 606 30331 606 30332 607 30333 607 30333 607 30334 607 30335 607 30336 607 30336 607 30340 607 30350 607 30350 607 30350 607 30350 607 30350 607 30358 607	0698 0699 0700 0701 0702 0702 0703 0704 0705 0706 0707 0708 0709 0709 0711	B B B B B B B B B B B B B B B B B B B	30515 30516 30517 30518 30519 30520 30521 30522 30523 30524 30525 30526 30527 30528	1 1 43 80 1 1 1 1 273 1 1169 1 1 13 270	2457 1156 4677 964 4521 2460 1854 1367 419 1786 1443 446 1260	
30331 000 30332 601 30333 603333 603 30334 603 30334 603 30335 607 30336 607 30337 607 30334 607 30341 607 30341 607 30344 607 30344 607 30344 607 30345 607 30346 607 30347 607 30348 607 30348 607 30349 607 30349 607 30359 607 30359 607 30359 607 30358 607 30358 607 30358 607 30358 607 30358 607 30358 607	0699 0700 0701 0702 0703 0704 0705 0706 0707 0708 0709 0711 0712	B B B B B B B B B B B B B B B B B B B	30516 30517 30518 30519 30520 30521 30522 30523 30524 30525 30526 30527 30528	1 43 80 1 1 1 1 2273 1 1169 1 1 13 270	1156 4677 964 4521 2460 1854 1367 419 1786 1443 446 1260	
30332 607 30333 607 30334 607 30335 607 30337 607 30338 607 30338 607 30338 607 30338 607 30339 607 30341 607 30342 607 30342 607 30344 607 30345 607 30346 607 30346 607 30347 607 30348 607 30349 607 30349 607 30350 607 30350 607 30351 607 30352 607 30355 607 30356 607 30356 607 30356 607 30358 607 30358 607 30358 607	0700 0701 0702 0703 0704 0705 0706 0707 0708 0709 0711 0712	B B B B B B B B B B B	30517 30518 30519 30520 30521 30522 30523 30524 30525 30526 30527 30528	43 80 1 1 1 1 1 1 273 1 1169 1 1 13 270	4677 964 4521 2460 1854 1367 419 1786 1443 486 1260	
30333 60°333 60°3333 60°3333 60°3333 60°3333 60°3333 60°3333 60°3333 60°3334 60°3334 60°3334 60°3334 60°3334 60°3334 60°3334 60°3334 60°3335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335 60°335	0701 0702 0703 0704 0705 0706 0707 0708 0709 0710 0711	B B B B B B B B	30518 30519 30520 30521 30522 30523 30524 30525 30526 30527 30528	80 1 1 1 1 1 273 1 1169 1 13 270	964 4521 2460 1854 1367 419 1786 1443 486 1260	
30334 607 30335 607 30337 607 30337 607 30337 607 30338 607 30339 607 30341 607 30342 607 30344 607 30344 607 30345 607 30346 607 30347 607 30348 607 30349 607 30351 607 30351 607 30352 607 30353 607 30353 607 30355 607 30355 607 30355 607 30355 607 30355 607 30356 607	0702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712	B B B B B B B	30519 30520 30521 30522 30523 30524 30525 30526 30527 30528	1 1 1 1 1 273 1 11169 1 1 13 270	4521 2460 1854 1367 419 1786 1443 486 1260	
30335 607 30336 607 30337 607 30338 607 30338 607 30340 607 30341 607 30342 607 30345 607 30345 607 30346 607 30347 607 30348 607 30349 607 30349 607 30349 607 30349 607 30350	0703 0704 0705 0706 0707 0708 0709 0710 0711	B B B B B B B	30520 30521 30522 30523 30524 30525 30526 30527 30528	1 1 273 1 1169 1 13 270	2460 1854 1367 419 1786 1443 486 1260	
30336 60:3 30337 60:3 30338 60:3 30339 60:3 30339 60:3 30340 60:3 30341 60:3 30344 60:3 30345 60:3 30346 60:3 30346 60:3 30347 60:3 30348 60:3 30348 60:3 30349 60:3 30350 60:3 30350 60:3 30350 60:3 30355 60:3 30355 60:3 30356 60:3 30358 60:3 30358 60:3 30359 60:3	0704 0705 0706 0707 0708 0709 0710 0711	B B B B B B	30521 30522 30523 30524 30525 30526 30527 30528	1 1 273 1 1169 1 13 270	1854 1367 419 1786 1443 486 1260	
30337 603 30338 603 30339 603 30340 603 30341 603 30342 603 30343 603 30345 603 30346 603 30346 603 30347 603 30348 603 30349 603 30350 603 30350 603 30350 603 30350 603 30350 603 30350 603 30350 603 30350 603 30350 603	0705 0706 0707 0708 0709 0710 0711	B B B B B	30522 30523 30524 30525 30526 30527 30528	1 273 1 11169 1 13 270	1367 419 1786 1443 486 1260	
30338 603 30339 603 30340 603 30341 603 30341 603 30342 603 30343 603 30345 603 30346 603 30347 603 30348 603 30348 603 30349 603 30351 603 30351 603 30352 603 30352 603 30353 603 30354 603 30354 603 30354 603 30356 603	0706 0707 0708 0709 0710 0711	B B B B B	30523 30524 30525 30526 30527 30528	273 1 1169 1 13 270	419 1786 1443 486 1260	
30339 603 30340 607 30341 607 30342 607 30343 607 30345 607 30345 607 30346 607 30347 607 30348 607 30351 607 30351 607 30352 607 30353 607 30353 607 30354 607 30355 607 30356 607 30357 607 30358 607 30359 607 30359 607	0707 0708 0709 0710 0711 0712	B B B B	30524 30525 30526 30527 30528	1 1169 1 13 270	1786 1443 486 1260	
30340 603 30341 603 30341 603 30342 600 30343 603 30344 603 30345 603 30346 603 30347 603 30348 603 30350 603 30350 603 30351 603 30352 603 30353 603 30354 603 30355 603 30356 603 30357 603 30358 603	0708 0709 0710 0711 0712	B B B B	30525 30526 30527 30528	1169 1 13 270	1443 486 1260	
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30348 607 30349 607 30350 607 30351 607 30352 607 30353 607 30354 607 30355 607 30356 607 30357 607 30358 607 30359 607		В	30531	1	4831	
30349 607 30350 607 30351 607 30352 607 30353 607 30355 607 30355 607 30357 607 30358 607 30359 607 30360 607	715	В	30532	184	1593	
30350 607 30351 607 30352 607 30353 607 30354 607 30355 607 30356 607 30357 607 30358 607 30359 607 30360 607	716	В	30533	1	615	
30351 607 30352 607 30353 607 30354 607 30355 607 30356 607 30357 607 30358 607 30359 607 30360 607	717	В	30534	1	3513	
30352 607 30353 607 30354 607 30355 607 30356 607 30357 607 30358 607 30359 607 30360 607	718	В	30535	113	1666	
30353 607 30354 607 30355 607 30356 607 30357 607 30358 607 30359 607 30360 607	719	В	30536	101	2667	
30354 607 30355 607 30356 607 30357 607 30358 607 30359 607 30360 607	720	В	30537	1	1692	
30355 607 30356 607 30357 607 30358 607 30359 607 30360 607	721	В	30538	51	142	
30356 607 30357 607 30358 607 30359 607 30360 607	722	В	30539	1	3198	
30357 607 30358 607 30359 607 30360 607	723	В	30540	251	1207	
30358 603 30359 603 30360 603	724	В	30541	1	1491	
30359 607 30360 607	725	В	30542	1	4024	
30360 607	726	В	30543	1	3316	
	727	В	30544	1	1342	
30361 603	728	В	30545	91	810	
	729	В	30546	17	489	
30362 607	730	A	30547	1	504	MGGSNRSAEAWKLANGINIIVA
						TSGRLLDHMQNTPGFMYKNLQ
						CLVIDEADRILDVGFEEELKQII
						KLLLTHRQTMLFSATQTQKVE
						DLARISLKKEP/LYVGDDDDNA
						NETVFG\TLLCTDVAARGLDITE
						VDCIVQYDPPDDPKEYIHSVGR
						TARGLNGRENWVFFAT
30363 607			30548	1	2676	
	1731	A		1	1071	
30365 607		A B	30549		348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30366	60734	A	30551	1	711	MAEIGHKTIRPLLEGRDLLAAV; KTOSGKTLAVLPAIELVVKLKE MPRNGTGVLILSPTRQLAMQTF GVLKELMTHHVHTYGLIIGGSN RSAEAQKLANGINIVVTFGRIL DHTONTPGFMYKNLQVEDLAR ISPKKEPLVVGVDEDKANATVD GLEGGHFVCPSERKYLLFTFL KKNQKKLMYFFSACMSVKYP YGLLKYIDLIPVLAIHGKQKQN KHTTIFF*YCNADSGTLL
30367	60735	A	30552	661	987	VTFYSSEHSNPCHKNLRKARRK DTKRIILKW*HTLV*GRDI*N*NI IITRNTRYSLLCPWATKKLKAC FISQK*KRDVIERNSAQCLQPKS IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	IFOGASNLTLSETQNODVSEET MGSRKVKKSKQKPMNVGLSET QNGGMSQEAVONIKVTKSPQK STVLTNGEAAMQSSNSESKGK MKKKRKMYNDNDEFDTKKAKT ENKGKSEESAETTKETENNVE KPDNDEDESEVPSLPLGLTGAF EDTSFASLCNLVNENTLKAIKE MGFTNNTEIQHKSIRPLLEGRD LLAAAKTGSGKTLAFLIPAVILISPITRE LAMAGSSGKTLAFLIPAVILISPITRE LAMAGSNESAEAQKLONGINIV ATFGRLDHMONTFGFMYKNL LUFTRQTMLFSATQTRKVE DLARISLKEEPLVODDIKA NATVDGLEGGYVVCPSEKRFL LLFTFLKKNRKKLMYFFSSCH LLFTFLKKNRKKKLMYFFSSGK QKQNKRTTITFQFCNADSGTL LCTDDVAARGLDIFFFR LL*HISKGFPLSGIWTFSWSLK SVCHYHELLNYIDLPVLAIGK QKQNKRTTITFQFCNADSGTL LCTDDVAARGLDIFEVDWIVQY LL*LSTRUGHTSWSLKEEPLWINGLEFFR LL*LSTRUGHTSWSLKEEPLWINGLEFFR LL*HISKGFPLSGIWTFSWSLK AVGANGLDIFEVDWIVQY RUFYLEY RUFYL RUFYL RUFYL RUFYL olynucleotide of claim 1 under stringent hybridization conditions
- An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
  - 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
  - 6. A vector comprising the polynucleotide of claim 1.
- An expression vector comprising the polynucleotide of claim 1.
  - A host cell genetically engineered to comprise the polynucleotide of claim 1.
- A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
   associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
  - 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
    - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
    - a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.
  - 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
  - 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
    - a) contacting the sample under stringent hybridization conditions with
- 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the
   15 sample.
  - 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annualed RNA molecule into a cDNA polynucleotide.
- 20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
  - 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

 a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so
   5 that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
  - A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and
- isolating the polypeptide from the cell culture or cells of step (a).
  - An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.
  - 21 The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
  - A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.
- 25 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
  - 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 30 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
  - The collection of claim 22, wherein the collection is provided in a computer-readable format

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27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaccutically acceptable carrier.

5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

IPC(7) US CL According to B, FIEL Minimum do	IPC(7) : C12N 15/00, 15/12   US CL : 55/23.1, 23.5; 455/6, 320.1, 325   According to International Patent Classification (IPC) or to both national classification and IPC						
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched NONE							
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) NONE							
C, DOC	UMENTS CONSIDERED TO BE RELEVANT						
Category *	Citation of document, with indication, where a	ppropriate, of the relevant passages	Relevant to claim No.				
X, P	Database Genbank, Accession No. AL135937, 15	March 2001 (15.03.2001),	1-8				
Α	particularly nucleotides 29925 through 30325.		9, 19				
x	Database Genbank, Accession No. AA004350, HI	LLIER et al., Generation and	1-8				
	analyhsis of 280,000 Human Expressed Sequence T						
A	(07.05.1997), Vol. 6, No. 9, pages 807-828,		9, 19				
Everban	documents are listed in the continuation of Box C.	See patent family annex.					
	pecial categories of cited documents:	*T* Later document published after the inte	emational filing date or priority				
*A" documen	defining the general state of the art which is not considered to be	date and not in conflict with the appli- principle or theory underlying the inv	estion but eited to understand the ention				
	plication or patent published on or after the international filing date	"X" document of particular relevance; the considered novel or cannot be consider when the document is taken alone					
establish							
	referring to an oral disclosure, use, exhibition or other means	being obvious to a person skilled in th	ie art				
*P* document priority of	published prior to the intermalonal filing date but later than the late claimed	"&" document member of the same patent	Lamiy				
	ictual completion of the international search	Date of mailing of the international sea	arch report				
	001 (23.10.2001)	Authorizad officiary					
	ailing address of the ISA/US unissioner of Patents and Trademarks	K Million Son	vistace L				
Box	PCT	Marianne P. Allen	- 4cg				

Telephone No. 703-308-0196

## INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/08631

Box	I Obse	rvations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This	internat	ional report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1.		Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2.		Claim Nos.:  because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:  .
3.	6.4(a).	Claim Nos.: because they are dependent claims and are not drefted in accordance with the second and third sentences of Rule
Box	Π Ob	servations where unity of invention is lacking (Continuation of Item 2 of first sheet)
		ional Searching Authority found multiple inventions in this international application, as follows: ontinuation Sheet
1. 2. 3.		As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4.		No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1
Ren	nark on	Protest The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS, named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO, or for Groups VIII and IX a specific combination of SEQ ID NOS, for searching. Due to the burden of search for sequences, only a single SEQ ID NO, or specific combination of SEQ ID NOS, for Groups VIII and IX is considered to meet unity of

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I-III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VIII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO, does not appear to share a common core structure, they are considered to be structurally and functionally distinct invention.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ IO. 1. If Group VIII is elected, the default polypricia stray is considered to be an array comprising all of SEQ IO NOS: 3096-6076. If Group IVII is elected, the default polynucloutide array is considered to be an array comprising all of SEQ IO NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ IO NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ IO NOs. present on the arrays if additional combinations are to be exercised.

Form PCT/ISA/210 (second sheet) (July 1998)